Student Poster Presentations

Does Arsenic and Uranium in the Bedrock Affect Water Quality?

Discipline: Geoscience
Subdiscipline: Earth Science

Clarene Davis*1; Clara Chang2; Benjamin Bostick2 and Paul Olsen2, (1)Dine College, (2)Columbia University

Abstract: The Navajo Nation is located in the Four Corners regions of Colorado, Arizona, New Mexico, and Utah. Water quality is a major problem in the Navajo Nation. Poor water quality is critical to people using untreated private wells and affects regulated water systems regionally. The Navajo Nation is particularly affected by contamination related to mining rocks enriched in toxic metals. Most of these mines are abandoned and improperly remediated, and left behind elevated levels of uranium (U) and arsenic (As) metals in the water.

The purpose of this project is to determine how geological sources of arsenic and uranium may contaminate the water. We hypothesized there is some relationship between bedrock chemistry and the water quality. We analyzed bedrock chemistry using X-Ray Fluorescence Spectroscopy (XRF) measurements on cores from the Colorado Plateau. XRF includes measurements of toxic elements such as U, As, and other elements important in regulating As and U solubility like Si and Fe. We compared XRF data to lithologic logs to determine the relationship between bedrock lithology and chemistry. We used QGIS to compare bedrock chemistry to As measurements in wells. Initial results show there is more As in the claystone than the sandstone. This is encouraging because water is more likely to flow through sand than clay, therefore, the most commonly used groundwater aquifer is less likely to be contaminated by the bedrock. However, water derived from the boundary between clay and sandstones may be susceptible to contamination because clays can contribute metals to the aquifer.

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Adrian Colazo[*] and Christopher Harrison, *San Diego State University*

Abstract: Performance enhancing methods are nothing new in the world of sports, and while there have been many advances in the way which we can detect for a range of doping methods, blood doping still remains at large a highly undetectable method, with autologous blood doping being especially difficult to detect. This is due to the fact that the red blood cells (RBCs) extracted, stored, and transfused back into the athlete originate from the athlete, making the transfused blood and the fresh blood nearly identical.

Stored RBCs differ from fresh RBCs in some respects however, namely in the stored RBCs exposure to high concentrations of sugar during the storage period. The concentrations of sugars result in the surface proteins of RBCs undergoing non-enzymatic glycosylation. The glycosylation predominantly alters the terminal amines of the proteins, resulting in a change in the surface charge, and thus the isoelectric point of the stored RBCs. This change in isoelectric points can be exploited through isoelectric focusing (cIEF) as a means to provide a reliable way to detect blood doping.

In order to perform a successful cIEF separation, it is imperative that the electroosmotic flow (EOF), or the movement of analyte due to the applied voltage, is suppressed so that the analytes can focus effectively on their isoelectric points. I will present the preliminary results of various capillary coatings used to suppress the EOF and as a result their effectiveness at separating the stored RBCs from fresh RBCs.

Optimizing the Separation of an Antiparasitic Medication Using High-Pressure Liquid Chromatography (HPLC)

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Karis Barnett[*] and William LaCourse, *University of Maryland, Baltimore County*

Abstract: Excess pharmaceutical waste in water is an emerging concern that can increase parasitic drug resistance, interrupt animal food chains, and threaten drinking water sources. A high-pressure liquid chromatography (HPLC) method with ultraviolet (UV) detection (210 nm) is under development for sensitively quantifying antiparasitic drug praziquantel (PZQ) and related compound metronidazole (MET). This method has the potential to commercially monitor PZQ dosages administered to aquatic species, which can ultimately limit pharmaceutical waste in water. The separation of PZQ and MET in an antiparasitic medication was achieved on a Phenomenex™ Luna C_{18} analytical column (150 x 4.60mm, 5µm, 100A) using acetonitrile:water at alternating ratios of 20:80 v/v and 80:20 v/v as a mobile phase. The compounds were successfully separated with an optimized method. The polarity of the compounds and the protocol proposed by Vignaduzzo et al. (2015) were considered to optimize the method. The method may require further improvement for compounds in a seawater matrix. Future work also involves validating the method with analytical figures of merit (e.g. linearity, limit of detection, and relative standard deviation). The optimized and validated method can be proposed to aquariums and related organizations for commercial use.

The Aroma Characterization of *Eugenia brasiliensis* Via Gas Chromatography-Mass Spectroscopy

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Matthiew Haines[*1]; Florença Borges[2] and Eduardo Purgatto[2], *(1)The Pennsylvania State University, (2)Universidade de São Paulo*

Abstract: Fruits native to South America have been used for centuries; however, these fruits have mostly gone unresearched. The ripening pattern, the production of volatile compounds, and their pigments have not been studied for their potential of bioactive compounds. This project aimed to characterize the profile of volatile compounds in a fruit native to southeastern Brazil, *Eugenia brasiliensis*, commonly known as *grumixama*. The fruits were harvested at three different ripening stages: green, intermediate, and mature, from Paraibuna, Brazil (23º23'10" S, 45º39'44" W), and stored at -80 ˚C. Each group of fruit was predicted to have differences in their chemical composition based on their ripening stage. Solid-phase microextraction (SPME) was used to analyze the samples in triplicates by gas chromatography-mass spectroscopy (GC-MS). The *grumixama* profiles were determined to contain aromatic compounds such as terpenes, alcohols, and aldehydes. The fruit in the intermediate stage had an increased concentration of dimethyl ether and acetaldehyde, which contributes to the fresh, fruity aroma of the unripe fruit. Hexanal was more prevalent in the ripened *grumixama*, along with acetoin and limonene, contributing to a sweet, citrusy aroma. The next steps in characterizing *E. brasiliensis* should focus on understanding the bioactive compounds and the nutritional or functional value for companies, such as those in the cosmetic or pharmaceutical industries. Future projects could also focus on the sensory-assisted breeding of *E. brasiliensis*.

Using CE-SELEX to Evolve a ssDNA Aptamer for Nicotine Capture

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Catrin Law[*] and Christopher Harrison, *San Diego State University*

Abstract: Third-Hand Smoke (THS) remains on surfaces such as a car or home for weeks to months after the cessation of tobacco smoking, leaving behind a toxic mixture of chemicals, despite cleaning house-hold cleaning products. Those concerned about common surfaces, like rental housing, do not have a cost-effective, non-laboratory test readily available. We aim to create a simple testing device, akin to a home pregnancy test, available for consumers to use to test their homes and obtain semi-quantitative data about potential nicotine contamination (the most abundant molecule in THS). This poster will present our work of finding a nicotine aptamer through Capillary Electrophoresis-Systematic Evolution of Ligands by EXponential enrichment (CE-SELEX). This is the process of identifying random oligonucleotide ssDNA sequences with an affinity for binding to nicotine, from within a large library of ssDNA and selectively evolving those sequences that bind to nicotine to have higher affinity. Once a selective aptamer has been identified we will incorporate it into a disposable device which exploits complexation reactions between nicotine and the ssDNA aptamer to quantify the nicotine contamination. Due to the limited electrophoretic mobility difference between free ssDNA and ssDNA bound to nicotine we are employing the Simul 5 Complex electrophoresis simulation software to determine optimal separation conditions.

Identification of Degradation Products Formed from the Thermolysis of Glycerol and Terpenes in Aromatherapy Devices

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Alisha Ortiz* and Robert Strongin, *Portland State University*

Abstract: Degradation chemistry has been widely studied to assess the safety of aerosols in many fields. The study herein investigates the degradation products formed from MONQ personal aromatherapy devices- a new non-nicotine vape pen device on the market. These pens are marketed to alleviate symptoms of an unrecognized medical syndrome called “terpene deficiency”. These pens contain a glycerin (GL), or glycerol (VG), base and a blend of terpene-rich essential oils. Previous studies have investigated the degradation of both GL and terpenes and shown that concerning compounds are released in the gas phase, including benzene, benzaldehyde, methacrolein and methyl vinyl ketone. Studies also conclude the formation of formaldehyde releasing agents (FRAs) from propylene glycol (PG) and GL. However, a study has not been done that focuses on the thermolysis reaction of terpenes combined with GL. Here, the purpose of these experiments is to bridge this gap in understanding. Proton nuclear magnetic resonance spectroscopy (^{1}H-NMR) and adsorption-thermal desorption gas chromatography-mass spectroscopy (ATD-GCMS) are implemented to identify the compounds in both the gas and particulate phases of MONQ devices. Methacrolein, benzene, benzaldehyde, FRA’s, and other organic acids and compounds were successfully identified in selected blends of MONQ devices. Considering most of these compounds are respiratory irritants, and benzene is a carcinogen, MONQ devices pose questionable benefits to consumers.

The Use of Neural Network Platforms for Chemical Characterization and Toxicity Prediction

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Bianca Flores* and Grady Hanrahan, *California Lutheran University*

Abstract: Artificial neural networks (ANN’s) are computerized models that mimic the brain, in that they can be trained for a specific purpose, and eventually, learn on their own. Optimized models can detect trends and make predictions with remarkable accuracy and robustness. In this study, an optimized neural network platform was created in a MATLAB format, including assessing network functionality, nodes, and related model factors. Using a model data set, neural network functionality was tested, trained and optimized. High correlation between model predicted and experimental results was observed, as well as low model error and discrepancies. This will prove useful as we begin to examine chemical data sets from the GC-MS analysis of urine and blood samples. In particular, how the structure of phenolic-related compounds corresponds to the chemical toxicity properties and thus human health consequences. ANN models will be used to assess these correlations and predictive capabilities.

Keywords: artificial neural networks; prediction, chemical toxicity; human health.

The Exploration of Fluorescence Flow Cytometry Microfluidic Chips for the Quantification of White Blood Cells

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Madison Noroña* and Christopher Harrison, *San Diego State University*

Abstract: Fluorescence flow cytometry (FFC) is a widely used technique in many biological and biochemistry laboratories in order to determine a range of physical and chemical properties of different cells within a sample mixture. One or more fluorophores are introduced to the sample, and they bind to the cells based on specific physical or chemical interactions. The sample then flows through a flow cytometer, where each individual cell passes the detectors independently. This technique makes it easy to detect, count, and even sort the cells in the sample based on each individual cell’s fluorescence signature.

Flow cytometers, however, can be rather bulky and expensive. To reduce cost and increase accessibility to these tools, we are exploring novel fabrication means. 3D printing is a relatively cheap and fast way to create templates for microfluidic chip systems. PDMS can be placed over the 3D-printed template, creating channels. Microfluidic chips can also be built using laser cutter plastic sheets and adhesives to form the channels. These chips can then be used for small scale flow cytometry with samples on the microliter scale.

This project will explore different methods of building pressure-based microfluidic FFC systems in order to count the number of leukocytes in a whole blood sample. In a whole blood sample, the only cells that contain DNA are the leukocytes, or white blood cells (WBCs). Therefore, when mixed with a DNA intercalating fluorophore, the only cells that should fluoresce in a whole blood sample are WBCs, allowing them to selectively be counted.

Characterization and Toxicity of 2D Nanomaterials with the Protein Corona

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Carmen castillo[*1]; Roxana Coreas[1] and Wenwan Zhong[2], *(1)University of California, Riverside, (2)University of California Riverside*

Abstract: Nanomaterials are studied in biomedical research because of their extensive properties. Furthermore, upon contact with biological media, nanomaterials form a surface layer called the protein corona, which is unique to each nanomaterial and can affect their behavior. Therefore, our interest lies in identifying the composition of the protein corona and its effect on their toxicity.

This study aimed to characterize the composition of 2D nanomaterials, predominantly used in electronics, in order to understand their toxicity. The viability of breast cells was measured after exposure to six materials (rGO, prGO, GO, MoS2, G-PF108, and hBN) at short incubation times. Additionally, the "protective effect" of the nanomaterial corona was studied along with the surfactant's role in the toxicological profile of these materials. Lastly, the material's characterization was done by measuring size change via nanoparticle tracking analysis and the formation of the protein corona on the pristine 2D nanomaterials and concentrated materials via SDS-PAGE.

Preliminary findings suggest that the six nanomaterials are slightly toxic to all cell lines, and the biocorona does not influence the toxicity. The concentrated materials are more toxic, suggesting that the surfactant is not solely responsible for the toxicity. Moreover, only graphene oxide-based materials showed an increase in size with the corona. SDS-PAGE results showed higher protein on the concentrated materials than the pristine, suggesting potential protein conformation and function changes.

Further studies will include measuring uptake, identifying proteins of the coronas, and the biological impact of the nanomaterial-protein interactions.

Effect of Phosphate Adsorption on Collodal Stability of $LiCoO_2$ Nanoparticles

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Miguel Nieves[*1]; Elizabeth Laudadio[2]; Robert Hamers[2] and Justin Rosa[3], *(1)University of Puerto Rico, Rio Piedras, (2)University of Wisconsin-Madison, (3)University of Puerto Rico, Mayaguez*

Abstract: The demand for sustainable technology has permitted the accelerated utilization of “greener” energy storage devices such as Lithium ion batteries (LIBs). The implementation of LIBs in electronics like laptops, cell phones and electronic vehicles has allowed the supply growth of these batteries (a 58% increase of electric vehicles is expected for 2035). However, the lack of regulatory policies has resulted in an unexpected environmental pollution. It is estimated that 55% of the LIBs produced in 2016 will end up in landfills in 2025, and a 192% increase of LIBs in waste streams between 2020-2040 is expected. These projections lead to toxicity concerns since cathode materials leached from LIBs, specifically $LiCoO_2$ (LCO), can suffer environment-induced modifications, thus potentially impacting the environment negatively. The goal of this project is to identify the adsorption strength and conformation of aqueous phosphate, a relevantly natural oxyanion, over LCO nanoparticles within common concentration conditions. We will unravel the impact of phosphate ions on the dispersibility and sedimentation state of LCO. Different spectroscopy techniques were used to determine various chemical interactions between them. These techniques and its interactions include FTIR (phosphate adsorption), DSC (Diffusion Coefficient), Zeta potential (Agglomeration) and UV-VIS (sedimentation). With the use of these techniques we were able to determine that phosphate binds strongly and irreversibly to LCO, and that it promotes LCO dispersibility and colloidal stability. This study elucidates the toxic potentiality of LCO by addressing the promoting effect on transport capacity that phosphate in freshwater systems has over the LIB cathode material.

Cobinamide-Based Rapid Detection of Cyanide in the Blood

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Sydney Williams[*1]; Sari Mahon[2] and Matthew Brenner[2], *(1)Hampton University, (2)University of California at Irvine*

Abstract: Cyanide (HCN) is a colorless and odorless gas that goes undetected in the air and metabolizes quickly in the blood. Lethal amounts of cyanide gas can be emitted in massive house fires and chemical warfare. The current rate of detection is 24 hours, but lethal amounts of cyanide poisoning can shut down the respiratory system in 15-30 minutes. This study focuses on the fast detection of cyanide poisoning using the color-changing properties of cobinamide, a vitamin B_{12} precursor, by visual analysis. This qualitative experiment was conducted using a UV-Vis spectrophotometer, 0.1 M HCl to extract HCN from the various solutions, 15 μM cobinamide, and concentrations of potassium cyanide (KCN) ranging from 10-100 μM. According to literature, the difference between mild and severe poisoning lies between 30 μM and 40 μM. When 15 μM cobinamide reacts with 10-30 μM cyanide, the solution color remained pink. However, when 15 μM cobinamide reacts with 40-100 μM cyanide solution the color turned orange within 15-20 seconds. This color change is due to the binding of a sufficient amount of cyanide molecules to the hydroxyl and water groups of cobinamide. The color changes are seen in the spectrophotometer. Cyanide solutions at or below 30 μM gave an absorption spectra with lower peak amplitudes at 350 nm, 420 nm, and 520 nm wavelengths compared to solutions at or above 40 μM. Using cobinamide for the visual detection of severe cyanide poisoning decreases the detection time for first responders and affects the treatment time for the patients.

Degradation of Ciprofloxacin Using Silver-Based Photocatalysts Under UV-Vis Light

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Bryan Bentz Cruet*, *Universidad Ana G. Mendez recinto de Gurabo* and Abniel Machin, *Arecibo Observatory/ Universidad Ana G Méndez -Recinto de Cupey*

Abstract: One of the main health challenges of the 21st century is the resistance to antibiotics. Researchers from all over the world are constantly looking for innovative ways to address this situation. A possible solution is to degrade these organic compounds by using photocatalysis. Is for that reason that the objectives of this investigation were: 1) Synthesize and characterize different silver-based (1 wt.%, 3 wt.%, 5 wt.%, 10 wt.%) zinc oxide catalysts; 2) Study the photocatalytic activity of the catalysts by the degradation of the antibiotic Ciprofloxacin. The hypotheses of the experiment were: 1) All the catalysts are able to degrade Ciprofloxacin by 85% or more in one hour under ultraviolet and visible light; 2) The catalyst containing 5% of silver will achieve the maximum degradation. The results showed that all the catalysts were able to degrade Ciprofloxacin by more than 91% in one hour, being the catalyst with 3% silver the one with the highest degradation percentage, 99.6%. These results demonstrate that high catalytic activity of the as-synthesized catalysts under ultraviolet and visible light. As future works, different morphologies of the support and the incorporation of the different metals will be evaluated.

Encapsulation of Virus-like Particles with Metal Organic Framework ZIF-8 to Analyze Stability and *In Vivo* immunogenicity

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Cesar Reyes*; Fabian Castro; Candace Benjamin; Michael Luzuriaga and Jeremiah Gassensmith, *University of Texas at Dallas*

Abstract: Virus-like particles (VLPs) are polyvalent structures of coat proteins which have been isolated to have their genetic cargo removed. Inside of these capsids, they can carry a multitude of proteins or drugs and thus may act as nanocarriers for therapeutics or vaccines. Along with having the capability to carry proteins, VLP's surface can be chemically modified to enhance their affinity to the desired target, improve their structural integrity, or tune their immunogenicity and stability. Bacteriophage Qβ and Pseudomonas phage PP7 are a *Leviviridae* derived VLPs. Though Qß has been shown to provide an immunologic response when injected in mice, a similar experiment hasn't been performed on PP7. Both are structurally similar, but studies have shown PP7 has a superior stability. This project focuses on determining the immunological response and thermal stability of PP7 in comparison to Qß and the encapsulated VLPs in zeolitic imidazolate framework-8 (ZIF-8). ZIF-8 is another nanocarrier which has also shown significant stability enhancement. This experiment analyzes immunogenicity of mice injected with native PP7, native Qß, PP7@ZIF-8, Qß@ZIF-8, & Saline (0.9%) on days (0, 7, 14). Blood samples from days (0, 28, 56) would be analyzed using ELISA to measure IgG1. Thermal stability of the VLPs is analyzed *in vitro* at various temperatures. The results of this project would give a direct comparison between PP7 and Qß as well as the stability effects of ZIF-8. VLPs have been effective as therapeutic nanocarriers and knowing their immunogenicity and stability would provide insight to future applications.

Moving from Community Concern about Air Quality to Citizen Science and Student Research

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Diana Rodriguez* and Deborah Gross, *Carleton College*

Abstract: Elevated production of smoke from burning biomass affects both global and local public health due to the negative effects of smoke inhalation. High concentrations of particulate matter (PM2.5) downwind of the source can increase the likelihood of respiratory illness. In this study, we illustrate how citizen concerns regarding a local restaurant potentially emitting high levels of smoke can be evaluated with a "citizen science" based approach. As a proof-of-concept, we recruited 7 people to measure the PM2.5 concentration at locations circling the restaurant in question in downtown Northfield, MN, to determine if the smoke complaints by a neighbor were consistent with this restaurant being the source. PM2.5 measurements were made with low-cost AirBeam sensors operated by participants at predetermined intersections downwind or upwind of the restaurant. Although the measurements obtained were all relatively low values of PM2.5, relative to one another the locations downwind of the restaurant had significantly higher PM2.5 levels than did those downwind. This study illustrates the opportunities available for utilizing citizen concerns to devise citizen science and student research projects, while providing data that can help citizens quantitatively assess the impact of local pollution sources on their health.

Computational Drug Discovery for a Protease Inhibitor as a Treatment for the Coronavirus Disease

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Marissa Pina* and Bill Miller III, *Truman State University*

Abstract: The disease COVID-19 first appeared in China on December 31, 2019 but quickly spread around the world to gain the designation of a pandemic by March 11, 2020. Thus, a viable treatment option is vital to ensure public safety. COVID-19 is caused by the novel coronavirus, SARS-CoV-2. The functional polypeptides of the virus are activated by a main protease that has no similar homologs in humans, making it a desired target for potential drugs. The structure of the main protease of the virus was solved by Jin, et al., in 2020. The goal of the present research is to find a suitable inhibitor for the main protease using a known drug database. In the present study, three of the most promising inhibitors from the Jin study (ebselen, cinanserin, and N3) were docked to the protease structure (PDB code 6LU7) and used as controls. To test for novel inhibitors, 5180 known protease inhibitors identified as “purchasable” by the ZINC15 online molecular database were screened in this study using Autodock QuickVina02. The 38 molecules that resulted in the lowest docking scores have been further investigated using molecular dynamics. The structure and dynamics of the complexes during their simulations have been analyzed, and their average binding free energies have been calculated. The average binding free energies of the controls (ebselen, cinanserin, and N3) are -17.0, -16.2, and -14.3 kcal mol^{-1}, respectively. The average binding free energies of the two inhibitors with the best scores were found to be -45.42 and -44.15 kcal mol^{-1}.

Anthropogenic Ramifications Affecting Arsenic’s Bioavailability in Fountain Creek Watershed

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Alejandra Chavez*[1]; Jim Carsella[2]; Nathan Gasparovik[3] and Debbie Crans[3], *(1)Adams State University, (2)Colorado State University Pueblo, (3)Colorado State University*

Abstract: Arsenic, a metalloid, exists naturally and anthropogenically in the environment. It is commonly discovered in volcanic fumaroles and can be identified at industrial working plants like mines. Exposure to arsenic is typically through contaminated potable water or inhalation from industrial pollution. Repeated exposure to arsenic can cause adverse health effects or in extreme cases, death. A major source of arsenic exposure is from leaching of tailing and slag piles at abandoned mines like the Golden Cycle Mill in Colorado Springs, Colorado. This site is known to have high concentrations of arsenic that has the potential to bioaccumulate, but what is unknown is how bioavailable that leaching arsenic is to organisms. The focus of this study was to identify the bioavailability of that arsenic by examining the dose response relationship of arsenic’s concentration in the water compared to the arsenic’s concentration in plants. The bryophyte plant *Hygrohypnum ochraceum* was used to identify arsenic's bioavailability. Water and submerged bryophyte samples collected at several sites along the Fountain Creek watershed were prepared via EPA protocols, analyzed by inductively coupled plasma mass spectroscopy (ICP-MS), and examined for dose response relationships by statistical analysis. Current results indicate bioaccumulation of arsenic in the bryophyte, but to what extent is still being analyzed. Further research is needed to identify which arsenic species are bioavailable within these creeks. It is imperative to continually raise awareness of arsenic's presence in Colorado due to increased housing developments near abandoned mines and its potential to contaminate potable drinking water.

Post-Polymerization Functionalization of Poly(Phenylene-Ethynylene) Type Water-Soluble Conjugated Polymers and Their Applications As Biological Probes

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Daniel Martinez*; Dr. Han Sun and Dr. Kirk Schanze, *University of Texas at San Antonio*

Abstract: Conjugated polymers (CP) are a class of fluorescent macromolecules that are well known for their photophysical applications (e.g. light emitters, energy acceptors/donors, charge transfer, etc.) Making CPs water-soluble enables their capabilities to interact with proteins, cells, and other biological systems. The purpose of this research is to present a common methodology for the synthesis and modification of a water-soluble poly(phenylene-ethynlene) (PPE). The method for appending targeting groups was optimized for the molecule Biotin, and the reaction’s effectiveness was determined through calculating loading percentages from high temperature nuclear magnetic resonance (NMR) spectra. This method was then applied to other biomolecules to demonstrate the versatility of the PPE. The functionality of the biotinylated polymer (PPE-B) was demonstrated by mixing PPE-B with neutravidin coated polystyrene beads and analyzing their binding via flow-cytometry. It was hypothesized that the PPE-B-neutravidin complex would produce more aggregated bead populations and would exhibit higher fluorescent intensities than simply mixing a plain PPE with the same beads. Two aryl-based monomers were accessorized with solubilizing groups and subsequentially polymerized. The resulting polymer was then functionalized with biotin, folic acid, cholesterol, mannose, rhodamine, and oxaliplatin through amidation reactions. The flow-cytometry analysis confirmed specific binding of PPE-B to the neutravidin beads and showed increased aggregate bead population. Additionally, those same bead populations exhibited far greater fluorescent intensities because of the polymer's chromophoric properties. These results indicate that the PPE-B successfully complexed with neutravidin and demonstrates the polymer's functionality and potential as a biological probe.

New Techniques for Improved Separation in HPLC

Discipline: Chemistry
Subdiscipline: Chemistry (general)

EZEKIEL OLUYADI*; Sergio Batres and Stefan Tsonchev, *Northeastern Illinois University*

Abstract: Carbon nanodots (CDs) are a new class of carbon-rich nanoparticles with physicochemical properties that make them a fascinating material for bio-analytical applications. We believe that using carbon nanodots can improve the separating capabilities of HPLC column materials. We have developed standard procedures and methods of processing nanodot-doped silica gels. This research work aims to determine whether adding carbon dots to a chromatography column will improve the separation time and resolution. From this point of view and based on some preliminary studies of ours, we expect positive results. We are also studying the effect of different solvents on the properties of CD-modified HPLC columns.

Global Emissions Changes in Particulate Matter Due to Mandated Responses to Covid-19 Pandemic

Discipline: Chemistry
Subdiscipline: Chemistry (general)

David K Stem* and Deborah Gross, *Carleton College*

Abstract: Over the past few months, there have been significant changes in the emissions of gas-phase pollutants observed throughout the world, likely due to countries' responses to the Covid-19 pandemic that have mandated various measures to counteract the spread of coronavirus. Using an open-source data platform called OpenAQ, this study gathers emissions data for particulate matter (PM2.5), which is typically emitted from both transportation and industrial sources, to investigate how emissions are impacted, based on the measures mandated by various countries. PM2.5 values are examined in various cities to investigate if preventative measures such as quarantine, isolation and social distancing have reduced particulate matter emissions, which would suggest that transportation is a dominant source. In addition, this study will explore locations where cooking with biomass fuel is prevalent in order to see if there is a less significant decrease in particulate matter emissions. This study will examine both short and long term emissions datasets for various cities around the world to try to determine the relative importance of transportation, industrial, and biomass cooking emissions. Overall this study aims to find significant evidence of changes in particulate matter emissions due to alterations in everyday human activity caused by the Covid-19 pandemic.

Characterization of $PM_{2.5}$ Emissions from Various Cookstoves Used in Restaurants in Ethiopia.

Discipline: Chemistry
Subdiscipline: Chemistry (general)

Mehdi Shahid* and Deborah Gross, *Carleton College*

Abstract: Emissions from biomass cookstoves pose adverse health concerns to millions of people worldwide and are responsible for significant environmental issues as well. The common practice of burning charcoal for cooking in Ethiopia poses health hazards whilst the inflating price of charcoal from mass deforestation and increasing transportation costs significantly affect impoverished communities. The Ethiopia Cookstove Project aims to introduce a more environmentally efficient cookstove and to develop a sustainable and economically viable model for the production and distribution of pellet fuels and the collection of charcoal waste. The goal of the project is to significantly reduce the impact of particulate matter (PM) and indoor air pollution (IAP) on those cooking in household and restaurant kitchens. Here, we compare the emissions of the improved cookstoves to charcoal, wood, LPG and electric stoves in the specific case of small and medium-sized restaurants in Addis Ababa. Using Berkeley Air PATS+ instruments, we sampled and recorded restaurant kitchen $PM_{2.5}$ concentrations over a 12-hour period on multiple days, and considered variables such as: number of cooks, kitchen dimensions, and ventilated zones. Our analysis and results show that the newly improved cookstove produced much lower $PM_{2.5}$ levels in comparison to other stoves and is a cleaner alternative. The results show that the Ethiopia Cookstove project can significantly reduce the health and environmental impacts of IAP on vulnerable communities through an environmentally sustainable and economically viable model.

Measuring Binding Affinity of SAR-Cov-2 Spike Glycoprotein with Heparan and Its Derivatives

Discipline: Chemistry

Subdiscipline: Chemistry (general)

Giovanni Lara* and Roland Faller, *University of California, Davis*

Abstract: The novel coronavirus SARS-CoV-2, which causes the COVID-19 disease, has created mass lockdowns world-wide due to its high transmission rate and lethal nature. It is well documented that the SARS-CoV-2 spike glycoprotein interacts with receptor ACE2 in order to enter cells to start replication. Recent research suggests that the glycosaminoglycan heparan may be able to bind to the SARS-CoV-2 spike glycoprotein which lowers transduction efficiency in cell culture. To validate this interaction, a SARS-CoV-2 spike glycoprotein fragment and heparan are tested in silico to find binding affinity by measuring the relative distances between the molecules at various time points. High binding affinity may reveal potential in heparan and its derivatives as drugs to reduce transfection rates.

Synthesis of Nickel Nitrosyl Complexes with Bidentate *N*-Heterocyclic Carbene Ligands

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Zijie Zhang*; Brenda Henriquez and Dr. Chantal Stieber, *California State Polytechnic University, Pomona*

Abstract: Activation of small molecules such as CO, N_2 or NO could harness new chemistry with underutilized starting materials and offer insight towards biological reduction mechanisms. NO is reduced by enzymes, but the redox activity of the metal and NO makes the characterization of the metal nitrosyl complexes complicated. The fundamental interactions between metals and NO could be elucidated with metal nitrosyl model complexes which are more easily studied than metal centers in enzymes. Nickel nitrosyl complexes with bidentate *N*-heterocyclic carbene ligands were synthesized to examine the effect of strongly sigma donating NHC ligands on the electronics of the nickel-NO bond. The ligand precursor mesityl bis(imidazolium) salt was synthesized and characterized by ^{1}H NMR spectroscopy. A new metal complex, ($^{Mes}NHC_2Me$)Ni(COD), was synthesized with the free carbene ligand and bis(1,5-cyclooctadiene)nickel(0), which was structurally characterized. A new Ni-NO complex [($^{Mes}NHC_2Me$)Ni(NO)][BF_4] was synthesized with ($^{Mes}NHC_2Me$)Ni(COD) and one equivalent of [NO][BF_4]. The presence of a new Ni-NO bond and a BF_4^{1-} counterion was demonstrated by infrared spectroscopy, which establishes a new example of a three-coordinate nickel nitrosyl complex with strongly sigma donating ligands. All complexes were characterized by X-ray absorption spectroscopy, supporting the proposed reactivity, and establishing rising edge features for NO complexes.

Iron Complexes with N-Heterocyclic Bidentate Carbene Ligands

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Alexis Hoxie* and Dr. Chantal Stieber, *California State Polytechnic University, Pomona*

Abstract: Iron complexes with bidentate *N*-Heterocyclic carbene ligands ($^RNHC_2$; R = alkyl or aryl) have not been widely reported and have potential to be used as catalysts for a range of chemical transformations. This work aims to make new Fe^0 pre-catalysts with $^{Mes}NHC_2$ ligands. Synthesis of $^{Mes}NHC_2$ was a stepwise process, starting with the synthesis of mesitylimidazole, followed by formation of the ligand precursor bis(imidazolium) salt after the addition of dibromomethane. The bis(imidazolium) salt, 1,1’-di(mesityl)-3,3’-methylene-diimidazolium dibromide, was then deprotonated with potassium bis(trimethylsilyl)amide (KHMDS), to form a carbene ligand ready for chelation. $FeCl_2$ was added to the ligand to synthesize the corresponding $FeCl_2$ complex, ($^{Mes}NHC_2Me$)$FeCl_2$. Sodium triethylborohydride ($NaEt_3BH$) was added to reduce Fe^{2+} to Fe^0. The complex was characterized by either ^{1}H NMR and IR spectroscopy. Further characterization is underway.

Cis Versus Trans Oxidative Addition of Arylfluorides to Nickel *N*-Heterocyclic Carbene Complexes

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Adrian Torres*; Justin Tabay Cortez; Nicole Avila; Jacob Brannon and Dr. Chantal Stieber, *California State Polytechnic University, Pomona*

Abstract: Activation of carbon-fluorine bonds has applications in pharmaceuticals, agrochemicals, and other subdisciplines in chemistry. Although the C-F bond typically has a high bond strength, nickel complexes have been reported to achieve C-F activation. Nickel *N*-heterocyclic carbene (NHC) complexes were reported to yield trans addition of aryl fluorides. In this work, a comparison of monodentate versus bidentate NHC ligands is reported to understand the effect of ligand chelation on oxidative addition of aryl fluorides at nickel. In a two-step reaction, the aryl fluoride nickel NHC complex was obtained from an oxidative addition of hexafluorobenzene to the nickel(0) NHC precursor. Complexes were characterized using NMR spectroscopy and X-ray crystallography. A cis addition product was observed for the bidentate NHC complex and a trans addition was observed for the monodentate NHC complex. Future work will involve reactivity studies.

Synthesis of Iron Nitrosyl Complexes with Diethyldithiocarbamate Ligands

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Evan Bonnand* and Dr. Chantal Stieber, *California State Polytechnic University, Pomona*

Abstract: Reduction of nitric oxide, a key reaction in the nitrogen cycle, lends itself to potential environmental and medicinal applications. Naturally occurring enzymes which facilitate this reaction contain first row transition metal centers, so there is interest in first row transition metals in the development of catalysts for NO reduction. In this work, iron complexes bound to a nitrosyl group (NO) with carbamate ligands are of interest. Literature indicates two approaches to synthesizing iron nitrosyl complexes with carbamate ligands. One approach involves two diethyldithiocarbamate (dtc) ligands coordinated to iron as a tetrahedral complex, which coordinates NO in the presence of nitric oxide gas. Another approach forms an iron nitrosyl complex first, followed by the coordination of two dtc ligands. This work explores the latter approach by varying stoichiometric ratios and types of reagents used with the goal of optimizing reaction conditions and establishing an air-stable synthetic method. Deviations from literature include using FeIII instead of FeII with both silver and sodium dtc salts. IR and NMR spectroscopy were utilized to verify the formation of the bis(diethyldithiocarbamato)nitrosyl iron complex. Further work will endeavor to isolate and obtain a crystal structure of the complex.

Effects of Methyl Versus Ethyl Linkers on Structural Characteristics of Bis(imidazolium) Bromide Salts

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Emily Thompson*[1]; Elisa Olivas[1]; Jacob Brannon[2] and Dr. Chantal Stieber[2], *(1)California State Polytechnic Pomona, (2)California State Polytechnic University, Pomona*

Abstract: Imidazoles have wide ranging applications as synthetic precursors, biological agents, and organometallic ligands. Bidentate *N*-heterocyclic carbene (NHC$_2$) ligands can be synthesized from imidazoles via bis(imidazolium) salt precursors. The bite angle of bridged NHC ligands may have an effect on the coordination and reactivity of the metal center. Bis(imidazolium) salts were synthesized and crystallographically characterized to determine the 3-D structures. The first step was the synthesis of *tert*-butyl imidazole (^{tBu}Im), mesityl imidazole (^{Mes}Im), and 2,6-diisopropylphenyl imidazole (^{Dipp}Im). The imidazoles were then reacted with alkyl bromides to furnish bis(imidazolium) salts. Bis(imidazolium) salts ([^{R}NHC$_2$R^2][Br]$_2$; R = ^{t}Bu, Mes, Dipp) with linkers were synthesized including a methyl linker (R^2 = Me) and an ethyl linker (R^2 = Et). Final salts were in the form of brown or tan crystals, and yields ranged between approximately 20% to 61%. 1H NMR spectroscopy and X-ray diffraction were used to verify the complete synthesis of the target structures, and bond lengths were compared. Further steps will include chelation to first row transition metal centers.

Nickel (II) Tris-(pyridinethiolate) and Its Derivatives for H$_2$ Production

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Alejandra Acevedo Montano* and Theresa McCormick, *Portland State University*

Abstract: Hydrogen gas is a carbon-neutral, renewable alternative energy fuel when made from water. A catalyst is required to convert protons from water into hydrogen gas, using solar energy. Nickel (II) tris-(pyridinethiolate) has been demonstrated to be an effective catalyst for the production of hydrogen gas in both electrochemical and photochemical water splitting. The proposed catalytic cycle undergoes a chemical-electrochemical-chemical-electrochemical (CECE) mechanism to produce hydrogen gas. Electron-donating groups (EDG) and electron-withdrawing groups (EWG) are currently being investigated to improve the initial protonation and reduction steps of the catalytic cycle respectively. A total of nine homoleptic and four heteroleptic nickel (II) tris-(pyridinethiolate) derivatives have been synthesized to further investigate individualized control of pK_a and E^0. Currently, homoleptic nickel(II) tris(6-methyl-2-pyridinethiolate) has been found to be the most efficient complex with high pK_a (10.7) and low E^0 (-1.25 V vs SCE). This study will continue to explore the effects of EWG and EDG on the efficiency of hydrogen gas production both electro- and photochemically for nickel (II) tris-(pyridinethiolate) derivatives.

Green One-Pot, Two-Step Synthesis of Polyurethanes from Cyclic Carbonates Prepared from Vegetable Oils

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Theresa Hinkle*, *Cameron university* and E. Ann Nalley, *Cameron University*

Abstract: As recent literature indicates, microwaves are quickly becoming an accepted tool for investigators in the organic laboratory. Microwave synthesis enables reactions to proceed more rapidly with greater yields than many conventional techniques. In parallel, there is a growing concerned about the isocyanate chemistry used to produce polyurethanes. Indeed, isocyanate are known to be toxic and are synthesized from phosgene which produces toxic gases. An alternative route to the isocyanate/alcohol chemistry is the cyclic carbonate aminolysis. However, the conventional synthesis of cyclic carbonate requires two-step procedure: epoxidation of double bond followed by carbonation.

In this research, we investigated the use of microwaves to synthesize cyclic carbonate from natural products such as soybean, olive oil, sunflower oil and corn oils in one-pot, one-step reaction. These monomers can then be converted to polymers using hexane diamines or ethylene diamines. We will compare the efficiency of microwave/ conventional synthesis of polymers from these different oils.

Aqueous Photocatalytic Modification of Peptides Enabled By a Novel Water-Soluble Iridium(III) Complex

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Gabriel Herrera*; David Anthony and Tianning Diao, *New York University*

Abstract: Previous research has shown that using photocatalysis to target dehydroalanine residues yields a promising method to achieve high selectivity for peptide and protein modification. However, these methods have been shown only to work on peptides in organic solvents. This poses a problem for the extension of this method into protein modification, as proteins would get denatured in these organic conditions. Through the use of a novel, water-soluble iridium photocatalyst, we aim to develop a way to modify dehydroalanine residues on peptides and proteins in aqueous conditions. By attaching polar poly(ethylene glycol) (PEG) groups to a known iridium (III) photocatalyst, one can solubilize this photocatalyst in water. Furthermore, one can attach various labels of interest onto an organoborane molecule. This PEG catalyst, activated by UV light, then reacts with the organoborane molecule and ultimately cleaves the label from the boron, forming a radical on the label of interest. This radical then adds into the electrophilic alkene, allowing for the tagging of these peptides and/or proteins with various molecules. This method provides a new approach to bioconjugation by taking a known reaction and developing it for aqueous conditions.

Synthesis, Characterization and Biological Activity of Ferrocenyl Furan Chalcones

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Alondra Rodriguez-Rolon* and Ingrid Montes-González, *University of Puerto Rico Rio Piedras Campus*

Abstract: Oxygen heterocycles have been studied due to their multiple's applications. In this work, we focus on furan because it is reported that is used as a key building block in medicinal chemistry. Furan derivatives have presented good activity against cancer, Parkinson's, and depression. That is the reason why it is present in many commercial drugs to treat the physiological diseases. Also, it has shown activity as antibacterial, antifungal, antiviral, and anti-inflammatory. Given the interest in design and explore new bioactive compounds with high bioavailability, we aim to synthesize and study a variety of ferrocenyl chalcones containing different substituents (-CH_3, Br, OH) in the furan ring. Our rationale is that incorporating ferrocene, chalcone, and furans on the scaffold, which presented effective activity separately, will increase the bioactivity. All products were obtained via a Claisen- Schmidt Condensation in a range of 54-89 % yields and characterized by ^{1}H-NMR, ^{13}C-NMR, UV-Vis, IR, Cyclic Voltammetry and in some cases the X-Ray crystallographic structure was obtained. The biological activity of the synthesized compounds was evaluated by radical scavenging and cancer cell lines (MDA-MB-231 and A549) assays. The findings were favorable to the bromo furan ferrocenyl chalcone. This data can be useful for identifying suitable candidates with high activity and a future potential candidate drug. In this presentation, synthetic methodology, analyses, and bioactivity results will be elaborated. This project was founded by MARC Program Grant: 5T34GM007821-39.

Developing a New Fluorogenic Cytidine Analogue to Examine Structure and Properties

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Casey Heaney*; George Samaan and Byron Purse, *San Diego State University*

Abstract: Fluorescent nucleoside analogues are important in advancing knowledge of the genetic code, especially in DNA replication, expression, and maintenance. However, differences in the fluorescent properties of these nucleoside analogues, as seen in response to base pairing and stacking, have yet to be fully understood. This has been shown for tricyclic cytidine analogues, such as 8-DEA-tC, that now include a family of compounds and exhibit a range of fluorescent properties. Fluorescent tricyclic cytidine analogues are currently widely used in DNA/RNA polymerase studies, measuring DNA–protein interactions, and FRET experiments. As a free nucleoside, 8-DEA-tC is nearly non-fluorescent (Φ_{em} = 0.006) and increases quantum yield of emission up to Φ_{em} = 0.12 when based-paired with guanosine in double-stranded DNA. We are synthesizing a related compound, 8-DEA-tC^{o}, to elucidate the mechanism for the exhibited fluorescence turn-on since it is not yet fully understood. The six-step synthesis of 8-DEA-tC^{o} includes the challenging step of adding a protected N^{4}-Boc-O^{1}-TBS-aminophenol (made in three steps) to a protected 5-bromouridine, with activation by $POCl_3$ and 1H-triazole. Once 8-DEA-tC^{o} is synthesized, a phosphoramidite derivative of the nucleoside will be synthesized in two steps to make oligonucleotides for further testing. Finally, a comparison will be made between 8-DEA-tC^{o} to 8-DEA-tC to better examine the photophysical properties as a free nucleoside in single-stranded and double-stranded DNA. These studies provide a greater understanding of the relationship between structural and photophysical properties of analogues and allow for better design of highly predictable fluorescent probes for studies on nucleic acid structure and dynamics.

Synthesis of Fluorinated Ladder Polymer and Its Use As a Low Refractive Index Layer in Optical Devices

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Amy Pollock[*]; Mike Larsen and Tierra Smith, *Western Washington University*

Abstract: Polymers of intrinsic microporosity (PIMs) are an interesting class of linear, solution-processable polymers that exhibit permanent porosity. The bulky, rigid backbone of PIMs causes the polymer to be unable to pack space efficiently, resulting in a network of interconnected pores. The presence of this porosity means PIMs tend to have a low refractive index, as the refractive index of the void space is effectively averaged with that of the polymer. Common applications of PIMs include generating membranes and making sensors due to their porosity, optical clarity and solution processability. These features hold great importance for our research because our goal is to spin coat and make thin films (ca. 50 nm) to be tested in optical devices. The following fluorinated ladder polymer has a combination of high rigidity and loosely packed chains, making it a promising candidate for our desired low refractive index layer. It was synthesized utilizing a simple one pot step-growth polymerization. Polymer size and structure can be confirmed utilizing proton nuclear magnetic resonance spectroscopy, gel permeation chromatography and infrared spectroscopy.

Reaction of Phenolic Antioxidants with Singlet Oxygen

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Matthias Selke, *California State University- Los Angeles* and Bliss Tafolla-Aguirre[*], *California State University Los Angeles*

Abstract: Resveratrol (trans-5-para-hydroxstryl)-resorcinol) is a polyphenol commonly found in the skin of grapes, mulberry, and wine. This trihydroxylated stilbene is said to exhibit therapeutic effects by preventing or alleviating photo-oxidative damage in epithelial cells; however, the mechanism describing how this occurs remains unknown. Resveratrol has two known pathways of reaction with singlet oxygen (^{1}O2): a [4+2] cycloaddition with the central double bond and adjacent double bond from the aromatic ring, and a [2+2] cycloaddition to form dioxetane. In vivo, resveratrol has been shown to react at its 4` hydroxyl group, which is either methylated or glycosylated. The Selke group has been exploring singlet oxygen scavenging by resveratrol and its methylated derivatives, as well as the reaction products formed during the interaction of resveratrol and singlet oxygen. In general, reaction of ^{1}O2 with trimethoxylated stilbene (3, 4`, 5 trimethoxy-trans-stilbene) and its methylated derivatives produces [2+2] cycloaddition products and a [4+2] reaction pathway is followed by a sequential [4+2] Diels Alder reaction to produce a bis-endoperoxide product in the case of the trimethoxy derivative. The kinetics of singlet oxygen removal by resveratrol and its derivatives have been determined using time resolved infrared luminescence spectroscopy. Scavenging rates are similar to an order of magnitude lower than those of antioxidants such as Vitamin E (alpha-tocopherol).

An Approach Toward the Total Synthesis of the Natural Product Piperine

Discipline: Chemistry
Subdiscipline: Organic Chemistry

mirka ortiz[*] and Dr. Robert Aslanian, *New Jersey City University*

Abstract: The mean for this study has been to synthesize Piperine through microwave promoted Wittig reaction. Piperine is known to assist in cognitive brain functioning, improve nutrient's absorption, and improve gastrointestinal functionality. In this experiment, Piperine was experimentally isolated from commercial ground black pepper using polar solvents such as petroleum ether and ethanol. Isolation of Piperine from commercial ground black pepper produces a low yield that makes it difficult to perform tests and to make analogs, thus Piperine was synthesized. Synthesis of Piperine was tried through Wittig and Heck reaction. Using the technique of thin-layer chromatography(TLC), nuclear magnetic resonance (NMR), and infrared spectroscopy (IR), results showed that the more effective synthesis of Piperine was through Wittig reaction. Using a Wittig reaction, it produced a product with minimal starting material and worked best for helping create the Piperic acid and lead to the final step of adding the piperidine (amine) to create Piperine.

Preparation and Toxicity of Phenanthroline-Based Anti-Tumor Agents

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Armenuhe Terzian[*], *California State University, Northridge* and Eric Kelson, *California State University Northridge*

Abstract: Although there are thousands of anti-tumor agents being developed with a range of targets within aberrant cells, these drugs are prone to inducing dangerous side effects that can complicate the recovery process. In our lab, we are looking to exploit the active transport processes cancer cells use to collect nutrients in order to target tumors even if they are unresponsive to other therapies. We have prepared a family of phenanthroline -based compounds to mimic natural polyamines and/or bind essential metals actively transported into rapidly dividing cells. This strategy was intended to entice tumor cells to import and concentrate the toxin while minimizing the impact on normal cells. These products were tested as anti-tumor agents against three breast cancer cell lines (MDA-MB-231, MDA-MB-468, and MCF-7) two of which are known to be particularly challenging “triple negative” cell lines. Our compounds demonstrated high toxicity levels with EC50s as low as 115 nM and varying selectivity among the cell lines. Correlations between structure and toxicity point to the importance of a phenanthrolinediimine motif and appear to validate the design strategy for these products. We hope this work will eventually lead to anti-tumor agents that minimize or avoid the detrimental side effects of current therapies.

Evidence of Active Transport of Phenanthroline-Based Anti-Tumor Agents into Cancer Cells.

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Erick Rios* and Eric Kelson, *California State University Northridge*

Abstract: Much progress has been made in the area of cancer research in terms of chemotherapies that have helped prolong the lives of many. However, despite making much progress over the decades, most cancer therapies have serious negative side-affects that stem from the fact that the treatments are not very selective, if at all, towards tumor cells. The Kelson lab has prepared a family of phenanthroline-based anti-tumor candidates with appendages resembling natural polyamines. These compounds are intended to entice tumor cells to import and concentrate the toxins through active transport processes intended to harvest nutrients. These compounds are indeed very toxic toward three breast cancer lines (MDA-MB-231, MDA-MB-468, and MCF-7) with EC50s as low as 115 nM. Competitive inhibition studies using spermine and tetraalkylammonium salts appear to confirm that these anti-tumor agents can indeed enter cells through polyamine and organic cation transporters. These results motivated the preparation of phenanthrolines with side groups resembling the essential amino acid phenylalanine. These agents had extraordinary toxicity toward MDA-MB-231 cells (EC50 if 73 nM) versus the others (EC50s around 230 nM) suggesting possible tumor targeting. Competitive inhibition experiments are also consistent with cell entry by amino acid transport channels. We hope that this work will eventually lead to chemotherapies that target tumor cells and minimize detrimental side effects.

Analysis of Flavor Extraction Rates in Wood-Aged Beer

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Rogelio Ordonez*; Caitlyn Berenson; Edward Banfill and Michael D. Mosher, PhD*, *University of Northern Colorado*

Abstract: Since the introduction of the barrel by the Celts around 350 BCE, the process of brewing beer was accomplished in wooden vessels. Wood vessels were replaced with stainless steel after the Industrial Revolution. Unfortunately, this resulted in a distinct change in the beer's flavor. The recent interest in craft beer has led brewers to bring back barrel-aged beer. On the contrary, this results many issues for the brewer. To be specific, it can take months to years to get the desired flavor character. Also, the cost in purchasing and warehousing barrels is considerable. One solution involves storing beer on pieces of wood. Previous research in this area has focused on studies in the wine and whisky industries. The major outcome is that as the surface area of the wood increases, the time to reach completion decreases. However, only limited research on wood-aging in beer and brewing has been generated. To address this lack of information, we measured the rate of extraction of principal flavor compounds from many wood types and particle sizes using GC/MS. By determining the rate of extraction, we could predict the optimum time for beer contact with wood. Our results illustrated that wood-dust has the slowest rate of reaction, wood-chips have an adequate rate of reaction, and wood-shavings have the highest rate. Our analysis reveals that a desired flavor can be obtained using the calculated extraction rates, in days rather than months. The details of the analysis and its implications will be presented.

Effect of Electron Withdrawing Groups on Benzoyl Amino Acids for Butyrylcholinesterase Inhibition in the Potential Treatment of Alzheimer's Disease

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Aaron Chavarria*, *California State University, Long Beach* and Jason Schwans, *California State University Long Beach*

Abstract: Alzheimer's disease (AD) is a neurodegenerative disease affecting 10% of people who are 65 and older in the United States. While there currently is no cure for AD, approaches are under investigation to slow the progression of the disease and mitigate its effects. For the two major classes of cholinesterases, previous studies showed acetylcholinesterase (AChE) activity showed little change, butyrylcholinesterase (BChE) activity increased activity in individuals with AD. The increased activity is suggested to deplete the neurotransmitter acetylcholine and may lead to dementia. Recently, our lab identified amino acids with a 9-fluorenylmethoxycarbonyl (Fmoc) group were selective inhibitors of BChE. The Fmoc group contains multiple aromatic groups similar to other cholinesterase inhibitors, and our hypothesis is the aromatic groups facilitate binding with active site aromatic residues via pi-pi interactions. To test this hypothesis, incorporation of electron withdrawing substituents in the aromatic groups is predicted to generate more potent inhibitors. Fluoro-substitution on the aromatic Fmoc group is synthetically challenging, so we turned to the more accessible benzoylated amino acids bearing quaternary ammonium group to facilitate binding. A series of benzoylated amino acids was synthesized, purified, and characterized by NMR. Initial kinetics studies showed the compounds are BChE inhibitors, and we are currently determining if incorporating electron withdrawing affects inhibition. Together, the results will evaluate the structural features important for enzyme inhibition. The results identified in this study may then be used to guide the incorporation of electron withdrawing or donating groups in a variety of different classes of cholinesterase inhibitors.

Gold (l) - Brønsted Acid Co-Catalyzed Synthesis of Substituted Isocoumarins

Discipline: Chemistry

Subdiscipline: Organic Chemistry

Angel Rojas*; Simrit Dhindsa and Hubert Muchalski, *California State University, Fresno*

Abstract: Heterocycles are small ring molecules that contain elements that are heteroatoms, such as oxygen, nitrogen, and sulfur. Heterocycles are an important class of organic molecules and are found in biologically active compounds, organic materials and drugs. This project focuses on the synthesis of heterocyclic esters called isocoumarins, which are benzo-fused lactones. Many biologically active compounds contain isocoumarin structural motifs. Isocoumarins are essential component molecules in several pharmaceutical applications to combat cancer, fungal infections and are a motif present in antiallergenic complexes such as thunberiginol A from the leaves of hydrangea dulcis folium. Isocoumarins are synthesized through the methology of gold (I) catalyzed reactions from 2-alkynyl benzoate esters. The 2-alkynyl benzoate esters are made through Sonogashira palladium cross-coupling reactions. This synthetic methodology was utilized to synthesize ten substrates with electron donating and withdrawing groups. In a typical reaction, 2-alkynyl benzoate ester undergoes cyclization reaction catalyzed by a gold (I) complex in toluene. It is established that less than 1 mol % of catalyst is needed to complete the reaction and the method tolerates a variety of substrates. These reactions are very efficient and result in high yields averaging around 80-90%.

Adipic Acid Synthesis from Cyclohexanone and H_2O_2 over Heteropoly Compounds

Discipline: Chemistry

Subdiscipline: Organic Chemistry

markus Potter*, *Texas A&M San Antonio* and Shane Kendell, *St. Philip's College*

Abstract: The synthetic polymer nylon 6-6 is produced from adipic acid and is one of the most manufactured plastics worldwide. In 2006, the Environmental Protection Agency (EPA) reported that 9,297,866 metric tons of nitrogen oxide gasses are released into the atmosphere every year as a side effect of adipic acid synthesis being used to produce nylon 6-6. Adipic acid is synthesized from the oxidation of cyclohexanone with nitric acid. This oxidation reaction is the source of nitrogen oxide emissions which produce chemical occurrences such as acid rain and ozone degradation. A clean chemical process for the synthesis of adipic acid is long overdue. The purpose of the research was to analyze the formation of adipic acid from the oxidation of cyclohexanone with H_2O_2 and different heteropoly catalysts. Phosphotungstic acid, phosphomolybdic acid, and tungstosilisilic acid, were used for the catalysis in their pure form, and also as salts of copper (II) or cesium. The catalyst most reactive for adipic acid production was a fully substituted cesium phosphomolybdate, $Cs3[PMo_{12}O_{40}]$. Copper salts, on the other hand, proved to be unreactive for this reaction, which may have been due to rapid oxidation of the cyclohexanone into carbon dioxide and/or other low light oxidation species. The aim of this work is to better understand how the synthesis of adipic acid, a key precursor for nylon 6-6, can be effectively synthesized without the emission of nitrogen oxide gasses from the oxidation of cyclohexanone with H_2O_2 via heteropoly acid catalysts, such as $Cs3[PMo_{12}O_{40}]$.

Design and Synthesis of Potential Anti-Fungal Agents

Discipline: Chemistry

Subdiscipline: Organic Chemistry

Jessica Villegas* and Jeffrey Pruet, *Valparaiso University*

Abstract: Fungal infections are of continuous concern, especially with regard to immunocompromised patients. In an effort to develop new potential anti-fungal agents, we have begun synthesizing a library of potential inhibitors of the fungal Methionine Synthase (MetSyn) enzyme. Key differences between the B_{12}-independant fungal MetSyn enzyme and the B_{12}-dependant mammalian form can allow for an antifungal drug to be developed to exclusively bind the fungal enzyme and inhibit fungal growth while leaving the host (patient) unaffected. We are currently exploring the synthesis of various pterin and deazaguanine-based molecules as these mimic folate, an essential substrate for MetSyn function. We have begun testing these new molecules for activity in a fungal growth assay, as well as a fluorescent assay for monitoring MetSyn activity.

Synthesis and Analysis of 1-Benzazepine Derivatives As Potential Therapeutic Drugs for the Treatment of Alzheimer’s Disease.

Discipline: Chemistry

Subdiscipline: Organic Chemistry

Christopher Nieves Escobar*; Margarita Ortiz Marciales; Carmelo Garcia Ruiz; Sandraliz Espinosa Diaz; Paola Colón and Luis Pinero Santiago, *University of Puerto Rico, Humacao Campus*

Abstract: Alzheimer’s Disease (AD) is currently the most common neurodegenerative disease among elders. Recent studies have shown that several conditions such as the excessive aggregation of β-amyloid plaques on the central neurological system and low levels of acetylcholine play a key role on the pathogenesis of AD. Consequently, the development of potential nicotinic agonists, acetylcholinesterase, and β-amyloid polypeptides (Aβ) inhibitors could be a valuable therapeutic strategy for the treatment of AD. Benzazepines are heterocyclic compounds used as intermediates for the synthesis of many pharmaceutical drugs. In our research group, these compounds are currently being studied to determine

their possible bioactivity as potential therapeutic drugs for the treatment of neurodegenerative diseases such as Alzheimer's. Presently, we are developing novel multi-functional 1-benzazepine (1-BNZP) analogues to study further their possible bioactivity as active binding ligands for the nicotinic receptors, Aβ peptides and acetylcholinesterase inhibitors. Methoxy substituted 1-BNZPs at the 7 and 7,8 positions were prepared with a good chemical yield of 85% (purified) by the regioselective ring expansion of 1-tetralone TIPS oximes using borane/BF_3. Further alkylations at the *N*-position were made to enhance the antioxidant properties of these compounds. Docking calculations have shown that compared to Galantamine, an anti-acetylcholinesterase agent currently approved by the FDA, 3-(2,3-dimethoxy-6,7,8,9-tetrahydro-5*H*-benzo[7]annulen-5-yl)propyl cinnamate, fitted very close to the nicotinic acetylcholine receptors with an electronic affinity of -9.2 kCal/mol (± 0.2 kCal/mol); indicating potential nicotinic agonist activity for this adduct. Therefore, the main goal of our laboratory team is to keep developing novel 1-BNZP derivatives to analyze their possible bioactivity.

Examining Photochemical Reactivity of Electron Rich Enediynes

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Michelle Moua* and John Spence, *California State University Sacramento*

Abstract: Enediyne natural products are known to inhibit the development of a neoplasm (cancer cell). Synthetic enediynes continue to be developed in laboratory to study their structure reactivity properties in an effort to develop more efficient drug candidates. The key event responsible for the biological properties is Bergman Cyclization of the enediyne unit to produce an aromatic diradical. These diradical then abstract hydrogen atoms from the DNA backbone in a tumor cell leading to apoptosis. Although enediynes may inhibit the development of neoplasm, they lack the selectivity to specifically target tumor cells. This project examines the incorporation of methoxy groups conjugated to the enediyne to improve photochemical activation towards Bergman cyclization. The methoxy groups are composed of an electron donating oxygen containing a methyl group that is attached to the enediyne core as a substituent. This project will examine the synthesis and photo-reactivity to better understand factors controlling light activated Bergman Cyclization. Overall, photoactivation may provide selective activation by delivery of light while electronic effects from the methoxy groups can increase reaction yield and reduce reaction time to help develop more efficient enediyne pro-drugs. The goal of this project is to study the methoxy effect at different locations within the enediyne structure.

Fluorescent Molecular Rotors (FMRs): Synthesis and Applications

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Gabrielle Balistreri*[1]; Emmanuel Theodorakis[2] and Jamie Lam[2], *(1)University of California San Diego, (2)University of California*

Abstract: Alzheimer's disease is a neurodegenerative disorder characterized by the abundance of protein, amyloid B-peptide (Aβ), that is aggregated, deposited in brain tissue and converted to fibrillar structures (amyloid fibrils) which are resistant to degradation and are considered as the starting point for Alzheimer's disease. Thioflavin (ThT), a fluorescent dye, can detect amyloids by binding to Aβ and emitting fluorescence that increases in intensity when the fibril structures become more abundant. However, there are limitations to using ThT, since this molecule cannot penetrate the blood brain barrier nor identify small fibrils that are formed at the initial stages of this disease. Thus, there is a need to design alternative fluorescent probes that are more sensitive and more biologically relevant than ThT. The Theodorakis group deals with the design of new fluorescent probes whose fluorescent emission varies as a function of their environment. We designed probes that upon binding to amyloids, emit fluorescent light with high intensity and sensitivity. Our cyano acrylate (ANCA) probe has shown a stronger fluorescence emission than ThT, when bound to the aggregated Aβ. A limitation of ANCA probes is that they contain an ester group that is susceptible to hydrolysis when used in vivo. I will modify the synthetic strategy of ANCA probes to replace the ester group by an amide functionality, thus increasing the molecules' stability. By improving the selectivity and affinity of the amyloid fibrils, this could potentially monitor and diagnose Alzheimer's disease, furthering other advancements in curing Alzheimer's disease.

Quantifying Hydrogen-Bond Accepting Ability of Organic Molecules Using 19F and 31P NMR Spectroscopy

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Madison Thompson*, *University of California Davis* and Annaliese Franz, *University of California, Davis*

Abstract: Hydrogen bonding is a vital aspect of organocatalysis and many drug receptor interactions. Current methods to measure H-bonds are time-consuming and costly. My research proposes a new method using ^{19}F and ^{31}P NMR spectroscopy, utilizing commercially available, inexpensive pentafluorobenzoic acid (PFBA) and phenylphosphinic acid (PPA) probes. Over 110 medicinally and catalytically relevant molecules and molecule fragments including heterocycles such as pyridines, quinolines, and benzotetramisoles, were examined with a variety of steric and electronic modifications. In addition, the hydrogen bonding ability of select drug molecules, organocatalysts, and ligands were quantified. Hydrogen bonding measurements showed strong correlations with Hammett parameters and proton transfer basicity (pK_{BH+}) ^{19}F and

^{31}P NMR spectroscopy offer rapid and simple tools to quantify HBA abilities, which may contribute to the understanding of H-bonding in the design of novel bioisosteres and organocatalysts for drug discovery and catalysis.

Computational Study of Reaction Mechanisms in the Catalytic Deoxygenation of Fats, Oils, and Greases (FOG) to Fuel-like Hydrocarbons

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Camron De'Vine*[1]; Chad Risko[1] and Eduardo Santillan-Jiminez[2], *(1)University of Kentucky, Lexington, (2)university of kentucky*

Abstract: As the need for clean energy rapidly grows in our society, research must be done to produce large amounts of clean energy that is also affordable for potential consumers. Ultimately, the goal of this research is to produce renewable hydrocarbons fuels through the catalytic deoxygenation of fats, oils and greases (FOG). Oxygen can be removed from FOG via decarbonylation (DCN) and/or decarboxylation (DCX), two reactions typically catalyzed by palladium-based catalysts. However, nickel is a more affordable material whose activity in DCN and DCX can rival that of costly palladium. This research aims at investigating the decarbonylation (DCN) and the decarboxylation (DCX) reaction mechanisms on nickel model surfaces *in silico* (i.e., computationally), employing propanoic acid as a surrogate for FOG. Using previous DCN and DCX mechanistic studies on a palladium model surface as a guide, similar methodology is being applied to elucidate the DCN and DCX reaction mechanism on a nickel model surface. In conducting work towards this goal, three-dimensional models were created for relevant gas phase molecules to depict their interactions with a clean nickel slab. The results of these tests provide information on the amount energy associated with these interactions. Armed with this information, other factors – such as geometrical and spatial arrangements – can be manipulated to refine the system and gain further insights. Notably, multiple iterations of the aforementioned steps need to be performed until the energy graph completely converges, convergence being indicative of the success of the experiment.

Brønsted Acid-Catalyzed Stereospecific Dearomative Spirocyclization of *Cis*-β-Meth(hetero)Arylstyrenes

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Victoria Lerda*; Anargul Tohti and Benjamin Stokes, *University of California, Merced*

Abstract: Spiroheterocycles and quaternary geminal dialkyl groups are both important molecular motifs in important synthetic and naturally occurring compounds. There are few direct methods available to install a spirocyclic quaternary center adjacent to a second quaternary center. We hypothesized that a geminal dialkyl carbon atom linking the 3-position of a benzo-fused five-membered heteroarene to the **β**-position of a styrene would lead to a dearomative Friedel–Crafts-type cyclization in the presence of acid, with the heteroarene serving as the electrophile. Herein, we describe a Brønsted acid-catalyzed stereospecific dearomative spirocyclization of benzothiophenes by pendant cis-configured styrenes linked by a geminal dialkyl carbon atom. The reaction optimization is described in detail and is accompanied by a preliminary reaction scope (specifically yield and regioselectivity outcomes due to substituent variation) and mechanistic discussion.

Identification of Compounds Against Glucocorticoid Resistant Leukemia Cell Models

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Calli Nguyen*[1]; Taotao Ling[2] and Fatima Rivas[1], *(1)Louisiana State University, (2)St. Jude Children's Research Hospital*

Abstract: The pro-differentiation and pro-apoptotic effects of glucocorticoids (GC) are central in the treatment of acute lymphoblastic leukemia (ALL) and initial treatment response is a key prognostic indicator. Resistance to GC treatment is observed in 10-30% of patients with untreated ALL and in relapsed ALL. Natural products (NPs) have been used as medicines throughout human history and continue to serve as potential sources of new chemical scaffolds.

The purpose is to identify potential new compounds to sensitize GC resistant ALL cellular models.

A high throughput primary screen cytotoxicity assay were conducted using NP fractions in a single-dose response. Hits were validated using a dose-response cytotoxicity assay and computational studies were conducted to predict potential biological targets.

We identified potent anti-proliferative triterpenoid NPs against ALL cellular models and discovered that these compounds affected the mitochondrial membrane potential (ΔΨm). Furthermore, their apoptotic effects were validated by annexin V staining. Preliminary molecular docking studies suggest potential biologic targets.

Herein we disclose the effects of a potent anti-proliferative NP against human ALL leukemia cell lines to be used in combination experimental therapeutics, and its potential mode of action will be discussed.

Hydrogen Production Via Water Splitting Using Titania-Based Photocatalysts.

Discipline: Chemistry
Subdiscipline: Other Chemistry

Carla M. Colon Cruz[*1]; Dr. Francisco Marquez Linares[1]; Dr. Abniel Machin De Jesus[2]; Kenneth Fontanez[1]; Loraine Soto-Vazquez[3] and Carmen Morant[4], *(1)Universidad Ana G. Mendez, Gurabo Campus, (2)Universidad Ana G. Mendez, Cupey Campus, (3)Materials Characterization Center, (4)Universidad Autónoma de Madrid*

Abstract: A potentially viable way to eliminate fossil fuels is to produce hydrogen from water by combining solar energy and heterogeneous photocatalysis. For these reasons, the objectives of this investigation were: 1) synthesize high surface area TiO_2 nanowires (NWs) catalysts in the rutile phase; 2) incorporate different amount of silver nanoparticles on the as-synthesized catalyst and on the commercial form of TiO_2 (P-25) using a chemical reduction method; and 3) produce hydrogen via water splitting using visible and UV light. The hypothesis of the study were: a) the catalysts with higher surface will produce the largest amount of hydrogen, and b) the silver nanoparticles will enhance the hydrogen production and will allow the use of visible light. Interestingly, the incorporation of silver nanoparticles on the titania surface enhanced the surface area in both P-25 and TiO_2 NWs. The hydrogen production obtained by using Ag@P25 catalysts was measured to be 653 µmolg-1h-1 under irradiation at 500 nm and 1,119 µmolg-1h-1 using Ag@TiO_2 NWs at the same wavelength. Both of the hypothesis were verified and all the objectives achieved. The characterization of the synthetized compounds were performed by: 1) X-ray diffraction (XRD), 2) Field emission scanning electron microscopy (FESEM), 3) Brunauer, Emmett and Teller (BET) surface area, and 4) UV-vis spectroscopy. The results of this study open the possibility to design green technologies contributing to the development of new and more efficient catalysts, and the development of alternatives for the production of clean and renewable energy.

Photodegradation of the Antibiotic Ciprofloxacin Using Ag@ZnO Catalysts

Discipline: Chemistry
Subdiscipline: Other Chemistry

Carlos Valentin Cruz[*], *Universidad Ana G. Mendez, Recinto de Gurabo*; Dr. Francisco Marquez Linares, *Universidad Ana G. Mendez, Gurabo Campus*; Dr. Abniel Machin De Jesus, *Universidad Ana G. Mendez, Recinto de Cupey* and Carmen Morant, *Universidad Autónoma de Madrid*

Abstract: One of the main health challenges of the 21st century is the resistance to antibiotics. Researchers from all over the world are constantly looking for innovative ways to address this situation. A possible solution is to degrade these organic compounds by using photocatalysis. Is for that reason that the objectives of this investigation were: 1) Synthesize and characterize different silver-based (1 wt.%, 3 wt.%, 5 wt.%, 10 wt.%) zinc oxide catalysts; 2) Study the photocatalytic activity of the catalysts by the degradation of the antibiotic Ciprofloxacin. The hypotheses of the experiment were: 1) All the catalysts are able to degrade Ciprofloxacin by 85% or more in one hour under ultraviolet and visible light; 2) The catalyst containing 5% of silver will achieve the maximum degradation. The results showed that all the catalysts were able to degrade Ciprofloxacin by more than 91% in one hour, being the catalyst with 3% silver the one with the highest degradation percentage, 99.6%. These results demonstrate that high catalytic activity of the as-synthesized catalysts under ultraviolet and visible light. As future works, different morphologies of the support and the incorporation of the different metals will be evaluated.

Prediction of Micelles Attributes Based on DFT-Calculated Molecular Physical Properties

Discipline: Chemistry
Subdiscipline: Other Chemistry

Jenlyan Negron[*]; Dalvin Mendez and Luis Negron, *Univeristy of Puerto Rico at Cayey*

Abstract: Thermosensitive micelles can work as effective drug delivery system because of their ability to transport poorly water-soluble anticancer drugs, improve drug stability, and have good penetration and site-specificity, leading to an enhance therapeutic efficacy. These structures are prepared through the self-assembly of amphiphilic molecules (monomers). One important characteristic of an amphiphilic molecule is that it has a polar and a non-polar region which allows it to interact with aqueous and non-aqueous solvents. Therefore, the orientation of the amphiphilic molecules depends on the surrounding medium and thus, physical properties of micelles are influenced by the chemical nature of the monomers that form them. However, very often these monomers can fail to form micelles under the desire conditions. Density Functional Theory (DFT) calculations can be used to look for correlations between theoretical parameters of monomers (e.g. solvation and binding energies) and experimental ones of micelles (e.g. transition temperature, cloud point temperature, and enthalpy of formation). These correlations could help in the design of new molecules based on predicted micelle properties. Herein, six monomers were draw using Gauss View 5.0 and DFT calculations were performed at the B3LYP/6-31g(d) level of theory using Gaussian 09. Our results show very weak correlations; however, a clear difference was noticed between the solvation and binding energies of the monomers that form micelles and the one that does not. This information can lead to identifying the monomers that form micelles from the ones that do not, which can preserve valuable resources.

Investigating Thermal Effects on Organic Photovoltaic Material Morphologies from Molecular Simulations

Discipline: Chemistry
Subdiscipline: Other Chemistry

Daniel Valenzuela*; Liang Shi and Yue Yu, *University of California, Merced*

Abstract: Organic Morphologies of donor/acceptor blends are meaningful to the developing of high-performance Organic Photovoltaics (OPVs). These devices are subject of importance for electricity generation, replacing silicon solar cells due to their cheap production, light weight, high flexibility and non-polluting nature. Although the OPVs have a lower energy conversion efficiency, it is possible to optimize schemes by looking at its morphology. However, these morphologies are easily predictible. In this study, we determine the thermal effects over OPVs material's morphology using the Coarse Grain (CG) Molecular Dynamic (MD) simulation. This method was developed by converting four heavy atoms into one interaction site called "bead". For this experiment it was used a blend of 50 PCBM and 146 P3HT molecules to mimic a 1:1 mass ratio. Four different temperatures: 350 K, 300 K, 250 K and 200 K; have been tested to obtain the morphologies of the coarsed blends of PCBM/P3HT. For each simulation run, both CG and AA models have been validated by comparing obtained free energies with experimental data. These obtained configurations were later remapped to an All Atom (AA) configuration to later obtain the specific properties lost by coarse-graining the molecules. The goal is to see the expected result of inverse relationship between density and temperature, where the density increased in the system as the temperature was lower. After remapping the model to an AA system, the radial distribution was computed in order to determine the thermodynamic properties that can achieve the optimized scheme, such as potential energy and pressure.

Modeling Drug-Protein Interactions within the Spleen Using Computational Chemistry

Discipline: Chemistry
Subdiscipline: Other Chemistry

Alexander Plonski*, *University of Colorado Denver* and Scott Reed, *University of Colorado, Denver*

Abstract: Many populations experience adverse drug reactions (ADRs) within the spleen after the use of a drug. ADRs such as splenomegaly can have damaging effects on the spleen. Through the use of computational modeling, we are able to understand the interactions between drugs linked to specific ADRs and a tissue. We are specifically interested in the interactions between drugs and proteins within the dark genome which are understudied and may have a linkage to an ADR. Being able to understand how a drug interacts with a tissue can help populations prone to ADRs avoid a specific side effect. Using public databases for protein and drug information, we are able to simulate protein-drug interactions with both the wild type protein and its single nucleotide variations (SNVs) through docking software. We are using existing metrics that measure the conformational change of a drug as well as developing metrics that record the proximity of a drug to an SNV site to help gage the role an SNV might play in an ADR. SNVs selected were filtered by a surface area change of less than 10 angstroms and a net charge of zero to select mutations with the least amount of structural change on a protein. We will present results from a study of 13 proteins within the dark genome and 19 drugs associated with ADRs within the spleen. We expect drug conformation and proximity to an SNV site to change if an SNV is linked to an ADR.

Modification of Iridium Alkane Dehydrogenation Catalysts for Site Isolated Reactivity

Discipline: Chemistry
Subdiscipline: Other Chemistry

Juancarlos Rojas* and Madalyn Radlauer, *San Jose State University*

Abstract: Catalysts play a key role in enabling chemical reactions to be faster and more efficient. Our research group studies ways to facilitate challenging chemical reactions with a synthetic catalyst. We hypothesize that using a polymer (a long chain of repeating subunits) as a scaffold for a catalyst will promote reactivity. We are developing a more efficient iridium catalyst for turning alkanes into alkenes (alkane dehydrogenation). If successful, our catalyst could work at significantly lower temperatures than previously reported systems. Alkanes are fully substituted carbons and they are not very reactive. However when you turn an alkane into an alkene that is when the real chemistry can begin. We have completed a series of synthetic reactions, most of which require oxygen- and water-free conditions accomplished with a glovebox. We started synthesis of the modified complex with 3,5 -dihydroxybenzaldehyde. Protection of the hydroxyls with silyl protecting groups allowed us to use a Wittig reaction to install an alkene in place of the aldehyde. Removal of the silyl groups was followed by phosphination to finish our modified ligand. My role includes performing laboratory techniques for synthesis, purification (like pumping down or filtration), and characterization. I use nuclear magnetic resonance (NMR) spectroscopy and thin layer chromatography (TLC) to identify the compounds I am making. Currently, we are working to incorporate this ligand into a polymer, and to metallate with iridium. Then we will begin catalytic trials with the iridium-containing polymers and study how the polymer structure affects the catalytic activity.

Computation of Host-Guest Free Binding Energies with a New QM-MM Mining Minima Algorithm

Discipline: Chemistry
Subdiscipline: Other Chemistry

Kilinoelani Montgomery* and Emilie Guidez, *University of Colorado, Denver*

Abstract: Some potential drug molecules are hydrophobic, therefore, insoluble in the human body. Drug carriers have hydrophilic and hydrophobic character, which allow drug molecules to be encapsulated in these systems to improve solubility and bioavailability as they travel to the target site. Since drugs are bound to the carrier through noncovalent interactions, the binding energy between them is difficult to predict accurately. The VeraChem VM2 software utilizes molecular mechanics (MM) methods to predict the binding energy between a host (drug carrier) and a guest (drug). A combination of quantum mechanics (QM) and MM is important to develop accurate yet cost efficient software. The QM-VM2 scheme searches for host-guest conformers using an MM mining minima method, then runs QM calculations to get accurate free binding energy values. The resulting software will aid drug developers and minimize computational cost.

Simulating Temporal Heterogeneity in Supercooled Liquids: Comparing Results from Time-Limited Single Molecule Trajectories

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Talha Rehman[*]; Nicole Mandel and Laura Kaufman, *Columbia University*

Abstract: In supercooled liquids, the dynamics are heterogeneous. As molecules rotate they display spatial heterogeneity, and as molecules translate they display temoral heterogeneity. Experimentally stretched exponential relaxations are shown to indicate heterogeneous dynamics in supercooled liquids. However, different interpretations are provided about the degree of heterogeneity by various experimental approaches. Earlier work had shown that even when spatially heterogeneous dynamics is existent, SM experiment time-limited trajectories can lead to a stretching exponent which suggest homogeneous dynamics. We scrutinize whether temporal heterogeneity accessible with single-molecule (SM) approaches are consistent with each other. In particular, the lognormal distribution of diffusion coefficients obtained from simulations is compared with the SM measurements. We will present the results from ideal case simulations with zero background conditions. The results would be compared to SM experiments in terms of mean square displacements and dependence of time-limited trajectory lengths.

Plasmonic Fluorescence Enhancement of Gold-Diamond Nanoassemblies for Biodetection Methods

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Davida Simpson[*1]; Nedah Basravi[1]; Camilla Hanson[1]; Karen Lopez[1]; Grace Jeanpierre[1]; Virginia Altoe[2]; Dennis Nordlund[3] and Prof. Abraham Wolcott[1], *(1)San Jose State University, (2)Molecular Foundry, (3)SLAC National Accelerator Laboratory*

Abstract: Nitrogen Vacancy Center (NVC) nanodiamonds (NDs) have potential applications in intracellular drug localization and cancer detection due to their electron spin properties, biocompatibility, molecular components, and stability. However, NVC imaging requires high light levels (1 mW/um^2), which increases fluorescence background signal from cells and tissues. ND-gold nanoparticle conjugates can achieve a 200X increase in light emission based on FDTD (finite difference time domain) calculations. We hypothesize that self-assembly of gold nanoparticles (AuNPs) with SiO_2-coated NDs into a hexagonal pattern will allow for plasmonic enhancement of NV fluorescence. We employ thiol functionalized ND-SiO_2 constructs for self-assembly of the gold-nanodiamond nanoarchitectures which is kinetically driven by gold-thiolate bond formation. Click chemistry with alkynes and azides are also used in conjunction with polyethylene glycol moieties for stabilization. We synthesize gold nanoparticles via a seeded growth mechanism to yield 60-80nm citrate capped AuNPs. SiO_2 shells of 15nm thickness were synthesized on nanodiamond cores to provide a chemical platform which does not change the properties of NVC nanodiamond. Both AuNPs and SiO_2 coated nanodiamonds were imaged via Scanning Electron Microscopy (SEM) and Dynamic Light Scattering (DLS). Here we have shown that self-assembly of dimers and trimers is possible and confirmed via SEM. The conclusion is that conjugation rates are highly sensitive to the coverage of moieties on the ND surface and the initial ratio of ND:Au NPs during the self-assembly process. Future work includes scanning fluorescence microscopy to confirm plasmonic enhancement and incorporation of the ND-Au NPs constructs into 3-D cancer cell models.

Semiclassical Approximation of Heat Capacities for Model Systems

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Sheindel Gamerberg[*] and Aurora Pribram-Jones, *University of California, Merced*

Abstract: Both quantum mechanical properties and temperature effects are important for certain systems, which are studied in astrophysics, fusion science, atomic and optical physics, and materials chemistry. Many quantum mechanical methods are ill-suited to high temperatures, suffering from substantially increased costs, a lack of explicit temperature dependence incorporated into their implementations, or treatment of quantum effects not usefully accurate in complicated systems. Semiclassical methods can be used under such conditions, and we apply this approach to approximating partition functions, bypassing computational bottlenecks to more directly compute energetic quantities and experimentally accessible properties like heat capacity. Semiclassical approximation of the partition function is expected to be more accurate as temperatures increase, while remaining more accurate at lower temperatures than approximations for high-temperature classical electronic systems. A python script designed to approximate the partition function through semiclassical methods is altered to generate the heat capacity for model systems, such as the harmonic and Morse oscillators. The calculated approximate heat capacities are compared to their exact heat capacities and analyzed in varying temperature and density conditions.

Substituent Effects on Microcapsule Ligand Self-Assembly from Density Functional Theory Calculations

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Estefania Cuevas-Zepeda*; Christopher Perez; Ryan P. Brisbin; Ryan D. Baxter and Aurora Pribram-Jones, *University of California, Merced*

Abstract: Self-assembled microcapsules, composed of nanoparticles and functionalized organic ligands, can provide a robust and tunable tool for targeted drug delivery. A collection of such assemblies has been produced by the Baxter and Ghosh Labs at the University of California, Merced, demonstrating stable encapsulation of cargo paired with bio-compatible release mechanisms. In this study, we use quantum mechanical simulations to investigate the dependence of the ligand's substituents and its geometry on the final conformation that is produced. The obtained results can be used to better understand existing microcapsule phenomena and contribute to the development of future designs.

Density functional theory (DFT), an electronic structure method with a useful balance of accuracy and computational cost, is used to determine the energies and geometries of various structurally related ligand structures. We hypothesized that the observed crystal configurations occurred in order to achieve more favorable interactions at the cost of the individual ligand's preferred geometry. The simulation results will be compared to both experimental crystal structure data and to DFT calculations conducted on theoretical molecules using experimental parameters. The trade-off between structural strain and advantageous intermolecular interactions will be analyzed using structural, energetic, and electronic perspectives. Our preliminary results support experimental observations that, surprisingly, the unsubstituted ligands produce the largest shell sizes, suggesting some competing influences on this behavior.

Using Spectroscopy to Investigate Photoprotection Mechanisms between Mthf and Fad in E. coli Photolyase

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Warner Carnero* and Johannes Schelvis, *Montclair State University*

Abstract: The ability for flavin cofactors – flavin adenine dinucleotide (FAD) and 5,10-methenyltetrahydrofolate polyglutamate (MTHF) – to become photoreduced in the presence of UV light and achieve different excited states describes the photochemistry necessary for photolyase systems to engage in pathways that result in DNA repair and degradation. The ramifications of understanding the energetics and kinetics involved in the flavin triplet state can address potential issues of further degradation caused by the triplet excited state. To test our hypothesis that MTHF has a photoprotective role, we aimed to compare results from fluorescence and absorption spectroscopic studies between the interactions of MTHF and FAD with MTHF and Riboflavin (Rf), serving as the base isoalloxazine ring for comparison with FAD. Fluorescence experiments on Rf samples with potassium bromide (KBr) quencher allowed us to measure the absorption maxima at 525 nm during singlet-singlet transition, resulting in a quantum yield Φ^{o}= 0.5. Absorption experiments during 30-minute irradiation runs aimed to study interactions of RF with KBr and RF with MTHF at longer timescales, indicating no significant correlation between concentration of MTHF and exponential decay constants obtained from decay fits of the absorption data. Preliminary results of the same procedure of the absorption experiment done on MTHF and FAD present a possible pathway of FAD conversion to Rf in the presence of MTHF. By expanding to shorter timescales by using phosphorescence and computationally simulating triplet-triplet transition between MTHF and FAD, we aim in the coming future to compare experimental and theoretical values of triplet-triplet energy transfer.

Why Don't Students Use RadGrad? A Qualitative Study of Factors That Inhibit Adoption of the RadGrad Software

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Quinne Uchida* and Philip Johnson, *University of Hawaii at Manoa*

Abstract: In 2017, RadGrad, a software application, was designed to address the short-comings of the University of Hawaii at Manoa's Information and Computer Science (ICS) Department ability to prepare students for the demands of a rapidly growing industry, as well as to address low enrollment of female and Native Hawaiian students. Unfortunately, despite intended benefits of RadGrad, student adoption is still relatively low after over 1 year of deployment. This research aims to answer why students are not using RadGrad by conducting a series of in person interviews consisting of 22 open ended questions with currently enrolled ICS students who were in the low adoption group for August 1st, 2019 to December 31st, 2019. Ideally, this project will be conducted on 15 - 20 student users. A pilot study has been conducted on 5 students, the results of which were transcribed and analyzed for words and phrases associated with student perception of RadGrad. The results of the pilot study indicate that gamification, user experience and user interface may be the reason why student use of the system is low according to students in the low adoption group. However, only the pilot study has been completed due to disruptions by COVID-19 and 5 participants is too small of a sample size to make a conclusion. By concisely identifying low adoption reasons, this research can lead to improvements in RadGrad, leading to an increase in users who will benefit from it, as RadGrad is to be launched to other departments in other colleges.

Using Social Media to Perform Parasocial Relationships with Celebrities

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Courtney Smith* and Lynette Yarger, *Pennsylvania State University*

Abstract: With the boom of technology and rapid growth of social media, it has become increasingly common to create one-sided parasocial relationships with celebrities and tv/movie characters. Considering this, it is important to determine what impact these relationships are having on society. My research question is “How do attachment styles and level of intensity of parasocial relationships exhibited in social media communities differ from actor to character and does this affect personal relationships?” To conduct this study, I will use the Absorption-Addiction Model and the Social Attraction/Physical Attraction scale to determine the level of attachment. Data collection will be carried out by a survey given to individuals 18-25 years old through social media sites, such as Tumblr, Instagram, Facebook, etc. The survey will include four main categories measuring emotional intensity, dedication, sharing, and technology. Currently, there is limited research on parasocial relationships and social media and even fewer studies on the differences in attachment between nonfictional versus fictional people. My intent is to contribute to this field by furthering our understanding of the complexity of parasocial relationships as well as relationships in general and how and why these attachments are created using social media. I currently do not have preliminary data on my research, but I received the Erickson Discovery Grant from Penn State to support data collection and analysis this summer and expect to gain strong results indicating a strong level of attachment more towards the actor than their character portrayal.

Designing the Creative Commute: Using a Car Simulator to Examine How Driving Impacts Creativity

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Kordell Schrock*, *Iowa State University* and Elizabeth Murnane, *Stanford University*

Abstract: Creativity, whether undertaken for pragmatic or playful goals, plays a key role in societal advancement as well as personal well-being. This research is aimed at better understanding how technology can foster creativity in everyday life, for instance as part of a daily commute. Conducting user-centered design activities and undertaking simulator-based experiments, we explore how a series of interactive in-car systems (e.g., conversational agents, haptic feedback, and ambient media such as light and sound) can engage with drivers and passengers to guide creative activities and novel ideas, in an effective, enjoyable, and safe manner that will boost creativity and well-being. On average over 76% Americans commute by car every day. We are seeing if driving is linked to creativity when they experience a defocused-attentional state.

In our study, we looked at the participant’s Convergent & Divergent thinking. We wanted to see if their creativity was affected when the participants were either a passenger or driver in a car-simulator. In our experiment, we had three quizzes to examine the participant’s Convergent & Divergent thinking. One quiz before the experiment to get a baseline (Pre), one after the 20-minute driving simulator (During), and one after the experiment (After). After running 15 participants, we had found that Convergent thinking decreases, and Divergent thinking increases, which supports that creativity is boosted when a participant was a passenger or driver of a car-simulator. Our next step would be using a real car instead of a car-simulator and increasing our participants to 50 to solidify our findings.

Deep Learning for Accurate Shape Representation Using the BMA

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Sophie Schaefer* and Kathryn Leonard, *Occidental College*

Abstract: The Blum Medial Axis (BMA) can be used to represent a two-dimensional image using a skeletal model. Unlike a simple binary image, the BMA stores geometric information about the boundary and connectivity information regarding different parts of a shape. This information includes the number of parts needed to describe a shape. For our research, we investigate methods to quantify the number of parts necessary to represent any given shape accurately. This prediction can later be used in a number of ways, including pruning unnecessary shape parts corresponding to boundary noise, evaluating shape complexity, performing parts decompositions, and generating comparisons between shapes. To predict the number of parts needed to represent a shape, we develop a convolutional neural network based on the ResNet structure. We train the convolutional neural network using the SkelNetOn data set consisting of 1,725 black and white shape images as inputs along with the number of Bezier curves representing the ideal parametric fit to the BMA of the shape as ground truth. The results of our prediction are evaluated using the F1 score the neural network attains. We also perform an analysis to determine for which categories of shape our predictions are and are not accurate.

Deep Learning for Accurate Shape Recognition Using the BMA

Discipline: Computer & Information Sciences

Subdiscipline: Computer & Information Sciences

Dyani Dillard* and Kathryn Leonard, *Occidental College*

Abstract: The Blum Medial Axis (BMA) is a skeletal model of a two-dimensional shape that stores geometric information about the boundary and connectivity information about different parts of a shape. As such, the BMA can yield more information about a shape than a simple binary image. The connectivity information includes information about how many parts are necessary to describe the shape. Our research aims to quantify the number of parts needed to accurately represent any given shape. This prediction can later be used in a number of ways, including pruning unnecessary shape parts corresponding to boundary noise, evaluating shape complexity, performing parts decompositions, and generating comparisons between shapes. We develop a convolutional neural network based on the ResNet structure to predict the number of parts needed to represent a binary shape. To train the convolutional neural network, we used the SkelNetOn data set consisting of 1,725 black and white shape images as inputs and the number of Bezier curves corresponding to the ideal parametric fit to the BMA of the shape as ground truth. We evaluate our results by considering the F1 score our model achieves and provide an analysis of the categories of shapes for which our predictions are and are not accurate.

Training a Convolutional Neural Network to Output a Blum Media Axis Skeleton

Discipline: Computer & Information Sciences

Subdiscipline: Computer & Information Sciences

Joaquín Madrid Larrañaga* and Kathryn Leonard, *Occidental College*

Abstract: The research objective is to use a Convolutional Neural Network to learn a Blum medial axis (BMA) skeleton representation of an object of interest from a typical RGB image. BMAs are useful for computing a shape parts hierarchy as well as for shape recognition and classification. By using a dataset of over 300,000 images and corresponding BMA skeletons (our ground truth), we trained an modified Mask-Resnet Convolutional Neural Network (Mask-RCNN) to output an image with a black background and a white skeleton which is a denoised version of the Blum medial axis. We then used 300,000 additional images to test and refine the Mask-RCNN. Once the Mask-RCNN was reliably outputting accurate skeletons from our test set, we tested 300,000 additional images and computed their accuracy. By continuing to refine the model, this accuracy can be increased in order to reliably output skeletons for a wide variety of input images for use in a shape parts hierarchy or for shape recognition and classification.

Path Planning for Underwater Crashsite Reconstructions

Discipline: Computer & Information Sciences

Subdiscipline: Computer & Information Sciences

Mugen Blue* and Zoë Wood, *California Polytechnic State University*

Abstract: Capturing a 3D computer model of real world geometry is useful for many domains, including archeology for site mapping, monitoring and producing educational visualizations. Using photogrammetry to reconstruct such 3D models from a sequence of photographs (or video frames) has gained wide spread acceptance. This project focuses on creating trajectories for an autonomous vehicle with the primary objective to capture `good views’ of the site of interest to then use video frames for photogrammetry reconstructions. Using a robotics motion planning algorithm integrated into a virtual testbed, this project includes trajectory refinement, especially with respect to translating a given digital path (defined by discrete points with `good views') into a usable geo-located way-points for an autonomous vehicle to follow and testing to evaluate the trajectories. This includes the development of an algorithm to optimally match pairs of existing path nodes to create a new AUV usable path. In addition, this research evaluates various trajectories using the virtual testbed and planned field deployments. This research builds on existing software written in C++ using OpenGL and algorithmically constructs paths from discrete nodes into viable AUV trajectories in a usable format by the AUV.

Diffusercam: Deep Image Prior on Reconstructing 2D Images for Lensless Camera

Discipline: Computer & Information Sciences

Subdiscipline: Computer & Information Sciences

Nguyen Thanh Vi Tran*; Kristina Monakhova; Grace Kuo and Laura Waller, *University Of California, Berkeley*

Abstract: Lensless camera systems replace the lens with a light-weight diffuser to map a point source in the scene to a caustic pattern on the camera sensor. The diffuser can be made from a low-priced material, which allows the imaging system to be compact and cheap. Traditionally, the scene is recovered from the multiplexed measurement by solving an inverse problem. However, the reconstructed image often suffers from artifacts and does not match the image quality of lens-based systems. Deep learning could be applied to train the neural network to improve the image quality, however this technique requires large training datasets, which is hard to obtain for these cameras. In this research, we explore unsupervised deep learning methods, which train neural networks on one single measurement image without the need for a ground truth label or large dataset. The network consists of many randomly-initialized convolutional and activation layers, whose output is passed through a known forward model of the imaging system, producing a simulated measurement. The weights of the network are updated by minimizing the difference between simulated measurements and experimental sensor data. This technique has the potential to perform deep learning on single measurement to reconstruct the scene image with better perceptual image quality compared to traditional models. Since ground truth data is hard to acquire for many mask-based imagers, this approach has the potential to produce high quality reconstructions in the absence of ground truth training images.

Towards Classification of Wound Stages Using Deep Learning Algorithms

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Héctor Carrión*, *University of Puerto Rico, Rio Piedras* and Mohammad Jafari, *University of California, Santa Cruz*

Abstract: Wound healing is a variable, complicated, painful, and often prolonged process that involves a series of different stages. Current healing solutions are passive in nature and do not account for the dynamic state of the wound. A proactive treatment solution could benefit extensively from real-time awareness of the different healing stages (i.e., what physiological process has just completed, what process is in progress, and what process should subsequently take place). Therefore, to enable such proactive treatments, our research focuses on an end-to-end deep learning pipeline that intakes a wound image and returns its size, healing stage, and other critical parameters related to the injury. We also aim to study the changes of wound conditions over time and integrate those findings back onto the healing solution. We hypothesize that well-known object detection and medical instance segmentation deep learning algorithms could be adapted to our particular task. Our preliminary results after developing customized algorithms based on the YOLO, U-Net, and DenseNet architectures are promising and can already locate and segment the wounded area. We also plan on exploring unsupervised methods and comparing their performances. Moreover, after post-processing our results, we expect to build a clear end-to-end graphical representation of the healing process. Ultimately, the results of this project should be an accessible, easy to implement, and robust wound monitoring Artificial Intelligence (AI)-based pipeline that will provide useful, actionable insights geared towards proactive wound treatments.

Angel SCAN: A Novel Approach to Medical Imaging Processing to Detect Abnormalities in X-Rays

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Georgiana Wright*[1]; Marius Schamschula[1] and Angelina Uno-Antonison[2], *(1)Alabama Agricultural and Mechanical University, (2)University of Alabama Birmingham*

Abstract: Approximately 41,000 women in the US are expected to die from breast cancer in 2018. Mammograms are needed to find breast cancer yet the cost for a mammogram from a radiologist is $730-$1,000. This cost exceeds the $50 Medicare reimbursement, which can cause financial burden onto patients. This can cause them turn away or delay proper treatment to protect their finances. To decrease this problem, we created a machine learning tool with image recognition features that reads mammograms and examines it into normal shapes or irregular abnormalities as well as a trained radiologists. The prototype, ANGEL SCAN, was established to be created with Python and PyCharm was used as the developing environment to use during this experiment. The data was collected from the MIAS Mini-Mammographic Database. The database contains 322 images of mammograms. The program associates the classifications to mammograms and inputs them into the ML algorithm for each of the mammograms. This establishes a model that can predict abnormalities in a mammogram. The images in the database are used to train the model to learn abnormalities. Developing the images to fit within these categories was done during the preprocessing stage. The computer ran for 7 hours for 345 iterations out of 30,000 iterations which was outputted in the Google Kubernetes system. For the current iteration of this project, past tools were replaced with Tensorflow within Google's Datalab and the data will be supplemented with Stanford's MURA Database

An Algorithmic Approach to Improving and Reannotating a Cyberbullying Youtube Dataset

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Phd. Marcelo O. Szteinberf; Luis Rosales*; Akshit Gupta and Rachel Trana, *Northeastern Illinois University*

Abstract: Cyberbullying has become a national mental health concern not only among adolescents, but also other age groups. Most of the cyberbullying occurs on social media platforms, such as Twitter, YouTube, and Instagram. In this work, we examine a previously collected YouTube dataset of approximately 19,000 comments that was subsequently labeled using Amazon Mechanical Turk commonly referred as MTurk. While using MTurk allows for the labeling of large amounts of data at relatively low cost and within a short period of time, there is limited quality control. Additionally, many of the posts include slang terminology to which many MTurkers may not be familiar, so it can result in mis-labeled data. It is essential to emphasize that a classification algorithm is only as good as the dataset on which it is trained, so it is vital to verify and improve the dataset annotation in an unbiased algorithmic manner. To do this, Naive Bayes and Support Vector Machine algorithms were used on smaller subsets of the dataset, in combination with LIME, which is a novel exploration technique that interprets and provides insights on classifier prediction results. Our goal is to relabel the data that may have been misclassified by Mturkers. We will train our classifiers iteratively, focusing on misclassified labels, and adjusting the thresholds for relabeling to improve the accuracy of our predictions.

The Computational Apprentice: Exploring a New Approach for AI Assistance

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Samantha Childers*[1]; J.D. Zamfirescu-Pereira[2] and Björn Hartmann[2], *(1)Citrus College, (2)University of California, Berkeley*

Abstract: Future intelligent systems often envision AI agents that aid users through mixed-initiative interaction. To make such agents effective, an understanding of the ways agents can learn from users' actions and explanations is necessary. To help develop this understanding, this work describes and explores the interactions between an AI apprentice and a human mentor through a series of studies. Prior work in Human Computer Interaction (HCI) typically conceptualizes AI agents as "experts" in narrow domains that observe event streams and offer assistance when they have high confidence about the user's goal and that the agent's assistance will be welcome.This study explores how a computational apprentice can engage in apprentice-style questioning and elicit a deeper and better-connected model of the user's tasks, actions, and goals. Beginning with insights collected from recorded interactions between two humans taking on the role of mentor and apprentice in a programming task, and culminating in the evaluation of an automated AI apprentice, these experiments provide insight into how apprentice agents should be designed, and how their design influences how human mentors use them and feel towards them. Initial results, including observations of recorded interactions between humans, suggest that a multimodal interface consisting of a voice interaction, combined with a code "window" that can be gestured upon, could provide a useful mechanism for AI agents to gather data about the meaning and context of program code as it is written.

Using Computational Models to Predict Reversals in Earth's Axial Magnetic Dipole

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Matthias Morzfeld and Travis Davis*, *University of California, San Diego*

Abstract: We study and build models that we can use to predict reversals, or other drastic events, of Earth's axial magnetic dipole field over time scales of millions of years. We focus on reversals of the dipole, or perhaps other dramatic events during which the dipole strength becomes very low (sometimes called such events are called excursions). We use paleomagnetic observations, simplified models and very complex models to study these questions. The simplified model we use is called G12 model and consists of a set of three differential equations, describing the time evolution of three quantities: the axial dipole, D, the quadrupole, or non-dipole field, Q, and a velocity, V. A reversal in the G12 model is a change in the sign of the quantity D. We present a program that detects reversals (changes in sign) in a time series of D and saves the time instances where reversals occurred. We compare the results with paleomagnetic records that describe the intensity of Earth's axial magnetic dipole over the past 2 Myrs. Additionally, we also search for reversals in outputs of a complex, magneto hydro dynamic (MHD) model.

Development of a Relevant and Self-Updating Slang Corpus

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Joanna Vaklin*; Marcelo Sztainberg; Ishita Verma and Rachel Trana, *Northeastern Illinois University*

Abstract: Slang terminology is abundant in user-generated content on social media platforms. It is a way of expressing societal and cultural experiences and emotions and is complex in that the language has layered meaning and is often not understood at first exposure. In textual analysis that incorporates sentiment detection, it is important to have a feature that considers the effect of slang on the entire text. The goal of our research is to create a slang corpus that identifies the sentiment value of slang terms and maintains its relevancy as new slang words are added. To do this, we collected a set of words and definitions from Urban Dictionary (UD). Because UD is not a curated website, we are developing a preprocessing algorithm to remove nonsensical and irrelevant entries. To accurately label sentiment of existing and new slang terminology, we plan to use an integrated approach of two machine learning algorithms and two existing sentiment detectors, SentiStrength and VADER, applied to the definitions of each word. The two machine learning algorithms, Naive Bayes (NB) and Support Vector Machine (SVM), will be trained on the definitions of an existing slang dictionary, SlangSD. By combining the average score found from VADER and SentiStrength as foundational sentiment values for the new slang definitions with the resulting score from NB or SVM, we can algorithmically annotate new slang. To keep the corpus accurate and relevant, we plan to implement a self-updating process to routinely gather, analyze, and annotate new words and definitions.

Predicting House Price Using Machine Learning

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Orlando Hernandez*[1]; Joshua Westgor[2]; Edwardo Torrez[1]; Manar Mohaisen[1] and Ahmed Khaled[2], *(1)North Eastern Illinois University, (2)Northeastern Illinois University*

Abstract: Machine learning (ML) algorithms teach our machines to learn and make accurate decisions for a wide range of engineering problems. In this project, we utilize the power of ML to design and implement a tool for predicting the prices of

houses according to the different characteristics (e.g., type, size, neighborhood, nearby school rating) of the house. The project is divided into three main stages. The first stage is about collecting data set that is used to build our prediction model and focusing on determining the essential characteristics. Each record in such a set is composed of the house characteristics along with its known price. We considered two cities with differences in home pricing: San Francisco and Las Vegas. The second stage is about cleaning and preparing the collected raw data to avoid data outliers and any bias towards certain characteristics. This includes dropping or filling in missing data, handling redundant information, and normalizing to weight the effect of each characteristic. The third stage is about utilizing the ML linear regression algorithm, among others, to build the prediction model. This step will determine the accuracy, complexity, and generalization ability of the model. This project is built using Python programming language with its powerful data analysis and ML packages. This tool enables the user (buyer and seller) to evaluate a house and view the main aspects that shape the predicted price for more balanced decisions. The model is evaluated verses different accuracy measures, and the developed model achieves high accuracy.

Development of an Interactive Framework for Identifying, Visualizing and Tracking Cyberbullying in Image Memes

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Amanda Bowers*; Sebin Puthenthara-Suresh; Christopher Gomez; Dr. Rachel Trana and Marcelo Sztainberg, *Northeastern Illinois University*

Abstract: Cyberbullying, or harassment on primarily social media platforms on the internet, has evolved from pure text commentary to a variety of other mediums, such as images with embedded text, also called memes. As a part of a larger project to identify and to broadly classify cyberbullying occurrences within the context of social media, our goal is to develop an interactive Flask web application that enables users to identify, visualize, and track cyberbullying in both comments and images. The application provides options for users to input images or text, which are then labeled as cyberbullying or not-cyberbullying using a machine learning model that was recently developed and trained on a diverse YouTube corpus collected within the last year. As part of the identification process, we plan to incorporate a feedback system that allows users to engage in further classification of additional images and text, thus further refining the algorithm, as well as maintaining a relevant and updated database of comments and images. A final component of this application is to develop a visualization of clusters of frequently-used cyberbullying text and memes, which can then help to identify current trends of cyberbullying occurrences. While identifying malicious content in multiple media sources can help to address the harmful impact of cyberbullying, the development of an easy-to-use web application that highlights the evolving nature of cyberbullying could help to educate users on the impact of their online posting choices, thus reducing likelihood of cyberbullying occurrences.

Cyberbullying Identification in Youtube Comments: An Analysis of Topic-Modeling Algorithms for a Multi-Stage Classification Schema

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Sebin Puthenthara Suresh*; Christopher Gomez; Dr. Rachel Trana and Marcelo Sztainberg, *Northeastern Illinois University*

Abstract: Cyberbullying is a broad term for various forms of harassment occurring on the internet. Our project's overarching goal is to develop an easy-to-use framework consisting of a multi-stage classification schema which can automatically detect harassment in text and images. Previous research has prepared a corpus of YouTube comments and used Amazon's Mechanical Turk (MTurk) to label the content as bullying or non-bullying. This data was then used to train and test two classification algorithms, Naive Bayes (NB) and Support Vector Machine (SVM). Further research showed that training these algorithms after grouping the data manually based on topics (body-shaming, sexism, racism, race, politics, a "general" category) further improved the accuracy of classification. As manually categorizing large datasets is work and time intensive, we tested several topic modeling algorithms:Latent Dirichlet Allocation (LDA), Biterm Topic Modeling (BTM), and Gibbs Sampling Dirichlet Multinomial Mixture (GSDMM). To verify our topic-modeling algorithm implementations, we reproduced previous findings for these algorithms using a corpus of Google News titles with 152 different topics. We then evaluated these models on the YouTube cyberbullying dataset and will report on their comparative performance. We will also present results on cyberbullying identification accuracy using both NB and SVM within the clusters identified by each of the three topic modeling algorithms.

Anonyrate Privacy-Preserving Recommender System

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Carlos Degollado*; Isaac Espinoza; Hiram Lin; Marcelo Sztainberg; Ahmed Khaled and Xiwei Wang, *Northeastern Illinois University*

Abstract: Location-based recommender systems present users with attractive options based on their geographical locations. The value attraction is strongly related to a user's previously recorded personal choices. The trade off for good recommender systems is personal information has to be shared with a central server, thus creating a potential privacy issue. Our proposal, built from our previous research on developing an algorithm that would generate recommendations while preserving privacy, defines a new framework where we remove personal information as we build a system in multiple layers.

The 3-tier system consists of user-end mobile apps, a central server, and several aggregate servers that act as a buffer between the first two tiers. It protects users' privacy at multiple levels: users' preferences are anonymously collected via Wi-Fi Direct by aggregate servers which reside at local business entities; these individual preferences are generalized into groups, which are later sent to the central server through the Message Queuing Telemetry Transport communication protocol; and the recommendations are personalized and generated completely on user devices.

We built the app with Android Studio and used physical devices as well as virtual emulators to test our application's connectivity and data transfer. The implementation used algorithms from data mining, machine learning and statistics. Our results show the framework can protect a user's privacy of choice by masking their preferences with that of others. By making this information increasingly challenging to trace back to an individual user, we have prevented any profiles from being created of them through their rating preferences.

Predators and Prey Interactions:Modeling Two Species Behaviors in the Presence of Food Oases and Deserts

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Jason Izui*; Paulo Acioli and Phillip Noffz, *Northeastern Illinois University*

Abstract: Computational modeling offers a means of rapidly recreating a scenario for all kinds of testing. The present work is designed to emulate a system of predators, prey, and plant life under a wide variety of scenarios that occur in the natural world.

These simulations are performed using the Python platform and are based on a three species predator-prey relationship with the intention of accurately modeling the spread of animals over a lush or food scarce environments, such as oases and deserts. Our model allows us to recreate a different set of scenarios including the ability to set parameters of the environment, the species of interest, and of the interaction between species. Methods of modeling the non-numerical interactions between predators and prey for computer application as discussed in literature are presented and tested. We examined how predator and prey species react to situations of pockets of low and high plant growth and determined "equilibrium" population settlement under these circumstances. These results are compared to more continuous models found in other literature. Comparisons include settlement rate and species persistence.

An Automatic Data Processing Pipeline to Reconstruct Coherent 3D Image Volumes from Cardiac Cine MRI Data.

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Rosario Martinez*[1]; Fanwei Kong[2] and Shawn C. Shadden[2], *(1)Long Beach City College, (2)University of California, Berkeley*

Abstract: Computational fluid dynamics (CFD) simulations of left ventricle (LV) flow combined with patient medical imaging data may facilitate a better understanding of cardiovascular diseases so patients can have improved diagnosis and treatments. These simulations usually require geometric models of the heart constructed from patient-specific cardiac image scans. The model reconstruction pipeline includes segmentation and surface reconstruction in 3D and is traditionally a time-consuming process when done manually. Deep learning-based methods can speed up this process. Cine magnetic resonance imaging (MRI) is a conventional image modality that is used for cardiac function evaluation which produces several time-series 2D image slices from different locations of the heart. These images must be reconstructed into a 3D image volume before a deep learning model can utilize it. Thus, we are creating a data processing pipeline that can automatically take in all 2D image slices for a patient and align them to produce a 3D image volume. We propose to apply inter-slice registration to reduce slice misalignment due to the 2D acquisition of cine MRI. The pipeline is validated on a large public data set, Data Science Bowl Cardiac Challenge Data. By converting 2D image slices into coherent 3D volumes, the proposed pipeline facilitates the use of cardiac cine MRI scans by deep-learning-based methods for constructing CFD-ready LV models and may ultimately enhance the treatment of cardiovascular disease.

Employing Machine Learning in the Study of Differential Equations Related to Nuclear Engineering

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Marina Zafiris*, *University of Houston- Downtown* and Katarina Jegdic, *University of Houston - Downtown*

Abstract: Differential equations model a variety of phenomena in sciences and engineering. The main focus of this project is on time-dependent partial differential equations known as conservation laws that are used to model multi-phase flows. In particular, these equations are of interest to engineers who design nuclear reactor pipes to ensure the optimal flow of gasses and liquids. Most of differential equations that describe the real-world phenomena cannot be solved exactly and one has to utilize an approximation method to obtain an approximate solution, such as finite differences. The goal of this project is to utilize machine/deep learning methods in study of conservation laws that model multi-phase flows.

Our project's emphasis is on relatively recent methods for solving differential equations that utilize machine learning and, specifically, neural networks, motivated by the universal approximation theorem. We review two such approaches. In the first approach a trial solution is proposed consisting of two parts – the first part, satisfying the initial/boundary conditions, with no adjustable parameters, and the second part consists of a neural network that is trained to satisfy the differential equation by minimizing the squared error loss. In the second approach, the solution is approximated by a deep neural network, derived using automatic differentiation. This results in a physics informed neural network. Within the two approaches, the common neural network parameters are learned by minimizing the mean squared error loss consisting of two terms. We have found that the machine learning approximation methods yield more accurate results than typical approximation methods.

Automated Quantification of Mosquito Behavior through Object Detection

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Jonathan Lacanlale* and Katya Mkrtchyan, *Cal State University, Northridge*

Abstract: Mosquitoes are historically known as carriers of infectious diseases, often infecting large scale populations. Understanding mosquito behavior may provide insight as to why mosquitoes are attracted to humans. Already, biologists are performing experiments in attracting mosquitoes to various odors, however quantifying the amount of mosquitoes attracted to an odor can be a laborious, time-consuming task as mosquitoes are small and difficult to track. We hypothesize that machine learning models can produce an accurate object detection system capable of quantifying mosquitoes on a frame-by-frame basis. We expect that this system can accurately count the amount of mosquitoes present and that the result will be close to a manually-counted ground truth. For our experiment, we utilize the videos recorded by biologists to construct a large dataset of 4000+ mosquito and non-mosquito images, and use these images to train our machine learning model. We then test this model on a given video, recording the accuracy of detection, detection time elapsed per frame, and detection time elapsed for the entire video. As an additional measurement of accuracy, we selected 1000 random frames from the video and manually counted the mosquitoes present, comparing the total produced by our model and our manual counts. Overall, we found that our model achieves an accuracy of 90%, with a deviation +/-1 from the ground truth. With this, we conclude that our object detection system is capable of quantifying mosquitoes, and that the usage of such systems can provide assistance in understanding mosquito behavior.

A Machine Learning Approach to Routing Information on a Satellite Network

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Huanxi Liu, *University of California, San Diego*; Anthony Meza, *University of California, Irvine*; Christina Tran*, *Harvard University*; Hwai-Liang Tung, *Brown University* and Thomas Merkh, *University of California, Los Angeles*

Abstract: Satellite networks are used for tasks such as GPS and communications. To perform these efficiently and reliably, suitable algorithms must be developed to decide how a packet of information should travel from satellite to satellite to reach its destination. Traditional algorithms direct packets on the calculated shortest path, but these cannot adapt to changes in satellite connections as they leave and re-enter service range. Furthermore, in a high-traffic network, they cause congestion in a few center satellites while underutilizing periphery satellites, slowing delivery time of these packets. We hypothesize that using machine learning to teach a satellite network how to route packets will result in faster delivery and less congestion.

To test this, the machine learning algorithm first randomly sends packets and is given a reward based on how much closer the packets get to their destination and how much congestion it causes. Based on these rewards, it estimates a quality value, or Q-value, for each possible routing decision. After it has sufficiently learned about the satellite network, it can choose actions based on the highest Q-value.

This newly trained algorithm, termed Q-Routing, lowers congestion on satellite networks by over 20%. This, in addition to learning the network's patterns of connection disruption, allows Q-Routing to deliver information faster than the traditional shortest path algorithm.

Q-Routing allows satellite networks to smartly avoid congestion and adapt to disappearing connections. Ultimately, these results can be used to improve the transmission framework of existing satellite systems and thus create faster, more reliable services.

Exploitation of Stationary Iot Cameras for 3D Modeling of Dynamic Objects

Discipline: Computer & Information Sciences
Subdiscipline: Other Computer and Information Sciences

Hector Delgado Marquez*, *California Polytechnic State University* and Steven Leung, *Air Force Research Laboratory*

Abstract: Structure from Motion (SfM), a technique of photogrammetry for 3D point cloud & surface reconstruction from image collections, has been notably used for the modeling of landforms and other static objects while offering comparable results to LiDAR-generated models at a fraction of the cost. SfM depends on prominent features in the 2D image sets to estimate geometry and point clouds, which limits the process modeling to static and quasi static environments. Considering this limitation, we propose two processes for modeling dynamic objects, such as a moving car or object, with a set of stationary cameras. To address the challenge of prominent features in the background of image sets that could distort geometric estimations from SfM, we completely removed image backgrounds and isolated our regions of interest, as well as removed glare/reflections visible on the object's surface. These two additional processes alone improve point cloud and surface model accuracy compared to the unprocessed 2D image sets.

Tuning Nanoparticle Interactions with Cells in the Brain with Peptide Physicochemical Surface Engineering

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Lauren Waggoner; Marianne Madias; Alan Hurtado* and Ester Kwon, *University of California, San Diego*

Abstract: Brain disorders are highly prevalent but lack viable treatment options. Cell-specific therapeutic development is challenging due to the structure and complexity of the brain microenvironment. Nanoparticle-based therapeutics are promising tools for cell-specific delivery as their surfaces can be engineered with targeting ligands, antibodies, and peptides to engineer their pharmacokinetics. Peptide-modification of nanoparticle surfaces is of particular interest due to the bioactivity and versatility of peptides. However, it is unclear how physicochemical properties of peptide-modified surfaces influence nanoparticle interactions with cells. To understand how the surface properties of peptide-modified nanoparticles influence nanoparticle-cell interactions, we designed a set of peptides with different physicochemical properties. We synthesized a nanoparticle library that display these peptides on their surfaces. In an analysis of the physicochemical properties of the nanoparticles using dynamic light scattering, we found that nanoparticles adopted the physicochemical property of the peptides on their surface. For example, nanoparticles with basic peptides on their surface led to nanoparticles with positive surface potential. We applied these nanoparticles into cell culture systems representing brain-specific cell types (neurons and microglia), and found that peptide-modified nanoparticle association was dictated by charge, with positively charged nanoparticles showing increased association with both cell lines compared to negatively charged or neutral nanoparticles. When injected into a healthy murine brain, peptide physicochemical properties had no influence on nanoparticle association with cortical microglia and minor influence with cortical neurons. Understanding how nanoparticle surface properties dictate their interaction with brain cells can inform the development of nanoparticle-based or virus-based cell-targeted therapies for brain disorders.

A Computational Model to Evaluate the Therapeutic Efficiency of an Adhesive Epicardial Patch for Tunable Mechanical Reinforcement.

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Diego A. Quevedo Moreno*; Claudia E. Varela and Ellen Roche, *Institute for Medical Engineering and Science, Massachusetts Institute of Technology*

Abstract: A heart attack or myocardial infarction (MI) occurs when the blood flow to a region of myocardium is interrupted. The damaged or infarcted zone loses its ability to contract resulting in mechanical disadvantages, adverse remodeling, and ultimately progression to heart failure (HF). Suturing patches to the epicardium for mechanical reinforcement has proven to be a promising preclinical strategy to prevent HF progression. Although a variety of patches have been studied, understanding how cardiac function is impacted by the 1) degree of mechanical reinforcement a patch can exert, and 2) patch-tissue coupling strategy which is typically achieved via sutures at discrete points or an adhesive applied globally to the surface, is warranted. To address this, we developed a computational model to evaluate how coupling and mechanical properties of a customized epicardial patch impact ventricular wall stress distribution and resulting cardiac function. First, we characterized the correlation between manufacturing parameters and patch mechanical properties and identified a mechanical reinforcement range. Next, patch designs with a low, medium, and high degree of reinforcement were coupled to a computational model of the left ventricle with MI, either by discrete points or by surface adhesion, and finite element simulations were conducted. We hypothesize that our simulated cardiac function parameters will match those of experimental data and different levels of reinforcement and coupling will modulate cardiac performance post-MI. The computational model developed in this study will serve as a versatile *in silico* tool to study and optimize reinforcement strategies for the treatment of post-MI HF.

iPSC-Derived Cardiomyocyte Model to Investigate Stretch-Responsive Signaling Pathways Involved in Hypoplastic Left Heart Syndrome

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Alyssa Salazar*[1]; Mallory Lennon[2] and Jeffrey Jacot[2], *(1)University of Colorado, Denver, (2)University of Colorado, Anschutz Medical Campus*

Abstract: Hypoplastic left heart syndrome (HLHS) is a congenital heart defect that results in the underdevelopment of the left ventricle, mitral valve, aortic valve and ascending portion of the aorta. This reduces the heart's ability to pump oxygenated blood through the body and is fatal without immediate intervention. For the majority of cases, the causes of HLHS is unknown. However, at a phenotypic level, cardiomyocyte (CM) deficiencies, such as cell function and structure, have been observed in HLHS. Given that CMs must respond to biomechanical stretch for proper heart development, we hypothesized that disruption of mechanical signaling pathways in CMs are responsible for the defects observed in HLHS. In order to test this hypothesis, we compared the stretch-induced proliferative and morphologic response of human iPSC-derived immature cardiomyocytes from infants with HLHS and controls with typical heart structure. CMs were differentiated using small molecular inhibitors impacting Wnt signaling and purified by glucose starvation. CMs were stretched for 48 hours at 10% strain at 1 Hz. Total cell area and proliferation rates were analyzed using ImageJ (NIH). Our results indicate that there was not a significant difference in proliferation rate or cell area between healthy control iPSC-CMs and HLHS CMs. Thus, stretch responsive signaling may not have an effect on the development of the defects observed in HLHS. Future experiments studying CM response to additional biomechanical stimuli, such as substrate stiffness, will provide insight into how HLHS develops and could lead to new therapies for the treatment or prevention of HLHS.

Identifying and Validating Wolbachia-to-Arthropod HGT Events

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Serafina Nieves* and Russell Corbett-Detig, *University of California, Santa Cruz*

Abstract: *Wolbachia* are gram-negative bacteria that frequently infect arthropods and form endosymbiotic relationships with the host (Werren 1997). Due to the close proximity of *Wolbachia* endosymbiont genomes and arthropod host genomes, horizontal gene transfer (HGT) has been shown to occur from *Wolbachia* to the host in several organisms, including mosquitoes, flies, aphids, and wasps (Hotopp 2011). However, studies documenting the presence of *Wolbachia* HGT in arthropod genomes are limited to a few species that have shown extensive transfer. We developed a high-throughput bioinformatics workflow that can identify and validate putative HGT events using publicly available sequence data. Using our comprehensive screening process, we found 1673 putative horizontally transferred protein coding sequences across 16 species, most of which do not have documented *Wolbachia*-to-arthropod HGT events. We also developed a method to validate these *Wolbachia*-to-host insertions using available whole genome sequencing data to compare the depth of coverage of putative *Wolbachia* insertions to coverage of exons in the host genome. We found that *Wolbachia*-to-arthropod HGT events may be more common than current literature, or lack thereof, seems to suggest.

Electrical Stimulation to Enhance Neural Stem Cell Proliferation and Differentiation

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Peyton Hamel* and Donald Sakaguchi, *Iowa State University*

Abstract: The brain and retina can be severely damaged by a number of conditions including physical trauma and neurodegenerative diseases resulting in irreparable damage to nerve cells. The very limited regenerative capacity of the central nervous system (CNS) makes it especially important to develop experimental strategies for brain rescue and repair. Electrical stimulation is a novel approach that may be useful to differentiate neural stem cells for cell-based therapies directed towards brain and retina repair. The goals of my research project are to study how electrical stimulation influences the proliferation, differentiation, and regenerative capacity of neural stem cells. This project utilizes graphene-based conductive and biodegradable poly-L lactic acid scaffolds designed for electric field stimulation. In this study I will examine different stimulation parameters (magnitude of the electric field (100-200 mVs) and stimulation duration (5 -15 minutes)) in order to identify optimal parameters for the electric field stimulation on retinal and brain neural stem cells. Through devising strategies for optimal neural stem cell differentiation via electrical stimulation, this study includes immunofluorescence labeling to identify specific cell types after stimulation. Currently, we are determining the best set of antibody makers to determine the types of cells that are differentiating from the neural stem cells. After devising an effective strategy for electrical stimulation for neural stem cell differentiation, future studies will aim to develop methods to effectively implant cells into rodent models of retinal degeneration or neurodegenerative diseases, where these stem cells will hopefully grow and repair the complementary tissues.

Quantifying the Functionality of the Gracilis Collateral to Assess Potential for Diameter Growth

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ada Tadeo* and Trevor Cardinal, *California Polytechnic State University San Luis Obispo*

Abstract: This research investigates the role of myoblast cells in enhancing arteriogenesis, the outward remodeling of pre-existing vessels. Muscle progenitor cells (i.e. myoblasts) are transplanted near the collateral bypass arteries in mice whose

femoral artery is ligated- to mimic the blockage that occurs in patients with ischemic diseases. Seven days after the operation, the hindlimb muscle containing the collateral bypass arteries is exposed and prepared for imaging. To quantify the functionality of the collateral arteries, pictures of the arterioles are taken from both the operated hindlimb and the sham side. Photos of the arteriole's resting state, electronically stimulated state (functionality), and chemically stimulated state (sodium nitroprusside, vasodilator, and norepinephrine, vasoconstrictor) are then used to measure the vessel diameter. The percent difference of the vessel diameters between the resting state and the functionally vasodilated state, show the potential for growth. In my research, the arterioles on the operated side showed close to 0% difference whereas the sham side showed roughly a 90% difference. This data suggests that the arterioles in the muscle whose femoral artery had been ligated have undergone arteriogenesis and the vessel sits in its maximum diameter. In future research, mice with diet induced obesity (DIO mice) would be used rather than lean mice in testing for this potential therapy, to more accurately represent the patient. These results can ultimately lead to the development of an alternative, minimally invasive, therapeutic product to treat patients with ischemic diseases that would benefit from natural bypass enlargement.

Incorporation of Decellularized Bovine Bone into PEGDA Scaffolds

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Durante Pioche-Lee*; Christina Salas; Marissa Perez; Lorraine Mottishaw; Christopher Buksa and Matthew Rush, *The University of New Mexico*

Abstract: Bone grafting, a surgical technique used to rebuild and repair damaged bones, has been performed over 1.5 million times annually. However, limited tissue donors and possible secondary complications associated with transplantation means that bone tissue engineering researchers are currently investigating and developing materials that can imitate the environment and strength of natural bone. This research examines poly(ethyleneglycol-diacrylate) (PEGDA), as a biomaterial scaffold, with microsized decellularized bovine bone (DBB) additives. DBB was added to increase mechanical compressive strength and bioactivity of the scaffold, but it has been shown to decrease the mechanical strength of the scaffold due to void creation within the PEGDA network. We hypothesize that functionalizing DBB with (3-Aminopropyl)triethoxysilane (APTES) and acrylic linkers (acrylic acid N-hydroxysuccinimide ester) will create a more homogeneous bone distribution and load-bearing structure with the bone crosslinking to the PEGDA. By using scanning electron microscopy (SEM), the results indicate that the functionalized DBB creates less voids within the PEGDA and increases the uniform inclusion of the microparticles. An increase in cell adhesion and viability of NIH 3T3 cells was shown when tested with Immunocytochemistry (ICC) staining and Live/Dead assay compared with PEGDA alone. A Mechanical Testing System (MTS) will be used to observe how the addition of functionalized DBB affects the scaffold's compressive mechanical strength. In addition, Fourier Transform Infrared Spectroscopy (FTIR) will be used to confirm the functionalization process of bone.

Development of a Portable, Phone-Operated, and Cost-Effective Digital Light Processing (DLP) 3D Printer

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Luis Santiago Mille*; Yu Shrike Zhang; Wanlu Li; Juan Robledo; Tlalli Uribe and Valentin Huerta, *Division of Engineering Medicine, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School*

Abstract: As an additive manufacturing technique used to fabricate complex structures, three-dimensional (3D) printing has been used in a variety of different fields. Digital light processing (DLP), as a major vat polymerization printing technique, has the ability to create high-resolution constructs. However, the dimensions of devices using this kind of technology and their high cost hinder their expansion into other fields or applications. In this study, a precise, portable, and cost-effective 3D printer was built based on visible-light DLP technology. The manufacturing of the device's structure was based on accessible components and materials, including acrylic, metal rods and PLA printed structures. Commercial microcontrollers and optic elements were also used. The system provides a phone-based and friendly mobile interface that allows the user to print high-resolution constructs for design and biomedicine applications. The printer has a speed of 96 $\mu m\ s^{-1}$ and enough resolution to print 5-10 mm long hollow channels (d = 1 mm) made with poly(ethylen glycol) diacrylate (PEGDA, 40% w/v) without supports. Porous scaffolds, channels, and constructs with surface details were successfully fabricated by the developed printer, using commercial resin, PEGDA, gelatin methacryloyl (GelMA), and allylated gelatin (GelAGE). The 3D printer also showed the ability to produce 3D scaffolds to encapsulate cells, which can be applied to model vascularized tissues using human umbilical vein endothelial cells (HUVECs) or mimic complex physiological structures accurately. With this kind of technology, the efficient fabrication of microstructures will be wider available allowing further advances in science and technology.

Lymphoid Immune Cells and Toll like Receptors Regulate Therapeutic Response in Human Lymphomas

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Nicole Felix Velez*; Shivem Shah and Ankur Singh, *Cornell University*

Abstract: Activated B-cell Like Diffuse Large B-cell Lymphoma (ABC DLBCL) is a type of Non-Hodgkin's Lymphoma in which 40% of patients are not curable with current therapies. Its pathogenesis has been linked to constitutive activation of the B-cell receptor (BCR) pathway, as well as the crosstalk of the BCR with the Toll like receptor (TLR) pathway. Within the BCR pathway, there is particular interest in MALT1 (Mucosa-associated lymphoid tissue translocation protein 1), an activator of the NF-κB pathway. Therapeutic inhibitors targeting MALT1 are used to treat ABC DLBCL, however, due to its genetic heterogeneity and the complex growth and signaling provided by the tumor microenvironment (TME), there exists discrepancies in drug response. Currently, there are no *in vitro* systems to understand how microenvironmental cues affect TLR signaling and MALT1 therapeutic inhibition. Here, we used an engineered maleimide-functionalized 4-arm polyethyleneglycol (PEG-MAL)-based lymphoid tissue to determine the impact of immune cell signals and TLRs on MALT1 signaling and therapeutic inhibition. These hydrogels encapsulated human DLBCL lines or patient derived xenografts along with other immune cells. Tumor survival, protein expression, and activity was studied with biochemical assays and flow cytometry. We found that human ABC-DLBCL cell lines responded to MALT1 inhibition with MI2 in an integrin-ligand dependent manner and that the presence of immune cells affected tumor progression and drug resistance, specifically through changes in MALT1 expression. With this 3D-microenvironment mimicking key lymphoid, we can understand how the TME affects complex signaling pathways in ABC DLBCL and inform the selection of patient-specific treatment plans.

Comparison of Plantar Pressure on Different Foot Prostheses in Non-Amputees during Locomotion

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jacqueline Puga*[1]; Rebeca Sicairos[2]; Aurora Alvarado[2]; Beatriz Alemon[2]; Carlos Huegel[2] and Bryan Cornwall[1], *(1)University of San Diego, (2)Tecnologico de Monterrey*

Abstract: Active foot amputees (AFA) refer to persons with foot amputation that have an active lifestyle. Due to the availability of different foot prostheses, prosthetists prescribe the ideal foot prostheses for each amputee. The use of different foot prostheses can lead to variations on the AFA's plantar pressures during gait. Uneven distribution of plantar pressure may lead to asymmetric patterns while walking. The aim of this study is to compare the plantar pressure between foot prostheses during locomotion. To simulate the AFA's prosthesis use, non-amputee volunteers, wear an Orthopedic Boot System that has attached the foot prostheses. The Solid Ankle Cushion Heel (S.A.C.H.) prosthesis is attached to the left orthopedic boot, while the articulated foot prosthesis is attached to the right orthopedic boot. The immobilization of the participant's ankle allows mobility only from the prosthesis, rather than from their natural ankle albeit with an exaggerated tibia length. Dynamic plantar pressure data is collected using the Tekscan F-Scan in-shoe measurement system as participants carry out 3 exercises: sit to stand, one-legged stance, and walk. Data is obtained while participants wear the same athletic shoes and walk at a self-selected speed for 3 m. The data obtained through the Tekscan F-scan serves to analyze peak pressure (PP), center of force (COF) trajectories, and to find similarities or differences between each foot prostheses. Results showed that the articulated foot prosthesis presents a smoother pressure distribution during walking in comparison to the S.A.C.H. foot; as well as more similar COF trajectories to the non-amputee gait.

Optimization of Manufacturing Conditions to Generate Induced Pluripotent Stem Cell-Derived Mesenchymal Stromal Cells

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Karen Mancera Azamar* and Ross Marklein, *University of Georgia*

Abstract: Mesenchymal stromal cells (MSCs) have the potential to modulate inflammation and are currently being explored in human cell therapies for the treatment of immune diseases such as osteoarthritis, diabetes, and Parkinson's disease. However, MSCs can lose their immunomodulatory potential during expansion, thus, having a limited lifetime in culture. Additionally, MSCs derived from different donors, tissues, and manufacturing conditions exhibit functional heterogeneity that can be reflected by differences in morphology and function. Induced pluripotent stem cells (iPSCs) have the ability to replicate indefinitely and differentiate into any cell type, thus making them an attractive and potentially limitless source of differentiated MSCs. There are currently no standardized methods for manufacturing MSCs from iPSCs (iMSCs) with consistent, reproducible properties. This study aims to optimize a protocol for the manufacturing of iMSCs by improving the post-thaw recovery and differentiation process. Post-thaw iPSC recovery variables measured include cell density plated, recovery drug type and concentration, and time. Results quantified cultures based on pluripotency or MSC marker staining, and area covered by cells per well i.e. confluency. RevitaCell and Y-27632 drug concentrations were compared and resulted in Y-27632 yielding higher percent confluence. Specifically, recommended concentrations of Y-27632 drug yielded a similar percent confluence to lower concentrations. Anticipated results should reflect a decrease in pluripotent markers and an increase in MSC markers as differentiation progresses, otherwise further identity characterization will be conducted. Optimizing a protocol would improve cell manufacturing and facilitate translation of large-scale iMSC expansion for promising therapeutic applications.

Wireless, Non-Invasive Force-Inducing Neuronal Stimulation Mediated By Magnetic Nanodiscs

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Claudia Collier*; Rohini Thevi G.V. and Gabriela Romero, *University of Texas at San Antonio*

Abstract: Parkinson's disease is a neurodegenerative disorder that affects the dopaminergic neurons and leads to plastic changes in primary cortex networks that can lead to a loss of control in body movement. The existing therapies that offer the ability to control neural activity result in poor treatment response and adverse drug effects. Our area of study is using magnetic nanodiscs (MNDs) under alternating magnetic fields (AMFs) for heat dissipation, which recently have been studied to control cellular signaling wirelessly. The goal of this project is to develop a novel wireless, non-invasive, and cell specific platform that allow for modulation of neuronal activity by transducing AMFs into mechanical stimulus. To conduct this experiment, Cortical neurons from newborn rats were extracted, transfected with a mechanosensitive ion channel eMscL, and combined with MNDs composed of permalloy and gold functionalized with a biocompatible polymer (POEGMA). Then Fluo-4 calcium imaging was performed on primary neurons under AMFs stimulation (6 Hz and 20 mT) using a custom designed electromagnet system. We were able to successfully passivate the surface of MNDs with a POEGMA coating. We found that the minimum concentration of MNDs to evoke mechanotransduction in neurons was 6 MNDs per cell, which is the number of MNDs needed to exceed the 1 pN force threshold for activation of mechanosensitive ion channels. In this study we develop a wireless strategy for neural modulation by transducing magnetic signals into mechanical stimulus and can be instrumental for the treatment of neurological diseases and mapping brain circuits.

A Three-Dimensional Convolutional Neural Network to Predict Fluorescent Protein Maximum Emission Wavelengths

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Michelle Garcia*[1]; Aiden Aceves[2] and Steve Mayo[2], *(1)Pomona College, (2)California Institute of Technology*

Abstract: The scarcity of far-red emitting fluorescent protein (FP) monomers is a major limitation for live-tissue imaging, where the near-infrared window is favorable for light penetration and necessary for deep imaging. The comparably smaller energy difference between the transition of HOMO and LUMO states in far-red FP fluorophores ensures a reduction of autofluorescence, light-scattering, and phototoxicity. In this work, we endeavor to contribute to the array of fluorescent protein monomers with peak emission wavelengths between 650nm to 700nm by creating a three-dimensional convolutional neural network to predict FP maximum emission wavelengths given a molecular structure. We use TensorFlow, an open source machine learning platform, and neural-network library to build Keras models consisting of 3D convolutional and pooling operations. Inspiration for network architecture was drawn from modern state-of-the-art networks from other domains such as image classification, medical image segmentation, lesion detection, and image reconstruction. While considering various potential architectures, hyperparameters such as learning rate, number of epochs, batch size, and more were automated using TensorFlow's Hparams module and performance was visualized with TensorBoard; all computations were conducted on the Caltech High Performance Cluster. After training models on data from extant public databases, we will execute in-silico sequence perturbations and input the augmented molecular models into the network. In addition to evaluating proteins with potential for subsequent synthesis and characterization, these experiments shed light on the use of three-dimensional convolutional models for the automated learning of features relevant to functional properties of biomolecules.

Maximizing Magnetic Heat Transduction for Fast Remote-Control of Temperature-Sensitive Ion Channel TRPV1

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Josiah Lozano*; Rohini Vishwanath and Gabriela Romero, *University of Texas at San Antonio*

Abstract: Nearly 20 million Americans suffer from neurological diseases and roughly one million new cases are reported annually. Current methods for treating neurological disorders involve the manipulation of neural signaling via application of drugs or the use of implantable devices in the brain. While these treatments have demonstrated a certain degree of effectiveness, the associated costliness and invasiveness have led to research in alternative therapies. Recently, there has been an increasing interest in the use of heat dissipation via magnetic nano-particles (MNPs) and alternating magnetic fields (AMFs) to manipulate neural circuitry as an alternative form of therapy. The successful application of MNPs and AMFs has been demonstrated through the excitation of the receptor TRPV1 , however this technique still requires optimization to ensure local and cell-type specific manipulation of biological signals. The purpose of this project is to accomplish the following specific aims: (1) Expose cells expressing TRPV1 to AMFs and MNPs using pre-existing lab procedures, (2) record cell activity in real time to determine effectiveness of each MNP in the transduction of AMFs into heat, (3) correlate neural activity response with magnetic nano-particles physical properties. We expect to evoke activity in cells expressing TRPV1 via the MNPs transduction of AMFs into heat and we hypothesize that cubic MNPs will be better transducers compared to spherical MNPs due to shape anisotropy. This study will serve to further refine and optimize the use of MNPs and AMFs to treat neurological diseases. Partially funded by NIH ESTEEMED 5R25EB027605

Novel Modeling of the Abdominal Aorta for Nano-Robotic Surgical Testing

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Tristan Pepper*, *The University of Texas at San Antonio*; Sergio Montelongo, *University of Texas at San Antonio*; Dimitrios Miserlis, *The University of Texas Health Science Center at San Antonio* and Teja Guda, *Department of Biomedical Engineering and Chemical Engineering, University of Texas San Antonio*

Abstract: Cardiovascular disease and sequelae such as plaque build-up within major arteries presents a major healthcare burden to the global community. Current solutions include lifestyle therapies, cholesterol medication, and in extreme cases, surgical interventions placing coronary stents or performing bypass surgeries. Risk factors and complications with surgeries remain high and depend on the location of constriction. We hypothesized that robust modelling of the aortic system will result in superior surgical outcomes. The purpose of this study was to develop patient specific arterial flow models, known as bioreactors, to train surgical interventions, including robotic surgery and intelligent navigation systems. Patient-specific contrast enhanced CT scans were rendered using Meshmixer and modeled in Fusion 360 for 3D printing. The 3D model was magnified by a factor of 4, dilated by wall thickness, printed hollow using ABS filament and used to create a paraffin wax cast of the abdominal aortic anatomy. The paraffin cast was then used to maintain inner structure in a transparent resin casting and melted out to create the bioreactor flow chamber. A rotary peristaltic pump simulated the fluid perfusion through the anatomical replica. Future studies will compare the perfusion bioreactor results to computational fluid dynamics modeling of the same architecture (using FEBio Studio). The ratified proof of concept will be expanded to a cohort of 21 patient anatomical scans, of different locations of the arterial tree most commonly needing atherosclerotic lesion correction. If such models prove beneficial for surgical intervention training, they may reduce mortality in complex cardiovascular surgeries.

Simulating and Mathematical Modeling of Vascularization in Bone Tissue Engineered Scaffolds

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Yohannes Akiel*, *University of Texas at San Antonio* and Teja Guda, *Department of Biomedical Engineering and Chemical Engineering, University of Texas San Antonio*

Abstract: The field of tissue engineering has shown tremendous progress in being able to successfully regenerate damaged bone. Some of the many ways to accomplish this are by using allografts, autografts, and scaffold-based synthetic graft materials. Scaffold-based tissues have shown great potential because of patient-specific customizability, minimal immune response, and no requirement for secondary donor tissue. Although scaffold-based tissues have shown promise, the main limitation is insufficient vascularization of the scaffolds post-implantation. A solution to this is to optimize the scaffold pore size and architecture to allow for greater and more rapid vascularization, but how to optimize the scaffolds has not yet been fully understood. We hypothesized that the rate of vacularization is determined by (1) distance of a vessel from the scaffold surface, and (2) size of the connections between pores. The purpose of this study is to develop a computational approach using Febio and AngioFe software to simulate vascularization and network development in a vessel fragment seeded scaffold. With this software, properties such as porosity, mechanical loading, vessel seeding and vessel growth rate in a matrix mechanics dependent manner can be analyzed to determine which scaffold properties simulate the best vascularization. A mathematical model to support these simulations has been previously determined by experimental validation. Once the properties promoting maximal network growth are determined, they can then be translated to the design of improved biomaterial scaffolds. This computational approach can aid in understanding the effects of the different properties mentioned earlier on vascularization and thus, on successful bone regeneration.

Development of a Pharmacodynamic Model for the Antimalarial Drug Artemisinin Needed to Reduce ***Plasmodium Falciparum L*****oad**

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ana Ibarra* and Brad Reisfeld, *Colorado State University*

Abstract: Malaria is a global health epidemic resulting in the deaths of nearly half a million people per year. The malaria parasite, which is transmitted by mosquitoes, infects hepatocytes in the liver and then damages red blood cells and their oxygen binding capacity. The World Health Organization recommends the drug artemisinin as part of the combination therapy for uncomplicated malaria. Although numerous clinical trials and research studies have focused on this drug, there is insufficient understanding of its disposition and mechanism of action to quantify the relationship between dose and parasite killing potential. Furthermore, there is limited information available about how the parasite affects oxygen binding availability through red blood cell destruction. The present study was aimed at the beginning to address these gaps by (i) collecting data from the literature related to how the dose of drug affects the parasite killing potential and the extent to which the parasite compromises oxygen binding potential, (ii) using the data to develop a mathematical pharmacodynamic model to predict how the amount of drug, coupled with the clearance owing to the immune system, affect parasite clearance, and (iii) extending the model to predict how various dosing regimens affected parasite load and oxygen levels.

Such a model is expected to be critical in the characterization of the role of parasite loading on oxygen availability in malaria patients and, ultimately, in the development of rational artemisinin-based drug therapies to treat this devastating disease.

Characterizing Cytotoxicity of a Novel Tendon Lubricant for Clinical Use

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Jannet Rivera*; Anne Gingery and Peter Amadio, *Mayo Clinic*

Abstract: Flexor tendon repairs are often complicated by the formation of adhesions post-surgery. These adhesions limit finger motion and hand function. While additional surgery, in the form of tenolysis, can remove the adhesions, such procedures are only successful roughly half the time. Thus, a treatment to both reduce adhesions primarily and to reduce recurrence of adhesions after tenolysis would be clinically helpful.

We have developed a lubricant based on two components in common clinical use, gelatin and hyaluronic acid (HA), that covalently bonds to the tendon surface with a carbodiimide (cd) reaction. This carbodiimide crosslinked hyaluronic acid and gelatin (cd-HA-gel) has functioned well to reduce adhesion formation and improve tendon gliding in a large animal model, but the mixture was also shown to have a negative effect on overall tendon healing. Therefore, the purpose of this study was to investigate the cytotoxicity of cd-HA-gel in vitro. Cell viability was measured and compared between human fibroblast cells that were cultured in media conditioned with cd-HA-gel and cells cultured in unconditioned media. The trypan blue assay demonstrated that cells treated with the conditioned media had an average viability of 86.3%, while the control cells had an average viability of 96.6%.

These preliminary results suggest that the cd-HA-gel mixture is toxic for cells. This could offer an explanation as to why the gel led to poor healing when tested in vivo. We are currently working to further validate these results with a secondary cell viability assay.

Septum Mechanical Testing Data Analysis and Histology Image Quantification

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ambrina Abbasi*, *University of Colorado at Boulder* and Zhijie Wang, *Colorado State University*

Abstract: The heart pumps blood throughout our bodies, and in order to do so, the cardiac tissues of the organ must be continuously able to contract. The heart has four chambers: two atria and two ventricles. Each ventricle contains a free wall and shares the septum, which is the structure that divides the two ventricles. Previous studies have been done on the ventricular free walls, and reported that they have different anisotropy, and thus may contribute to pumping differently. However, no research has been done to study these passive biomechanical properties of the septum tissue. Understanding the properties of the septum tissue will lead researchers one step closer to understanding the structure-function relations of the septum and how this may change in disease. When heart failure occurs, the mechanical properties of the heart are altered and understanding the passive mechanical properties of the different parts of the ventricles is crucial in order to study the remodeling that occurs in pathophysiology.

For this study, biaxial mechanical testing will be conducted on the septum tissue of animal hearts. During biaxial tensile mechanical testing, the tissue undergoes a fixed displacement while deformation and force are recorded. Tissue deformation, tracked by a camera taking pictures every second, will be converted into Green strain using an in-house MATLAB code. The force, measured by load cells, will be converted into Cauchy stress. Then, Green strain-Cauchy stress curves will be produced. Histology image analysis will then be conducted to assess cardiomyocyte size and collagen angle and content.

Matrix Stiffness and Applied Pressure Dictate Capillary Network Formation in Tissue Engineering Scaffolds

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Mistica Lozano Perez*[1]; Gennifer Chiou[1]; Joo Ong[1] and Teja Guda[2], *(1)University of Texas at San Antonio, (2)Department of Biomedical Engineering and Chemical Engineering, University of Texas San Antonio*

Abstract: Critical size bone defects are injured volumes of bone that are often too large for the surrounding bone to regenerate of its own accord. Much research has been conducted to support the use of porous, osteoconductive, biomaterial scaffolds either by themselves, or seeded with mesenchymal stem cells (MSC) to aid bone regeneration in large defects. Ceramics such as calcium phosphates, polymers such as polyurethane, polycaprolactone and poly-propylene fumarate and natural materials such as collagen and chitosan have all shown great promise in manufacturing scaffolds for orthopedic regeneration. In this study, we propose culturing MSCs in polyurethane foams of different pore sizes infiltrated with a fibrin gel matrix, all of which have shown the potential to support regeneration and integration, while being mechanically much softer than native bone matrix. We hypothesize that larger pore sized scaffold result in an effectively softer substrate and poorer cell growth and proliferation rate, despite greater nutrient and oxygen availability. To test our

hypothesis, PUR foams with different pore sizes will be created by varying the water composition in the urethane polymerization mixture, and seeded with MSCs and cultured for 28 days. The outcomes measured will include cell proliferation, metabolic activity, osteogenic differentiation and genetic markers of hypoxia (HIF1a), as well as evidence of mineralization. This research will provide insight into effective methods to culture and seed MSC in vitro and enable the design of optimal pore sized scaffolds that promote maximal cell attachment and growth, and hence improve chances of bone regenerative success.

Quantifying Disruption in Dry Powder Flow through Dry Powder Insufflation (DPI) Device

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Alexandro Lopez[*1]; Carlos Ruvalcaba[2]; Lisa Tell[1] and Jean-Pierre Delplanque[2], *(1)University of California, Davis, (2)University of California Davis, Mechanical and Aerospace Engineering*

Abstract: Aspergillus fumigatus, a common fungus, usually inhaled as a spore causes aspergillosis, a fungal infection that severely impacts rehabilitated avian wildlife. Treatment of this infection in avian patients is typically done prophylactically through oral administration of itraconazole. However, this treatment is unable to distribute sufficient amounts of anti-fungal medication to pulmonary parenchyma, leaving patients with continued susceptibility to aspergillosis. The inability to prevent this fungal infection from developing is a paramount because treatment is typically unsuccessful once the infection is contracted, quite possibly resulting in death of the bird. Our research team—the Delplanque Research Group in collaboration with Prof. Lisa Tell's laboratory—has developed a dry powder insufflation (DPI) device to address this issue by distributing amphotericin B intratracheally, allowing for a greater deposition of the medication into the respiratory tract of birds. The physio-chemical properties of the medication render it susceptible to agglomeration which disrupts the flow. As a result of these properties, our device is unable to bilaterally distribute the medication. To better understand this issue and its implications, we are developing a quantitative experiment that will measure pressure changes inside the dry powder insufflation device. Building a more comprehensive understanding of the underlying physical properties that limit our success will allow for more positive results: greater deposition efficiency and a more uniform bilateral distribution.

Pressure Generating Capacity of the Diaphragm Is Compromised during Forceful Efforts at High Lung Volume in Dogs

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Nora Rodriguez[*1]; Aubri Ford[1]; Violet Kimble[1]; Shari Wynd[2] and Aladin Boriek[1], *(1)Baylor College of Medicine, (2)Texas Chiropractic College*

Abstract: We wondered whether the pressure generating capacity of the diaphragm is compromised due to loss of curvature or maximal muscle contraction. Radiopaque markers were placed along three nearby muscle fibers in the midcostal diaphragm in six dogs (7- 8.6 kg). Using biplane fluoroscopy, locations of the markers were determined during quiet breathing and inspiratory efforts at lung volumes from functional residual capacity (FRC) to total lung capacity (TLC). Pressure-length relationships of mid costal diaphragm muscle fibers were measured in supine and prone postures. Three-dimensional software modeling techniques were used to compute volume displacement (VD) and surface area of the mid costal diaphragm and lower three ribs during inspiratory efforts against occluded airway at three lung volumes spanning the vital capacity. We computed muscle shortening and curvature of the mid costal diaphragm. We also computed normalized VD relative to surface area of contracted state during forceful efforts. Our data show that transdiaphragmatic pressure (Pdi) at TLC was reduced by 80% and surface area of the diaphragm at contracted state during airway occlusion at TLC decreased by 20.2% from their values at FRC. Normalized VD of midcostal diaphragm during forceful efforts against airway occlusion at TLC decreased by 3.8% from its value at FRC. Regardless of posture, muscle fiber curvature was not significantly different across lung volumes spanning the vital capacity. These data support a mechanism by which Pdi is reduced, and consequently its reduced VD at high lung volume, mostly due to higher muscle contraction rather than loss of diaphragm curvature.

Matrix Stiffness and Applied Pressure Dictate Capillary Network Formation in Tissue Engineering Scaffolds

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Naomi Alyafei[*]; Gennifer Chiou; Rena Bizios and Teja Guda, *Department of Biomedical Engineering and Chemical Engineering, University of Texas San Antonio*

Abstract: Large-scale tissue defects, observed in over 40% of traumatic injuries, need replacement of both the missing volumes as well as functional deficits. Successful engraftment requires robust vascular network formation; however, challenges such as cell types, cell numbers, ratios, and spatial distribution of cells within implant material scaffolds have delayed progress. Recent research efforts have involved using co-culture of microvascular fragments (MVFs) and Mesenchymal Stem Cells (MSCs) in order to mimic the physiological microenvironment of bone tissue. The objective of the present study is to investigate the effects of pressure on a co-culture of MSCs and MVFs, seeded within a hydrogel scaffold. We hypothesize that hydrostatic pressure will promote a faster vascularization of the co-cultured cells. To study our hypothesis, cells will be distributed in collagen: fibrin 3D gels. We will examine various ratios of the gel composition to determine the optimal ratio of collagen to fibrin that will result in successful, rapid vascularization of the constructs. The effects of hydrostatic pressure on the proposed cell co-culture system will examined by comparing to a control group without MSCs. The constructs will then be prepared for immune-histochemical analysis. Lectin staining will aalow visualization of the developing microvascular network. These results will enhance our understanding of cell co-cultures, the role of both mechanical properties of the scaffold and the external physical stimulation on cell biochemical signaling leading to the development of vascularized tissue.

Preliminary Study of a Two-Bar Nano-Mechanism Design Formed Primarily out of DNA

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Kimberly Lopez-Zepeda*[1]; Nina Robson[2] and Madeline Rasche[2], *(1)California State University, Fullerton, (2)California State University Fullerton*

Abstract: DNA origami mechanisms (DOM) are active biological nanostructures, made entirely out of DNA, with the potential to revolutionize biological machinery, stem cell research, and drug delivery systems. The design of current DOM are limited by function and mobility. The goal of this research is to synthesis, design, and experimentally validate a kinematic 3D two-bar DOM. We choose the two-bar mechanism because of its utilization as the core building block for several complex multi-functional mechanisms. This two-bar DOM design consists of two 3D DNA origami structures connected by two single-stranded DNA oligomers. Our design procedure begins with the use of Mathematica for the desired motion/functionality, SolidWorks for a 3D solid model, and caDNAno to obtain the required nucleotide sequences. Proceeding work will consist of a successful synthesis, imaging and verification using Atomic Force Microscope of the two-bar DOM. As well, the synthesis, design, and experimental validation of a kinematic four-bar DOM, consisting of two connected two-bar mechanisms.

Prevascularization of Porous Polyethylene Glycol Scaffolds Using Rat Derived Microvascular Fragments

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Favour Obuseh*; Binita Obuseh and Eric Brey, *The University of Texas at San Antonio*

Abstract: One of the major challenges in engineering viable tissues is forming functional and stable blood vessel networks within the tissue, which supply oxygen and nutrients to the cells. The use of Microvascular fragments (MVFs) for pre-vascularization of scaffolds are explored in this study. Microvascular fragments are a randomized mixture of arteriolar, capillary and venular vessel segments which have a high proliferation rate. Transplanted MVFs rapidly interconnect with each other and the surrounding microvasculature to form blood perfused vascular networks. In our study, microvascular fragments isolated from rat fat, were seeded into a (poly)ethylene glycol diacrylate-poly lactic acid (PEG-DA-PLLA) hydrogel. Varying concentrations of fibrinogen (Fg) and thrombin (Tb) were utilized. MVFs were added at various concentrations to the fibrinogen solution prior to loading into the pores. To optimize the working concentrations for Fg and Tb, fibrin gels were utilized initially. To analyze the vasculature in vitro, after 21 days, the gels were fixed using formaldehyde and stained using lectin, Dapi and actin to visualize the endothelial cells, nuclei, and actin filaments, respectively. In-vitro results show that the 30mg/mL-40U Fibrinogen-thrombin concentration provides the largest vascular density upon seeding into the PEGDA-PLLA scaffolds. Concentrations of fibrinogen greater than 80mg/ml as well as 40 units per ml of thrombin appear to prevent adequate vascular sprouting. 3D volumetric analysis was performed using Leica Las-X Software. Image J was used to calculate the vessel density, diameter, and sprout length. Advancement in this project could revolutionize the field of tissue engineering and regeneration application.

Monitoring Swallow Activity with Multi-Electrode Electromyography over the Neck

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ruby Rios Ramirez*[1]; Gladys Ornerlas[1] and Todd Coleman[2], *(1)University of California San Diego, (2)University of California, San Diego*

Abstract: High-density surface electromyography (HDsEMG) introduces a non-invasive approach towards studying muscle activity for the purpose of improving our understanding of muscle health. Laryngeal HDsEMG uses an array of multiple electrodes over the throat to capture spatiotemporal information about the complex and dynamic activities of throat muscles during voicing and swallowing. Our aim of using laryngeal HDsEMG is to improve the non-invasive assessment of swallow disorders such as dysphasia and enhance existing applications of traditional surface electromyography. This study uses a 20-channel HDsEMG array to capture salivatory swallows from ten subjects. Data analysis consists of first identifying the EMG tracings assumed to represent the contractions due to the pharyngeal phase of swallowing. Secondly, the peaks of these tracings are monitored across time and channels for differences in their time-stamp that may be related to spatial parameters associated with wave propagation through the muscles. This preliminary attempt aims to pave the way for HDsEMG usage as a biofeedback tool during swallow therapy.

Development of an Autonomous Perifusion System for Artificial Pancreas Devices

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Eleazar DeAlmeida*[1]; Alonso Torres[2]; Ana Santandreu[2] and Shuvo Roy[2], *(1)Skyline College, (2)University of California, San Francisco*

Abstract: According to CDC reports, over 100 million adults in the US live with diabetes or prediabetes. Studies have linked diabetes to heart disease, strokes, neuropathy, kidney disease, and in severe cases, blindness. Diabetes results from elevated blood glucose levels, insufficient insulin production, and destruction of β-cells within islets of Langerhans. Advancements in perifusion systems have characterized and quantified kinetics of biphasic insulin responses in healthy β-cells through *in vitro* glucose-stimulated insulin secretion (GSIS) assays. Perifusion systems are the standard in *in vitro* GSIS experiments to perfuse islets in temporal solutions to profile biphasic insulin kinetics. Current perifusion systems have several limitations in the following areas: high purchase price, data collection, automation, portability, and integration with current artificial pancreas systems. With our new custom, automated perifusion system, we hypothesized producing comparable insulin production and secretion to standard *in vitro* GSIS experiments. Our automated system was developed with a 3-axis mini-CNC machine, multi-channel peristaltic pump, dynamic sample collection platform, and temporal control of islet culture media with 5mM, 28mM, and 5mM glucose concentrations for 16, 30, and 44 minutes, respectively. The automation was programmed in a GRBL software using G-code. Our version reduced the cost and size while increasing the scalability of data, and improved integration with current bioartificial pancreas systems in incubators at physiological CO_2 and temperature. Lastly, the post-GSIS assay validated the quantitative characterization of biphasic insulin kinetics and our prototype. Ultimately, autonomous systems are of great importance to simulate *in vivo* conditions to improve intravascular bioartificial pancreas systems.

Reconstituting the Assembly of Extended Synaptotagmin 1 on Membranes

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Sybrina Kerr*[1]; Kasey Day[2] and Jeanne Stachowiak[2], *(1)Claflin University, (2)The University of Texas at Austin*

Abstract: In the past decade, exciting work has shown that at membrane contact sites (MCS), two organelles meet to facilitate cell signaling and molecular transport. Extended synaptotagmin-1 (E-Syt1) is a protein found between the endoplasmic reticulum (ER) and plasma membrane (PM). E-Syt1 mediates lipid transport and the direct transfer of calcium to the exterior of the cell. Calcium regulation is important for cell metabolic activities including cell signaling and muscle contractions. Improper calcium regulation may lead to health issues like heart failure, Alzheimer's, and ischemic stroke.

E-Syt1 contains C2 domains that bind calcium and mediate PM binding. Interestingly, these C2 domains are connected by long, disordered regions. At high calcium concentrations, E-Syt1 drives the formation of ER-PM contact sites. How E-Syt1 participates in defining these sites and the role of the disordered regions remains unknown. This study focuses on characterizing the behavior of E-Syt1 on membranes; how does E-Syt1 assemble itself and how is it influenced by calcium binding?

To visualize E-Syt1 in vitro, we affinity-purified a His-tagged version of E-Syt1 and fluorescently labeled it. Giant unilamellar vesicles (GUVs) simulated the ER and plasma membranes. We assessed the behavior of E-Syt1 on GUVs in the presence and absence of calcium. Without calcium, E-Syt1 decorated membranes smoothly. Upon adding calcium, bright dense E-Syt1 patches localized to the interface between GUVs. Thus, calcium not only causes E-Syt1 to tether membranes, but also induces strong E-Syt1 self-association at the MCS. Further studies will investigate the role of the disordered regions in driving E-Syt1 self-association.

Developing a Portable, Solar-Driven, Water Desalination Unit with Heat Recapture

Discipline: Engineering
Subdiscipline: Chemical Engineering

Emily Barragan*; Shane Ardo; Simon Luo and Sunny Jiang, *University of California, Irvine*

Abstract: Because dependable sources of water are required to sustain life on Earth, disasters restricting access to potable water are grievous concerns. For such events, a rapidly-deployable device which generates life-sustaining water must be available for mass distribution. This research focuses on the assessment and optimization of a portable device that is driven by sunlight and operates passively by membrane distillation. Membrane distillation relies on a porous, hydrophobic polytetrafluoroethylene membrane, such that a temperature gradient between solar-heated saline water on one side and cold pure water on the other drives potable, water vapor through the membrane pores where it condenses. After the lab designed a tangible, handheld device based on this concept; temperature gradients using hot water feeds, simulated sunlight, and natural sunlight were evaluated. Upon assessing various heat capturing materials, it was found that a carbon fiber weave atop of the membrane most effectively captured and maintained thermal energy. Based on this, a handheld

construct was developed which recycled the latent heat of condensation in the distillate side back to the permeate side, instead of traditionally dissipating it to a heat sink. Thermally conductive materials were strategically placed in regions of the device to optimize the formation, use, and recycling of heat; and the optimal design's efficiency will be reported and related to peer-reviewed, solar thermal distillation concepts that lack heat recycling mechanisms. Large strides have been made toward the critical need of a small-scale, handheld desalination device that can be mass distributed to in-need regions across the globe.

Optimizing Polymeric Nanoparticle Formulation and Characterizing Peg Degradation

Discipline: Engineering
Subdiscipline: Chemical Engineering

Michael Chungyoun*, *University of Washington* and Elizabeth Nance, *Department of Chemical Engineering, University of Washington*

Abstract: Drug delivery-enhancing platforms are vital to overcoming the blood-brain barrier that prevents sufficient accumulation of drugs in the brain during treatment. Although nanoparticles can improve diffusion and treatment of neurological diseases, the formulation process must be optimized. The goal of my project is to 1) optimize nanoparticle formulation parameters to maximize therapeutic enzyme activity, and 2) characterize the extent of nanoparticle degradation due to sonication. Within part 1), formulation methods were composed of poly(lactic-co-glycolic) acid copolymerized with poly(ethylene glycol), cholic acid (CHA) or polyvinyl alcohol surfactant, and the enzyme catalase. Each of the nanoparticles were formulated at varied sonication times during the emulsion step to measure differences in therapeutic activity using UV-Vis spectroscopy. It was revealed that the 30s sonicated CHA double emulsion and nanoprecipitation methods yielded the greatest enzymatic activity (2.10% and 3.72% activity, respectively). In the presence of degradative pronase, CHA double emulsion nanoparticles exhibited better retention of enzymatic activity than nanoprecipitation (75.66% and 9.22% retention, respectively). Within part 2), heat flow was monitored to identify the melting temperature in a sample of PEG exposed to varying sonications and degradation was assessed using differential scanning calorimetry. 5kDa PEG exhibited a melting temperature of 60.792C, while 5kDa PEG exposed to 2x150s of sonication exhibited a melting temperature of 59.450C, correlating to 4.8kDa. The 30s sonicated CHA double emulsion formulation yielded the highest enzymatic activity with protection from external proteases, yielding a promising polymeric nanoparticle platform that may help in the development of more powerful treatment options for neurological diseases.

Carbon Dots As Theranostic Agents for the Epithelial Cell Adhesion Molecule Expressed in Canine and Human Carcinomas

Discipline: Engineering
Subdiscipline: Chemical Engineering

Jeannine Marie Dizon*; Priyanka Ray and Dipanjan Pan, *University of Maryland, Baltimore County*

Abstract: The emergence of nanomaterials has created a new field of science impacting various spheres including medicine, imaging, electronics, agriculture and a host of others. Among nanoparticles, Carbon Dots have attracted much attention due to their unique photoluminescent properties and biocompatibility. In our project we plan to synthesize Carbon Dots from naturally occurring sources using greener methods. Different techniques including microwave synthesis, solvothermal method and surface passivation will be used to prepare CDs. We will characterize our materials using NMR, FTIR, UV-Vis and fluorescence spectroscopy as well as DLS, TEM and zeta potential measurements followed by in vitro studies on different cell lines. By harnessing the luminescent properties along with their ability to act as drug delivery agents, we plan to test the capability of the prepared CDs as theranostic agents.

Supramolecular Poly(Amino Acid) Vectors for Gene-Editing Therapy

Discipline: Engineering
Subdiscipline: Chemical Engineering

Elia Natalia Gonzalez*; Tina Rodgers and Gabriela Romero Uribe, *University of Texas, San Antonio*

Abstract: In recent years, gene editing technologies have achieved ample consideration as a therapeutic tool for treating different diseases. Many cancer types are applicable for gene therapy as it can inhibit or edit the expression of any specific gene of interest. Gene-editing tools like CRISPR/CAS or the BAC transposon/transposase apply a “cut-and-paste“ approach to replace distinct DNA sequences however, a major challenge for clinical translation of gene-editing therapies is finding a vehicle that ensures the cell delivery of the nucleic acids. A vector that guides nucleic acids into the cell efficiently is needed, as free exogenous DNA cannot enter mammalian cells.

Here, we aim to develop a novel approach for the nano architectonic design of non-viral vectors based on biopolyelectrolytes (poly(amino acids)) and lipids through supramolecular self-assembly. These vectors will carry Bac tansposon/transposase for cancer therapy. By utilizing poly(amino acids) we aim to develop a biocompatible nanocarrier with enhanced nucleic acid loading that facilitates nuclear targeting for more efficient gene editing.

Hydrodynamic size and surface charge of nanoparticles fabricated by different methods and with different poly(amino acid) compositions will be characterized and analyzed using Dynamic Light Scattering for an optimal size that will facilitate

plasmid intracellular delivery with potential enhanced circulation time. Surface charge will be studied to target a nanoparticle composition with adequate surface chemistry and architecture for plasmid intracellular delivery. We expect to find at least one poly (amino acid) vector with a positive surface charge between 10 and 20 mV, and hydrodynamic diameter below 200 nm.

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Impacts of Climate Change on Coastal Erosion

Discipline: Engineering
Subdiscipline: Civil Engineering

Kelsey Perez*, *University of Central Florida* and Talea Mayo, *Emory University*

Abstract: The world has been transitioning away from fossil fuels due to the large amounts of greenhouse gas emissions. The use of renewable energy resources, like wave power, has been increasing over time. Wave energy converters (WECs) function by extracting energy from waves to convert it into electricity in order to support local communities. There are many types of WECs that accommodate different wave climates and beach profiles, accounting for various factors such as wave heights, wind speeds, sea levels, and sediment transport. Through the extraction of wave energy from WECs, the dissipation of wave power can reduce wave heights. As a result, WEC farms can act as coastal defense mechanisms against erosion due to the reduction of wave power. In this study, we use a wave and sediment transport model, XBeach, to assess the potential morphodynamic impacts on the coastline with the presence of WEC farms. We examine the effects while considering the effects of climate change, which have direct and indirect impacts on wave energy and coastal erosion. We aim to show how climate change impacts that can intensify the effects of hurricanes may impact erosion on the coast. Additionally, we aim to show the potential of WECs to reduce erosion in both present and future climate scenarios. We use Hurricane Katrina as a case study.

Pfas Removal from Drinking Water Sources By Activated Carbons

Discipline: Engineering
Subdiscipline: Civil Engineering

Chantaly Villalona*, *Wellesley College* and Kurt Pennell, *Brown University*

Abstract: Amidst a growing global water crisis, legacy contaminants produced by industries can persist in the environment for long periods of time and may contaminate surface and groundwater globally. Per and polyfluoroalkyl substances (PFAS), known as "forever chemicals," are cytotoxic at high concentrations and are associated with cardiometabolic dysfunction alongside many other risk factors. PFAS are anthropogenic chemicals introduced in the 1930s for use in non-stick coatings and firefighting foams. Despite government efforts to reduce PFAS industrial emissions, PFAS products and materials remain widespread sources of soil and groundwater contamination. To minimize PFAS exposures, scientists have been working on remediation technologies to remove these chemicals from groundwater before they enter drinking water systems. This study discusses and compares three materials used for removal of perfluorooctanoic acid (PFOA) from drinking water via an adsorption process. The review evaluates the advantages and disadvantages of each approach, and discusses adsorption mechanisms, method accessibility, and retention efficacy. This analysis suggests that material favorability is not solely attributed to retention capabilities, but rather a holistic exchange, that favors coal-based agglomerated carbons who remain accessible with respect to cost and environmental sustainability.

Designing an Adjustable Suspension for Oscillating Mass Payloads in Legged Robotics

Discipline: Engineering
Subdiscipline: Electrical Engineering

Alyssa Giedd*; Keely Hall; Joey Sullivan; Raghav Duddala and Sam Burden, *University of Washington Seattle*

Abstract: The mobility of autonomous walking robots is an essential characteristic in their operation. Due to currently imposed constraints in battery technology, the optimization of robotic locomotion for energy efficiency is paramount. Previously, elastic payload suspension has been employed to reduce the cost of transportation in a hexapedal robot. Prior results suggest that the optimal load suspension characteristics are a function of robot morphology and locomotion strategy. A payload suspension system that can be easily adjusted would allow for the accommodation of a variety of these morphologies and locomotion strategies. We have designed a tunable suspension system that will allow for experimentally determining optimal suspension characteristics in a cost-effective manner. The design enables continuous adjustment of the suspension stiffness and damping, so optimal parameters can be determined through hardware experimentation. This hardware experimentation allows for the creation of a numerical model for an oscillating payload’s behavior, which can be compared to simulations. We have completed calculations and design of this hardware, and anticipate seeing that the data collected from its usage will verify the utilization of a haptic testing system in robotics development and allow us to determine methods for calculating the best parameters for elastic payload suspension. This verification of simulated data will allow for further research in developing more efficient methods of payload attachment to legged robots, examination of locomotion when carrying payloads, and design of payload management methods.

Novel Methodologies for Studying Yellow Music and Musical Identity in Vietnam and the U.S.

Discipline: Engineering
Subdiscipline: Electrical Engineering

Tedmon Tran[*] and Margaret Bodemer, *California Polytechnic State University, San Luis Obispo*

Abstract: This research utilizes a novel, music information retrieval (MIR) approach to investigate *"yellow music"* (nhạc vàng) and the extent of its role in forming a Vietnamese musical identity. Singer-songwriters in the yellow music era (1950-1975) of the Vietnam Wars produced controversial, but popular musical works which have been banned up until recently. A renewed prominence of yellow music in Vietnam provides a rare opportunity to explore a transnational musical identity for Vietnamese nationals and Vietnamese Americans. In addition, the consequences of the abrupt refugee exodus and resettlement after 1975 has taken a toll on memory among older Vietnamese Americans which warrants prompt, but thorough inquiry.

Efforts were made to preserve the core methodologies employed in existing MIR research while utilizing ethnological fieldwork approaches both in Vietnam and the United States in this project. Metrics of success were defined to identify the efficacy of project-based learning and interdisciplinary approach to the case study. After preprocessing and extraction of the empirical data, feature selection proved a critical step in the pattern recognition system to reduce classification uncertainty because of nonlinearity in the dataset. The existing recognition system-in-development employs supervised-learning and includes measures of valence, memory, and arousal by comparing the content of yellow music and other music genres, suggesting inherent sociocultural qualities in the music. This project also includes discussion of unfamiliar technology such as the newly released Daisy-embedded platform which can ease MIR and fieldwork data collection.

Current Induced Switching in Antiferromagnetic Multilayer System

Discipline: Engineering
Subdiscipline: Electrical Engineering

Menucha Winchell[*1]; Sucheta Mondal[2] and Jeffery Bokor[2], *(1)Los Angeles Valley College, (2)University of California, Berkeley*

Abstract: Although ferromagnets currently dominate spintronics, antiferromagnets may be faster and more reliable alternatives, promoting robust designs of magnetic memory devices and sensors used in electronics. Antiferromagnets emit negligible stray fields and exhibit ultrafast switching speeds. They also demonstrate powerful exchange coupling, resulting in eigenfrequencies in the THz range. However, manipulating their magnetization on a nano scale is difficult. This research study utilizes 'Object Oriented Micromagnetic Framework' (OOMMF), a micromagnetic simulation software, to layer nanoscale strips of antiferromagnets, ferromagnets, and nonmagnetic heavy metals. The manipulation of magnetization within the system is studied by injecting an electrical current through the nonmagnetic layer. The flow of charge current results in the generation of pure spin currents due to spin-orbit coupling, exerting spin-orbit torque on the interfaces. This torque influences the ultrafast dynamics in the ferromagnet's magnetization as well as magnetic switching in the antiferromagnetic sublattices. Static magnetic properties are also observed through varying the Zeeman field surrounding the multilayer system, thus numerically describing antiferromagnetic coupling within the system. This experiment aims to observe the dynamic and static properties of antiferromagnets within this multilayer framework.

Design and Optimization of Lidar Beam Scanners

Discipline: Engineering
Subdiscipline: Electrical Engineering

Musaiel Gebremariam[*1]; Xiaosheng Zhang[2] and Ming Wu[2], *(1)Santa Rosa Junior College, (2)University of California, Berkeley*

Abstract: Light detection and ranging (LiDAR) technologies are being used in the industry to generate 3D images by emitting a laser to measure a scene of interest point-by-point. In commercial LiDAR products, mechanical beam scanners are currently used, whereas solid-state beam scanners that are constructed with silicon photonics and micro-electromechanical (MEMS) technologies are under intensive research and development. The goal of this research is to determine how to improve the efficiency of mechanical and solid-state scanners and understand the correspondence and trade-off between each design. We analyzed the properties of the galvanometer mirror, such as the mirror size and scanning speed, and investigated the optomechanical package design of a solid-state focal plane switch array beam scanner. The galvanometer mirror was examined through a physical model along with mathematical derivations to demonstrate the relationship between the light beam diameter, scan angle range, and the mirror shapes and sizes. An optimized design will lead to a galvanometer scanner with efficient mirror dimensions and fast scanning speed. We also demonstrated the trade-off between the beam diameter and angle range, and discussed their effects on a LiDAR. For the solid-state focal plane switch array beam scanner, we analyzed the relationship between the lens and output beam properties by geometric and wave optics models. We developed an optical measurement procedure to characterize the relative position between the lens and chip, and designed an optomechanical package to ensure the correct lens and chip positions and thus achieve the best beam quality and the highest optical power efficiency.

Enhanced Luminescent Cooling in the Stimulated Emission Regime

Discipline: Engineering
Subdiscipline: Electrical Engineering

Adrian Pizano[*1]; Ibrahim Dursun[2] and Christopher Giebink[2], *(1)Georgia Southern University, (2)Penn State University*

Abstract: Laser cooling or optical refrigeration is an idea that started in the mid 1900's with the observation of anti-Stokes fluorescence by Pringsheim. The use of laser cooling offers a cryogenic refrigeration that is free of moving parts thus eliminating vibrations, which is especially useful in vibration sensitive environments. Since its initial conception the field of optical refrigeration has been expanded and where before it was limited to gasses and rare earth metals today it can be applied to a wider range of materials such as semiconductors. In this project we used MATLAB to solve coupled differential laser rate equations to determine whether optical refrigeration can be enhanced through stimulated emission for organic and perovskite semiconductors. We find that operating in the stimulated emission regime enables cooling to occur in materials with photoluminescence quantum yields that are well below unity and predict that this phenomenon can be experimentally observed in perovskite semiconductors under pulsed optical pumping.

Developing a Self-Regulating Solar Powered Watering System to Further Revitalization Efforts on Kahoʻolawe

Discipline: Engineering

Subdiscipline: Engineering (general)

Mia Fong[*], *Honolulu Community College* and Shidong Kan, *University of Hawaii at Manoa*

Abstract: After the bombing of Pearl Harbor, the United States seized the island of Kahoʻolawe under martial law for use as a bombing range. Since the transfer of the land title back to Hawaiʻi in 1994, the Kahoʻolawe Island Reserve Commission has been working to restore the island. Due to challenges such as limited access to fresh water and electricity, as well as hard packed soil, the reintroduction of native species to the island has been a difficult task. Through the use of moisture sensors, the system will be able to determine when the plants need water. This will then trigger the watering system and the sprinklers will water until the soil is once again within the satisfactory saturation range. The watering system will include its own water catchment and measurement system allowing it to report the amount of water it catches. This will allow the system to make further decisions about watering based on the amount of water available to it. By doing so, we ensure that the naturally occurring fresh water will be conserved as much as possible. Future goals include the WiFi transmission of the system's moisture readings to the University of Hawaiʻi Maui College for remote monitoring. This project would serve to further restoration efforts on the island of Kahoʻolawe and blend modern science with traditional practices. By taking the good of technological advancements and our kupuna's (ancestors) ʻike (knowledge) we will be able to create a system that promotes native practices in a modern world.

Investigating the Difference in Power Generated By Fixed and Solar Tracking Photovoltaic Panels during a 12-Hour Period

Discipline: Engineering

Subdiscipline: Engineering (general)

Kimberlymae Rodriguez[*] and Aaron Hanai, *Kapiolani Community College*

Abstract: Hawaiʻi's intense ultraviolet rays makes it an ideal location for solar energy. However, the high initial installation costs of photovoltaic (PV) panels prevents consumers from using them in their homes. Currently, an increased quantity of fixed panels need to be installed in order to achieve reliable efficacy. By maximizing the power collected from each panel, the quantity of panels can be decreased which will help to reduce cost. The purpose of this project is to test the difference in power between fixed versus single-axis tracking panels as part of a larger collaboration to improve solar energy in Hawaiʻi.

Panels were secured on a model house using a computer-aided design mount and placed below a LED arch that is programmed to simulate the sun's position throughout the day. The fixed panel remained stationary on the roof while the solar tracker panel was motorized to move at different angles of the sun. A circuit board was programmed to measure the voltage from each panel. Solstice and Equinox simulations were included to examine how seasons affect voltage. The voltage was then converted to power by factoring in current and resistance. An experiment with different resistors determined what resistance to use for the load.

Data collected from a fixed versus solar tracking panel provides evidence that a panel with a solar tracker does obtain a greater yield of energy. Providing a comparison model of solar panel options will play a key role in helping Hawaiʻi to be 100% dependent on renewable energy by 2045.

Aspire, Learn, Mentor, Achieve (ALMA) Science Academy: Early Exposure to STEM Has Lasting Effects

Discipline: Engineering

Subdiscipline: Engineering (general)

Jose Rea III[*1]; Destiny Macias[1]; Martha Romero BS[1]; Dr. Frank Zaldivar PhD[2] and Jose Rea MA[1], *(1)University of California, Irvine, (2)Department of Pediatrics, University of California Irvine*

Abstract: The ALMA program engineering component emphasizes exposure of STEM topics in the form of hands-on experiments focusing on engineering, coding, 3D printing, and basic circuits. The aims of our program are to develop critical thinking skills and assess interest in engineering and technology concepts in elementary and middle school students from underrepresented communities. We recruit 85 elementary and middle school students. Parents are required to attend 3 workshops on educational development. A pre- and post-test are administered to the student participants. Over the course of 10 weeks**,** the students are taught engineering subjects with hands-on lab activities. Overall, students showed an increase in understanding of engineering technology concepts. In addition, we evaluated a standardized test given annually, Measure of Academic Progress (MAP), and compared to students not enrolled in ALMA. Students enrolled in our program outperformed their counterparts and scored at or above state guidelines in MAP. MAP is a strong indicator of how well students will perform on the college entrance exams, SAT and ACT. The majority of ALMA students increase their interest in engineering and technology indicating their interest in pursuing degrees in those fields. This increase in knowledge and interest will also help them pursue STEM in higher education and careers, in which skilled workers are in high demand. We must prepare underrepresented groups to fully participate in the future work market where 2 out of 3 jobs will be in STEM and where currently there is a lack of skilled workers.

Enhancing Seagrass Monitoring Using a Small Unmanned Vehicles

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Marvin Hernandez*, *Texas A&M University- Corpus Christi* and Hua Zhang, *Texas A&M University- Corpus Christ*

Abstract: Seagrasses are an essential component of the marine environment and provide important ecosystem services such as nursery habitat, food source and sediment stabilization. Human activity and environmental disturbances can be threaten the health of seagrasses and results in significant biological and economic consequences. Seagrass beads have been monitored regularly along the Texas Coast based on the 2012 Texas Seagrass Monitoring Plan, in order to understand their changes over time. However, the establishment method are time-consuming and requires extensive work. Using Redfush Bay as the study area, here we propose a new approach that uses small unmanned aerial vehicles (UAVs) to help gather the data of seagrass percent cover. While being sent on a set path, a UAV takes images that can later be pieced together in a computer software. While the raw RGB images are nothing more than digital number between ranging from 0 to 255, they can be calibrated using ground truth of seagrass coverage to estimate bottom reflectance which is important for identifying the spectral signature of seagrass. The accuracy of images has been substantially improved by including ground control points strategically placed across the study area. Imaging over a large area with high resolution allows researchers to see patterns that wouldn't be recognizable from just several sampling locations in traditional efforts. Images from different surveys can be classified and compare to find change in seagrass. By comparing results from a control and an affected site, effects on the environment disturbances such as wastewater effluent could be analyzed.

Numerical Modelling of Dry Aerosol Drug Delivery in the Avian Respiratory System

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Lay Heng Teng*[1]; Carlos Ruvalcaba[2] and Jean-Pierre Delplanque[2], *(1)University of California Davis, Biomedical Engineering, (2)University of California Davis, Mechanical and Aerospace Engineering*

Abstract: One method to treat fungal disease in the lungs of mallard ducks involves using a liquid atomizer that produces a spray. However, that method has been shown to result in asymmetrical drug delivery due to a high momentum spray jet. To address the asymmetric delivery, we are developing a dry powder insufflation device that will allow for the drug to have a better penetration and more symmetric distribution in the lungs. To assess the development of the device, we numerically modelled the behavior of the spray inside the trachea. We create a model of a trachea, using an idealized cylindrical geometry to validate the numerical modeling approach. The mallard duck breathing rate during the day is 34.9 mL/min, which results in a calculated Reynolds number of approximately 36. The spray injection velocity is high and the flow is unsteady. Thus, the governing equations used are the unsteady Navier-Stokes equations. They are solved using the open source library, OpenFOAM, which uses a finite-volume approach. First, we run a mesh sensitivity study to determine the mesh resolution, then introduce a spray model to capture the medication insufflation process. To model the spray, we use the multiphase particle-in-cell (MPPIC) method to track Lagrangian pointwise solid parcels that mimic the solid spray injected by our device. We find that MPPIC is sufficient to capture the bulk spray distribution at the trachea outlet with the appropriate Reynolds number derived from the basal breathing rate for a mallard duck.

Optimizing Millifluidic Channel Geometries to Reduce Dynamic Shear Stresses on Coral Propagates

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Isaiah Cuadras*[1]; Jinkyu Yang[1]; Nastassja Lewinski[2]; Liza Roger[2] and Shuaifeng Li[1], *(1)University of Washington, (2)Virginia Commonwealth University*

Abstract: Millifluidic devices isolate biological specimens to create an environment where fluid flow rates and fluid properties can be controlled. The rapid decline of coral reef populations has led to an increased interest in using these devices to study the patterns exhibited during “coral bleaching”, a phenomenon where corals expel algae (their primary source of nutrients). To properly investigate the ways in which the changing chemical makeup of the ocean induces coral bleaching, corals must be evaluated under conditions of minimized dynamic shear stress to reduce the possibility of flow-induced stress. Previous research suggests feasible flow conditions for defined millifluidic geometries; however, there is still a need to identify the result of changing channel geometries within millifluidic devices. This study uses COMSOL Multiphysics (a software that allows Computational Fluid Dynamic Analysis) to simulate the velocity and shear stress fields and investigate the effects of simultaneously changing pipe length, width, position, and well (the coral propagate location) geometry. Shear stresses in the well are anticipated to increase when the pipes are shorter and narrower, and when the well is smaller in radius. These expectations are a result of the shear stress being proportional to the horizontal velocity, which typically increases in more confined spaces for a constant mass flow. The findings of this research would help provide a framework for developing millifluidic devices for use in the coral research community, and any other research that needs to minimize dynamic shear stresses in their millifluidic devices.

Tribological Effects of Varied Operating Conditions on Pressure and Film Thickness

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Tanner Ragan* and Ashlie Martini, *University of California, Merced*

Abstract: Information of the tribological behavior of a mechanical system can be extracted by capturing its pressure and film thickness distribution. Effects such as friction and wear can be obtained for design considerations on components such as gears and bearings. However, pressure and film thickness are variables that primarily depend on operating conditions such as flow speed and load. A numerical simulation will be applied using the Python coding program for efficient calculations that will provide an overview of how independent factors will affect tribological properties. The numerical model generally simulates a specified lubricant flowing between a ball and a flat surface. Ultimately, maximum pressure and minimum film thickness are plotted against conditions including the modulus of elasticity, flow speed, and/or load. This simulation will provide more insight on the effects of the operating conditions in the tribological system which will then be used for future investigation.

Synchronization in Collective Oscillatory Locomotion for Swarm Robotics Applications

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Jaquelin Dezha Peralta*; Wei Zhou and Nick Gravish, *University of California, San Diego*

Abstract: Swarm robotics draws inspiration from the collective behaviors of organisms in nature. Large groups of robots, called swarms, have many applications such as environmental monitoring and nanomedicine. The multi-agent character of robotic swarms creates desirable qualities such as robustness and scalability but introduces the challenge of coordination. This work explores a hypothesis of motion coordination: robots that use body undulation can passively synchronize their movements through spatial re-arrangement without changes to their actuation phase. The bio-inspired system in this project consists of two snake-like robots made to collectively travel within a confined channel. We demonstrate that robot pairs undulating at different phases will push each other by means of collisions along the longitudinal direction until they reach a spatial shift distance in which collisions no longer occur, we call the displacement shift versus phase shift relationship the gait compatibility threshold. A mathematical model approximating the robots as sine waves agrees well with the measured spatial shift versus phase shift experiments. Experimental results showed robots in collective motion with any phase difference achieved gait compatibility within 30 seconds and time to gait compatibility increased with phase difference. Simulations of the robots agreed well with the experiment and further showed that the initial distance between the robots and the area of confinement also determined the spatial reconfiguration for gait compatibility. These results show that coordinated motion can emerge without active feedback from the robots themselves. This work advances the aim of understanding the collective behavior in robotic swarms necessary for complex applications.

Validation of Water Contaminant Structure Libraries for Activated Charcoal Filtering Models Relevant to Atwater, California

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Emily Junez* and Aurora Pribram-Jones, *University of California, Merced*

Abstract: Water contamination is a global health issue that results in millions of deaths annually. Safer drinking water can prevent these deaths, but requires efficient and stable purification techniques. This study focuses on the water supply in Atwater, California, a small and rural agricultural town. The Atwater supply is heavily contaminated, exceeding the health and safety guidelines by up to 58 times, according to the Environmental Working Group database. Filtering with activated charcoal has been proposed as a solution, but the effect of multiple contaminants on its efficacy presents complications to this plan's implementation. Computational investigations have been used in the past to examine adhesion of contaminants to filter materials, though some of these methods are computationally demanding or focus on single contaminants. We have constructed a library of locally relevant contaminant and charcoal model structures for theoretical modeling in order to support development of a computationally efficient and flexible modeling protocol for multi-contaminant studies. As a validation of the model and first inquiry, we will examine combinations of water contaminants and their relative binding to an activated charcoal cluster model. These quantum mechanical simulations will use density functional theory, which has a useful balance of accuracy and computational cost, to determine the binding energies of contaminants and their combinations on models of activated charcoal fragments. Our preliminary results will justify the use of our selected charcoal model and may suggest locally significant contaminant combinations to investigate in more detail.

Three-Year Comparison of Springtime Saharan Dust Peak Season 2017 – 2019

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Juan Alape*, *Universidad de Puerto Rico*; Vernon Morris, *Arizona State University* and Juan Arratia, *Ana G. Mendez University System*

Abstract: Over half a billion tons of mineral dust particles are ejected annually from the Saharan desert. The Aerosols and Ocean Science Expeditions (AEROSE) cruises have studied the different aspects of these dust storms for over a decade and the data that were collected provided National Oceanic and Atmospheric Administration (NOAA) with datasets that show the intricacies of Saharan dust events, its life-cycle, and the relationships to other weather-related events like Atlantic storms, cloud properties, and retrieval of satellite data; found by the AEROSE instrumentation. These datasets were compared, for measurements of reliability, with the datasets from the Navy Aerosol Analysis and Prediction System (NAAPS) and Hybrid Single-Particle Lagrangian Integrated Trajectory (HYSPLIT) trajectories. The study has enabled a quantification of the error margin for the 2017-2019 Springtime Dust Seasons; ensuring the quality of these datasets for the purposes of forecasting through NOAA's mission of providing information that will help all communities respond intelligently to weather disasters and environmental threats.

Evaluating the Demand for Truck-Only Toll Lanes in Southern California Freeways with Owner-Operator Truck Drivers

Discipline: Engineering
Subdiscipline: Other Engineering

Samuel Dominguez* and Joseph Kim, *California State University Long Beach*

Abstract: With Southern California being home to the two busiest and growing ports in the United States, the demand for truck-only toll lanes by the freight industry is of great interest to transportation agencies as they are concerned with safety, traffic flow, and traffic demand. This study evaluates the demand for truck-only toll lanes in Southern California Freeways with owner-operator truck drivers. The study implemented the stated preference survey method to estimate the values of time, reliability, and safety for owner-operator truck drivers' travel routes by using various scenarios geared towards assessing the values. The study also utilized the face-to-face interview process with 31 owner-operators near the Ports of Los Angeles and Long Beach to understand the drivers' perspectives regarding truck-only toll lanes on Southern California freeways. The results indicate that the highest costs per mile on any day that drivers are willing to pay for when the main factor being compared are $0.31/mile with $18.35/hr, $0.30/mile with $8.94/hr, and $0.22/mile with $11.01/hr for the values of time, reliability, and safety, respectively. On average, interviewees disapproved of truck-only toll lanes, alleging that owner-operators were already burdened with the increasing costs of regulations and cannot afford tolls. Participants also found that it was unlikely that their clients would recompense their tolls. These results are meaningful for legislators and transportation agencies as they help them better understand the utility and demand for truck-only toll lanes by owner-operator truck drivers.

A New Web-Based Graphical Tool for Organizing and Visualizing Sets of Species for Large-Scale Phylogenetics Studies

Discipline: Engineering
Subdiscipline: Other Engineering

Lorenzo Chavarria Vargas*; Walker Pett and Dr. Tracy Heath, *Iowa State University*

Abstract: Revbayes is a program for Bayesian phylogenetics that provides a flexible framework for modular model design, enabling applications to a wide range of biological questions. The core interface of RevBayes is an interpreted programming language that may be challenging for scientists with no programming experience. Therefore, a graphical user interface–called RevScripter–was developed for users new to RevBayes. RevScripter is a web-based tool that generates analysis scripts for RevBayes while allowing the user to see details of how the script is created. To improve the utility of RevScripter we have added features that enable organization and management of taxon sets (a taxon represents a tip in a phylogenetic tree, usually a species). This feature in RevScripter allows users to input a data file, which is then parsed and then incorporated into the taxon-set organizer. Like RevScripter, this tool was implemented using JavaScript, CSS, and HTML. The libraries that were used were jQuery and Bootstrap. Using this new tool, users can create overlapping groups of taxa and visualize the groups as a cluster graph. The taxon sets created in RevScripter can then be exported for use in phylogenetic software or incorporated into a full analysis script for RevBayes. Tools like RevScripter improve the accessibility of complex statistical tools for analysis of biological data and allow researchers to create robust and reproducible analysis pipelines. RevScripter is an open-source project and is available on GitHub: *https://github.com/revbayes/revscripter*.

Ready to Rock: Modeling Excavation Costs for Embedment of Nuclear Reactors

Discipline: Engineering
Subdiscipline: Other Engineering

Kennard Johnston*[1]; Jacopo Buongiorno[2]; Enrique Velez[2] and Robbie Stewart[2], *(1)Morgan State University, (2)Massachusetts Institute of Technology*

Abstract: Nuclear energy remains a key solution in mitigating climate change and meeting current and future sustainable energy demands, but natural disasters and increasing capital costs in new built Nuclear Power Plants (NPPs) during the past few decades persists as an increasing threat to its implementation. A robust configuration that perhaps reduces capital cost while also increasing safety is embedding them in a silo fashion. Key benefits of an embedded nuclear reactor configuration might include lower civil infrastructure costs, natural protection against natural disasters and terrorists' threats, and protection of the environment and surrounding populations in the case of an accident. Due to a lesser requirement for structural robustness with embedment, determining the costs of excavation is critical in distinguishing whether it is more cost-effective than above grade siting. To achieve this, an excavation rate ($/m^3) was extrapolated using data from various below-grade construction projects. It is expected that the benefits of having an embedded nuclear reactor will exceed the costs incurred by additional excavation volume due to the most cost influential parameters. Those parameters are rock presence and quality, excavation technique, and project type: not volume. Key future work includes integrating this rate into a cost model that predicts economic gain from the level of reactor embedment. This model could be utilized as validation for supporting or discouraging reactor embedment as a design option at the initial stages of future NPP construction projects.

Application of Smart Irrigation Scheduling to Improve Water Use Efficiency for Sustainable Agriculture in the Pacific Island of Guam

Discipline: Engineering
Subdiscipline: Other Engineering

Joseph Lance Casila*[1]; Maegan Marie Delfin[1]; Mohammad Golabi[1] and Sayed Bateni[2], *(1)University of Guam, (2)University of Hawaii at Manoa*

Abstract: The unpredictability in rainfall patterns throughout the Pacific region presents a major problem for efficient water irrigation for vegetable crops. This has the potential of unsustainably increasing costs of crop production long-term. In Guam alone, approximately 67,443,000 gallons of water were used by 345 farmers surveyed in FY2015 costing about $330,222. The cost and amount of water-use is projected to increase as demand for crops increase. Thus, implementation of efficient water-use is imperative. CropManage (CM) is a smart online irrigation advising tool for farmers that can significantly reduce these irrigation costs while also maintaining/increasing a farm's crop production. First, CM intakes factors from a particular farm such as soil type and crop coefficients, which creates a profile for a specific crop in that farm. Next, CM evaluates rainfall and proximal evapotranspiration data to generate irrigation rate recommendations that meet the plant's water requirement. CM generates efficient irrigation rates daily so that farmers can adjust their irrigation schedules to ameliorate the practice of daily constant-rate irrigation, which may not benefit crops during the intermittent rainy days prevalent in the Pacific region. Trials comparing crops irrigated through CropManage are hypothesized to have similar, if not better, yields than crops with constant-rate irrigation. In this study, 3 trials of eggplants will be used, which preliminary data has shown to have consistent growth under controlled conditions. 30-minute/day and 1-hour/day constant-rate irrigation will be compared to CropManage's irrigation rates. Crop yield and %canopy growth rates of each trial will be used to assess CropManage's effectiveness.

Failure Analysis of Transition Regions in Hybrid Laminates between Regions with and without Metal Ply Reinforcements

Discipline: Engineering
Subdiscipline: Other Engineering

Itzel Salgado* and Satchi Venkataraman, *San Diego State University*

Abstract: Carbon fiber reinforced polymers (CFRP) are composites which have high potential for use in the aerospace industry due to their high strength and stiffness to weight ratio. However, these polymer matrix composites exhibit low bearing strengths. This requires increasing the regions where composites are connected with mechanical fasteners (bolts). This added thickness adds weight, and also increases load eccentricity in the fastening region thereby introducing additional bending loads into the joining region. Local metal hybridization of CFRP laminates only in the regions where a higher bearing strength is needed has been proposed. This introduces a transition zone created between the areas with and without metal plies. Although some researchers have investigated the failure modes of the composites in the transition zone, there are no good guidelines on how to design the transition zone region. In this study, we present results from a computational finite element analysis of the hybrid laminate with a transition zone. The plies are modeled with continuum shell elements with a continuum damage model for progressive failure and with cohesive elements for the ply interfaces to model interlaminar delamination. The analysis results are compared to experimental test results. The validated models can

be used to understand the static behavior of the transition zone and develop design specifications for the transition zone to maximize the bearing strength without failure at the transition region.

Creating an Arduino Based Sanitizing Robot to Reduce the Spread of Viruses in Grocery Stores

Discipline: Engineering
Subdiscipline: Other Engineering

Jeraldine Milla* and Jacob Tyler, *Kapi'olani Community College*

Abstract: Coronaviruses can potentially stay on plastic and stainless steel for 2-3 days, which means viruses can infect us just by touching objects in a store. While hospitals use ultraviolet disinfection (UVD) robots to disinfect rooms, they can cost between $80,000 to $90,000. Grocery stores rely on staff to constantly clean and disinfect, which increases the number of people that can potentially be exposed. The research objective is to design and prototype a low-cost robot that can spray 70% isopropyl alcohol onto surfaces. Isopropyl alcohol was chosen because it could safely be used on a variety of surfaces. To do this, an Arduino microcontroller will be used to control the mechanism of the spray. First, an off-the-shelf Arduino kit will be used to understand its capabilities. The Arduino will be programmed in C to control a servo that will activate the aerosol spray bottle trigger to produce several releases of isopropyl alcohol. A second servo attached to a base on the bottom of the bottle will be programmed to make the spraying device move to reach different areas. The result is a mechanism that can spray a sanitizing liquid in more than one direction. Future research will be to design and prototype a maneuverable robot and to test the effectiveness of this sanitation method and how it would work on different materials. This research can be used in other settings to help protect essential workers and slow the spread of viruses.

Coronavirus (COVID-19) Pandemic Impacts on Air Pollution: Comparison of Ground-Level Ozone (O_3) and Particulate Matter ($PM_{2.5}$) in Rural San Joaquin Valley to Urban Areas in California

Discipline: Engineering
Subdiscipline: Other Engineering

Julianna Porraz* and Colleen C. Naughton, PhD, *University of California, Merced*

Abstract: Pollutants like Ground-level Ozone (O_3) and Particulate Matter 2.5 ($PM_{2.5}$) are associated with poor air quality and are linked to negative health effects particularly for low-income and minority populations. During the Coronavirus (COVID-19) pandemic, shelter-in-place orders were enacted across California on March 19, 2020 to contain the spread of the virus, thus leading to substantially lower O_3 and $PM_{2.5}$ emissions in urban regions with less emissions from transportation. Most researchers have focused on air pollution in cities. There is a need to analyze COVID-19 shelter-in-place impacts on air pollution in rural areas compared to urban areas. Rural areas may not have as drastic of a reduction in air pollution from shelter-in-place orders given less traffic congestion and continued agricultural cultivation and associated emissions. However, urban area pollution still spreads to rural areas. Data was obtained from the Air Quality and Meteorological Information System (AQMIS2) through the California Air Resources Board (CARB). Statistical analysis, Analysis of Variance (ANOVA), was performed in RStudio to see if there was a statistically significant difference in O_3 and $PM_{2.5}$ levels compared to previous years within the San Joaquin Valley (SJV) and compared to urban areas. The results indicate there is a difference in the rural SJV in comparison to urban regions. Air quality data should be further monitored and analyzed to determine sustained impacts of the COVID-19 pandemic on air quality in rural and urban areas in under resourced communities.

Molecular Dynamics Simulations of Binding Energy between Single Strand DNA and Silver Nanoparticles.

Discipline: Engineering
Subdiscipline: Other Engineering

Kyle Skelil* and Tod Pascal, *University of California, San Diego*

Abstract: Large-scale Atomic/Molecular Massively Parallel Simulator (LAMMPS) molecular dynamics (MD) software was used to study binding energies of silver nanoparticle (AgNP) and DNA complexes after heating the system to 298K. Two silver nanoparticles were each bonded to the 5’ end of an 11-nucleotide complementary single-strand DNA (ssDNA). These AgNP-ssDNA complexes were each then solvated in their respective neutral water box to calculate their potential energies. The two AgNP-ssDNA complexes where then combined in their own water box to calculate this total system’s binding energy. Molecular motion is approximated classically by using the AMBER force field to describe forces experienced by the DNA atoms, and the EAM potential designed by Finnis and Sinclair(1) to describe the Ag atomic forces. Binding energy was found to be 2.14 kcal/mol for the combined AgNP-ssDNA complex, which is within 78.3% error of experiment. This model effectively simulates the hydrogen bonding energy that helps stabilize the DNA strands together, as well as the overall binding energy of the combined AgNP-ssDNA complexes in solution. The computational environment used is understood as a predictive model for studying the conformation and binding energy of our nanoparticle/DNA systems.

A Comparison of Ammonia Inhibition on the Anaerobic Digestion of Organic Acids between Digestate from Anaerobic Co- and Mono-Digestion Systems

Discipline: Engineering
Subdiscipline: Other Engineering

Gloria Ruiz-Orozco*; Ana Aranda; Ashley Berninghaus and Tyler Radniecki, *Oregon State University*

Abstract: Anaerobic digestion is a common terminal step in wastewater treatment systems and produces valuable by-products such as biogas, a combination of carbon dioxide and methane. Biogas can be used to off-set energy costs, and along with the anaerobic co-digestion of fats, oils, and greases (FOG) has been found to increase biogas production and enables some plants to become self-sufficient and a net-exporter of energy.
Operational difficulties, such as ammonia inhibition, can prevent treatment plants from implementing anaerobic digestion. This is due to high concentrations of FOG, which includes protein, that produce ammonia at levels that may be inhibitory to the anaerobic digestion process. While ammonia is not harmful to the system in quantities smaller than 2500 mg TAN/L, concentrations larger than that can lead to inhibition.
Two different lab-scale facilities were used to seed the batch bottle experiments. One from Gresham, OR which has used FOG successfully for years and the other from Corvallis, OR which has never been exposed to FOG. The digestate was put into batch bottles in five different conditions: control, volatile fatty acid control, +500 ppm NH 4 + , +1000 ppm NH 4 + , and + 1500 ppm NH 4+ . Anaerobic digestion activity was monitored through daily biogas volume measurements and methane composition measurements. The results found that while the ammonia levels of the digestate were comparable, the biogas production from the Gresham digestate was much higher. These results provide insight into how ammonia inhibition, and methane production, are affected by FOG co-digestion.

Water Quality Assessment and Modeling of Recreational Waters within an Urban Watershed

Discipline: Geoscience
Subdiscipline: Earth Science

Jennifer Williams*; Jose Congo; Jensen DeGrande and Philippe Tissot, *Texas A&M University - Corpus Christi*

Abstract: In coastal cities, recreational water quality can be substantially impacted by stormwater runoff leading to beach advisories and potential health hazards. The Poenisch Park beach, a segment of Corpus Christi Bay, was placed on the 2014 Texas Water Quality Inventory and the 303(d) list of impaired waters for not meeting the contact recreation single sample criteria of no more than 25 percent of measured values exceeding 104 Colony Forming Units (CFU) per 100mL for the indicator bacteria (Enterococci). A Total Maximum Daily Load (TMDL), which is a process with goals to restore impaired waters, was initiated. For this study, historical Texas Beach Watch (TBW) measurements were complemented by flow rate and water quality measurements at the Poenisch Park stormwater outfall. Results showed that there are two distinct components to the water quality impairment in this segment: runoff from the adjacent watershed and a dry weather load of unknown origin estimated as 68 CFU for all model calibrations. All precipitation information for the study was based on Multi-sensor Precipitation Estimates (MPE) as there are no rain gauges located within the watershed. Based on the TBW data, a statistical analysis of the correlation between measured Enterococci concentrations in nearshore water, and precipitation within the watershed, elevated bacteria levels tend to occur within 72 hours following the onset of precipitation. The main recommendation of the study was to avoid recreational contact at the start of precipitation within the watershed and up to 72 hours after the end of the precipitation event.

Identification of Fenton Reactions and Fe(II) Stabilization in Microbially Incubated Soils

Discipline: Geoscience
Subdiscipline: Earth Science

Joshua Thedford* and Aaron Thompson, *University of Georgia*

Abstract: During oxidation events in soil, Fe(II) can participate in Fenton reactions when it oxidizes, generating reactive radical species that can destroy organic material in the process. Prior work has noted that even during Fenton reactions in soils certain quantities of Fe(II) are resistant against oxidation over the time span of at least two hours. We hypothesized that in these cases Fenton reactions are occurring, but the Fe(II) is regenerated during the oxidation of the organic matter. Identification and quantification of Fenton chemistry intermediates—namely H_2O_2—will be used to ascertain Fenton reactions are taking place. We will incubate soil samples at field capacity in an anoxic environment to encourage microbial reduction of iron. After the incubation period, the samples will be exposed to oxygen and at five minute increments for thirty minutes, they will be flooded with 0.001 M HCl to halt reactivity and stabilize H_2O_2. Amplex UltraRed fluorescence reagent will be used to quantify the presence of the H_2O_2. Should Fenton chemistry occur, the concentration of the H_2O_2 will start high and decrease. If it does not occur, there is should be no H_2O_2 produced. By investigating this marker for Fenton chemistry, we hope to better understand the redox processes in soil and the cycling of carbon on local scales.

What Can the Variability of Hematite Tell Us about the Climate of the Triassic?

Discipline: Geoscience
Subdiscipline: Earth Science

Owen Yazzie*, *Arizona State University*; Christopher Lepre, *Rutgers University* and Paul Olsen, *Columbia University*

Abstract: Hematite is a common iron oxide found in mudstone layers and can display numerous colors. Experiments have determined that the color of hematite can be used as an indication of climate. Hematite appears redder in arid climates and bluer in humid climates. In addition, it can be determined where hematite particles may be much finer, as red hematite is smaller than blue hematite. Using diffuse reflectance spectroscopy, visible light concentrations from rocks, soils, and sediments can be collected. From the visible light data, hematite concentrations and its predominant red or blue color can be determined, based on the absorbance characteristics within the wavelength band of ~530-580 nm. For our study, a Varian Cary 50 spectrophotometer fitted with a diffuse reflectance spectroscopy sensor was used to collect diffuse light data from Late Triassic fossil soils preserved in sediment cores of the Chinle Formation, AZ. We conducted a meta-analysis of these data and compare the results to CIE color space data measured by the Geotek Multi-Sensor Core Logger at the national repository of LacCore, MN. Our preliminary results indicate that hematite concentrations in the younger half of the sediment core correlate to redder CIE color data, whereas color data for the older half appears to indicate bluish and/or purple hematite. These observations suggest that, similar to hematite concentration, color changes are indicating a progressive drying of the Late Triassic monsoon. Understanding Late Triassic climate provides insights into environmental conditions under which the major elements of modern animal communities on land first evolved.

Does Arsenic and Uranium in the Bedrock Affect Water Quality?

Discipline: Geoscience
Subdiscipline: Earth Science

Clarene Davis[*1]; Clara Chang[2]; Benjamin Bostick[2] and Paul Olsen[2], *(1)Dine College, (2)Columbia University*

Abstract: The Navajo Nation is located in the Four Corners regions of Colorado, Arizona, New Mexico, and Utah. Water quality is a major problem in the Navajo Nation. Poor water quality is critical to people using untreated private wells and affects regulated water systems regionally. The Navajo Nation is particularly affected by contamination related to mining rocks enriched in toxic metals. Most of these mines are abandoned and improperly remediated, and left behind elevated levels of uranium (U) and arsenic (As) metals in the water.

The purpose of this project is to determine how geological sources of arsenic and uranium may contaminate the water. We hypothesized there is some relationship between bedrock chemistry and the water quality. We analyzed bedrock chemistry using X-Ray Fluorescence Spectroscopy (XRF) measurements on cores from the Colorado Plateau. XRF includes measurements of toxic elements such as U, As, and other elements important in regulating As and U solubility like Si and Fe. We compared XRF data to lithologic logs to determine the relationship between bedrock lithology and chemistry. We used QGIS to compare bedrock chemistry to As measurements in wells. Initial results show there is more As in the claystone than the sandstone. This is encouraging because water is more likely to flow through sand than clay, therefore, the most commonly used groundwater aquifer is less likely to be contaminated by the bedrock. However, water derived from the boundary between clay and sandstones may be susceptible to contamination because clays can contribute metals to the aquifer.

Do Freshwater Foraminifera Disturb Stromatolite Fabric?: A Hypothesis for the Decline of Stromatolites on Early Earth

Discipline: Geoscience
Subdiscipline: Earth Science

Leena Sen[*1]; Joan M. Bernhard[2]; Veronique Le Roux[2] and Pieter T. Visscher[3], *(1)Cornell University, (2)Woods Hole Oceanographic Institution, (3)University of Connecticut*

Abstract: Microbialites are lithified microbial mats, with an extensive geological record dating back to >3.4 Ga. They exemplify the earliest pervasive life on Earth. A decline in stromatolites (layered microbialites) during the Neoproterozoic (700-541 Ma) remains a topic of controversy. A popular hypothesis to explain the Neoproterozoic decline of stromatolites is the radiation of eukaryotic predators that disrupt microbialite mesofabric, yet there is little fossilized evidence for this. Some foraminifera that lack mineralized shells, and thus do not easily fossilize, have been shown to disrupt the mesofabric of marine stromatolites. As part of a project studying Fayetteville Green Lake, NY (FGL) stromatolites in an alkaline setting considered an analog for Proterozoic oceans, we seeded FGL stromatolites with a freshwater foraminiferal species. Short cores of stromatolites (n=3) were placed in cut syringes with FGL water, imaged via microCT scanner, and seeded with ~10 individual *Haplomyxa saranae,* which were added to the stromatolite surface. After ~3.5 months, cores were scanned again via microCT. The before and after scans were analyzed in the softwares CTVox and CTAn from SkyScan to assess the degree and presence of disturbance to the mesofabric to microfabric. Preliminary results show limited disturbance to the large-scale stromatolite lamination, but ongoing textural analyses aim to quantify differences between pre- and post-experiment scans. While extant stromatolites are not ideal analogs for all early Earth microbialites, experimentally investigating their interaction with protistan inhabitants may further elucidate the biological processes that account for their demise in the Neoproterozoic. Supported by NSF 1561204.

$PM_{2.5}$ and Confirmed Positive Tests for COVID-19 in Illinois By County

Discipline: Geoscience
Subdiscipline: Earth Science

Eric Friedman*[1]; Madison Torrey[2]; Kenneth Nicholson[3]; Gregory Anderson[1] and Elisabet Head[1], *(1)Northeastern Illinois University, (2)Arizona State University, (3)Northeastern Illinois University, Chicago*

Abstract:

With the potentially dire respiratory effects on someone infected with COVID-19 it is natural to wonder whether or not air quality has any impact on the number of positive COVID-19 cases in a particular area. Recent studies have examined the connection between long-term exposure to $PM_{2.5}$ and COVID-19 mortality. This study explores the connection between long-term exposure to $PM_{2.5}$ and the number of confirmed positive tests for COVID-19 in the state of Illinois by examining whether or not there is a connection between higher levels of said exposure and an increased number of cases in a particular county. With the hopes that said findings will inform future research decisions regarding the study of air quality and COVID-19. Using established long-term mean $PM_{2.5}$ measures for every Illinois county and Johns Hopkins University data for confirmed positive tests of COVID-19 in each respective county to examine whether or not there appears to be a relationship between higher long-term mean $PM_{2.5}$ exposure and positive COVID-19 cases. At the time of writing this abstract the data has been gathered, but the statistical analysis portion has yet to be completed. Further information can and will be provided as it becomes available.

Tracking Ozone Plumes from Chicago to Wisconsin

Discipline: Geoscience
Subdiscipline: Earth Science

Oceana Chavez*[1]; Gloria Rios[1]; Gregory Anderson[2]; Elisabet Head[2] and Kenneth Nicholson[1], *(1)Northeastern Illinois University, Chicago, (2)Northeastern Illinois University*

Abstract: The stratospheric ozone shield is an essential region of Earth's atmosphere that protects life from harmful ultraviolet (UV) rays. However, ozone is created in the Earth's troposphere is dangerous to human health and the environment. Ozone is created when nitrogen oxides (NOx) and volatile organic compounds (VOCs) from the emissions of cars, power plants, chemical plants, and other sources react in the presence of sunlight. Human health is negatively impacted by ozone, creating, and exacerbating conditions such as asthma. In Chicago, Illinois the consequences of poor air quality are apparent. There have been roughly 85k COVID-19 cases and 5k deaths due to the pandemic. As the virus attacks the inner lining of the lungs, causing severe respiratory issues, poor air quality can exacerbate COVID-19 and increase fatalities. Investigating air quality, such as ozone, in Chicago and surrounding areas is necessary if we are to understand how COVID-19 and comorbidities such as asthma are connected. In this study, we examine movement of ozone from Chicago to Wisconsin on high ozone days to determine whether ozone created in Chicago affects the air quality of surrounding regions. R studio databases and EPA databases are used to plot and visualize ozone concentration, as well as ozone precursors such as NOx. Preliminary data from 2017 show that ozone plumes can be tracked along the west shore of Lake Michigan and we hypothesize that this same movement can be seen for 2019. This ozone may have affected communities along the path, negatively impacting their respiratory systems.

Analysis of Small-Scale, Spatial Variability within High-Density Arrays of Passive Fog Collectors to Determine the Optimal Location for Fog Collection at a Foggy Site

Discipline: Geoscience
Subdiscipline: Earth Science

Daniel Fernandez and Conor Rickard*, *California State University, Monterey Bay*

Abstract: Wind-driven fog can be collected passively and inexpensively, and fog water can supplement the needs of a site or community. The small-scale variability of fog deposition has not yet been researched. In Monterey, CA considerable variability of water collection has been observed within high-density arrays of fog measurement instruments, known as standard fog collectors (SFC). SFC consist of a square meter of mesh mounted 2 to 3 meters above ground. A trough beneath the mesh routes fog water to a tipping-bucket, rain-gauge, measurement device. Spring 2018, an array of ten standard fog collectors was installed at California State University, Monterey Bay on level ground, nearly vacant of vegetation within 4,500 m^2. Less than 4 km north, in 2019 an array of eight collectors was installed at the University of California, Fort Ord Natural Reserve, amidst sloping chaparral within 130,000 m^2. Both sites are about 2.5 km from the coast. Every collector was identical in design and orientation. It is anticipated elevation changes and surrounding vegetation play a role in wind speed and direction, affecting fog deposition and liquid water content available at each SFC. A large set of interannual fog collection data, and site-specific weather data is used in conjunction with topographic detail, vegetation characterization, and regional meteorological history to analyze small-scale variability and determine the optimal placement for a fog collector within a foggy site. This research has implications for fog collector installations worldwide and will interest the general public, cloud physicists, and environmental scientists.

Impact of Particulate Matter on COVID-19 Patients in the State of Illinois

Discipline: Geoscience
Subdiscipline: Earth Science

Samran Mirza*[1]; Gregory Anderson[1]; Elisabet Head[1] and Kenneth Nicholson[2], *(1)Northeastern Illinois University, (2)Northeastern Illinois University, Chicago*

Abstract: COVID-19 is having a massive impact on residents of the state of Illinois. As of July 10th, there have been 151,767 confirmed cases and 7,144 people have died in Illinois. Long term exposure to Particulate Matter (PM2.5) effects human health, such as decreasing lung function and exacerbates the respiratory symptoms of illnesses such as asthma and chronic obstructive pulmonary disease. It has been shown that these existing conditions put COVID-19 positive persons more at risk for worse outcomes. Preliminary work from Harvard University has demonstrated a correlation between COVID-19 impact and air quality around the United States. This research focuses on specific counties of Illinois and how the air quality has an impact on its COVID-19 mortality. The approach involves comparing counties in Illinois to other counties around the United States that have a strong statistical similarity score derived from population density, number of cases, and the number of hospital beds available. Johns Hopkins University, The United States Census Bureau, and the Environmental Protection Agency provide detailed and up to date data for this investigation. The goal of this study is to establish the connection, if any, between air pollution and COVID-19 in select counties in Illinois.

Did Iceberg-Discharge Events Influence the Climate and Circulation of the Central North Atlantic Ocean during the Main Würm Glaciation?

Discipline: Geoscience
Subdiscipline: Earth Science

Ava McIlvaine*, *Scripps College* and Jerry McManus, *Lamont-Doherty Earth Observatory, Columbia University*

Abstract: The chemical, biological, and physical impacts of iceberg-discharge events in the North Atlantic Ocean are well-studied for the late Quaternary period. However, a broad glacial-interglacial timescale defines the pattern of these intense iceberg-discharge events observed throughout the existing paleoclimate record. The following analysis of ocean sediment from Integrated Ocean Drilling Program (IODP) Core Site U13-13 (41°0.0'N, 32°57.42'W) is therefore limited to iceberg-discharge episodes during the Main Würm Glaciation to potentially enhance the resolution of the current record both temporally and spatially for the central North Atlantic. IODP Site U13-13 is a reoccupation of Deep Sea Drilling Project (DSDP) Site 607 which has already proven to be a useful site for reconstructing deep and surface ocean circulation during the last glacial period. IODP Site U13-13 is situated on the western flank of the Mid-Atlantic Ridge (3413 m) at a climatically sensitive boundary between sup-polar and sub-tropical Atlantic waters. Initial investigation into the core's sediment (>63µm fraction) detected the presence of polar planktonic foraminifera species *N. pachyderma*, sub-polar species *T. quinqueloba,* and Ice Rafted Debris (IRD), indicating a possible past extension of polar water into the central North Atlantic Ocean. Further research may allow for the addition of a reconstructed regional signal into the complex history of iceberg-discharge events in the North Atlantic. This study aims to expand present research on abrupt climate change in the North Atlantic and potentially provide new insight into the role of deep ocean circulation during the last glacial period.

Using Excel to Teach Polar Data to High School Students

Discipline: Geoscience
Subdiscipline: Earth Science

Isabella Hedly*[1]; Augustin Kalytiak-Davis[2]; Penny Rowe[3] and Steven Neshyba[3], *(1)Wellesley College, (2)Williams & Mary College, (3)University Of Puget Sound*

Abstract: ENgagement through GUided INquiry modules, or PENGUIN modules, give students hands-on experience working with polar data and research, using topics such as polar ice melt and ice cores. The modules include working through Excel spreadsheets or coding in Python through Jupyter notebooks. The original goals of the study included determining whether these modules could teach undergraduate students about polar regions. Student survey results indicate that students felt they knew more about polar data after completing the modules.

In the current project, the aim of the study is to convert the modules to the High School level. Modules modified to the High School level include a sea level rise one, an ice core one, and a penguin one. In the module about sea level rise, students view different scenarios for sea level rise, link them to melting of polar land ice, and see how this affects flood levels. In the ice core module, students examine oxygen isotope data from ice cores and use it to track temperature over time. Finally, we created a new module about how warming waters kill krill and how this impacts penguin populations. To improve usability at the High School level, modules that use Jupyter notebooks were modified to use Excel spreadsheets. In addition, math standards were incorporated into the modules. The three modules will be used in an Algebra 2 class in Tacoma, Washington. Based on lessons learned, the modules will be revised and improved so they can be used more broadly.

Validation of Wavewatch III Simulations Under Hurricanes in Shallow and Deep Water

Discipline: Geoscience
Subdiscipline: Earth Science

Avery Barnett*, *Grinnell College* and Brandon Reichl, *NOAA Geophysical Fluid Dynamics Laboratory*

Abstract: The validation of surface wave models in shallow water under hurricanes remains a difficult task due to the limited number of observations taken in this regime. In this study we utilize airborne SRA observations of the hurricane wave field under three hurricanes (Hurricane Irene, 2011; Hurricane Ingrid, 2013; and Hurricane Karen, 2013) and use this data to assess the skill of wave simulations from NOAA's surface wave model WAVEWATCH III. This dataset includes several examples of observed wave spectra in shallow water conditions (<20 m), which allows us to analyze model performance in shallow versus deep water. Our results focus on the sensitivity of the WAVEWATCH III skill to three model factors: the wind forcing, the topography, and the use of a structured grid versus an unstructured coast following grid. By focusing on wave height and dominant wavelength, we conduct statistical analysis to analyze the similarities between the observations and different model configurations. We also compare wave spectra simulated from the models to the observed SRA spectra for further skill assessment. This study is important to increase our confidence in employing the model for shallow water conditions, which contributes to ongoing research efforts to improve prediction of the impact of hurricanes along coastal regions.

Pd and Cd contamination in the Los Angeles County

Discipline: Geoscience
Subdiscipline: Geology

Melissa Aros*, *California State University, Northridge* and Michael Vendrasco, *Pasadena City College*

Abstract: This research project analyzed the possibility of lead contaminated soil in three residential areas that resided within a 5-mile radius of the Exide Company. The U.S. government has identified this company as a superfund area that poses a threat to human health. To establish a control sample, Eaton Canyon was used to determine the amount of lead that is naturally present in soil. At California State University, Long Beach the acid digestion process was utilized to prepare the soil samples for chemical analysis using the ICP-MS. The results revealed a correlation between the Exide Company and the residential areas as they both had more than 200 ppm of lead and cadmium particles in their soil.

Creation of a Fire Catalog Using a Core Sediment Sample from Lake Namonte Site in South Western Madagascar

Discipline: Geoscience
Subdiscipline: Geology

Azaria Davis*; Jose Capriles and Alejandra Rivadeira, *Pennsylvania State University*

Abstract: It is well known that global warming rapidly changing the world, and many have questions about how it will impact endemic species. This study utilizes microcharcoal analysis to reconstruct the fire activity over the last 1,400 years before present at Lake Namonte in south western Madagascar. The study is being conducted using microscopy and ImageJ software to quantify and identify charcoal particles deposited in the soil. The analysis will help determine approximately the frequency of fires and whether the fires were fueled mainly by woody or leafy vegetation. Furthermore, it can clarify how human activity and climate change have impacted the Madagascar dry deciduous forest, a unique ecoregion inhabited a high number of endemic species. Thus, insight gleaned from the study can be used to infer possible consequences of the climate change taking place today. Preliminary results of the samples from the sediment core contain very low concentrations of charcoal relative to most macrocharcoal studies (from 30 to 130 cm in depth). However, when taking into consideration data from a microcharcoal analysis done on the same core, there is indication of numerous fires. The variability in the concentration of charcoal particles along the sediment core suggest events of high and low fire intensity, or alternatively a small number of fires that took place at the site of the core (natural or manmade) and decent fire activity taking place near enough to deposit ash in the soil of the core.

Water Chemistry and Quality in Texas River Basins

Discipline: Geoscience
Subdiscipline: Geology

Lourdes Moreu*; Victor Garcia; Jason Ricketts and Lin Ma, *University of Texas at El Paso*

Abstract: There is a lack of understanding of how climate, geology, and land use impact water quality in rivers across the State of Texas. It is vital to understanding surface water chemistry and quality because of its many impacts on society, agriculture, and human health. The surface water chemistry and quality of four Texas rivers basins (Brazos, Colorado, Pecos, and Red) will be investigated to gain an improved understanding of how climate, geology, and humans impact water quality in rivers. This is a newly funded National Science Foundation project to UTEP. We will start the planning work for this project during summer 2020 for the Pecos river, Colorado river, Brazos river, and Red river. Fifteen water sampling locations along each river for future water sampling were determined based on proximity to USGS and TWDB stream gauges and accessibility. Future water sampling locations were mapped in Google Maps. Historical data for sampling locations with stream gauges was utilized from the United States Geological Survey's (USGS) website. This historical data included hydrographs of stream discharge and gauge height, and water chemistry data such as conductivity, pH, and total dissolved solids (TDS).

The "Rocket Storm" of 1954: Evidence for Inclusion in Hurdat

Discipline: Geoscience
Subdiscipline: Other Geoscience

Audrey Flores* and Patrick Fitzpatrick, *Texas A&M University-Corpus Christi*

Abstract: The purpose of this research is to substantiate that a landfalling tropical disturbance near Brownsville, Texas, on October 4, 1954, was likely a tropical depression. It then traversed the Texas-Mexican Border causing abundant rainfall accumulation until it dissipated near Roswell, New Mexico, on October 7, 1954. This cyclone's uniqueness was discovered visually on a set of two 16-mm cameras that were mounted on a Navy Aerobee rocket launched on October 5, 1954, in White Sands, New Mexico. These cameras captured visual evidence of an apparent tropical cyclone near the town of Del Rio, Texas, and is the first known high-altitude visual evidence of a tropical cyclone in recorded history. However, despite the low pressure values, a heavy rainfall swath, and the photo, this likely tropical cyclone is not included in the North American hurricane database (HURDAT), an archive of Atlantic basin tropical cyclones.

The rocket test was a historic event. This photo clearly demonstrated the value of space-borne visualization. In addition to the first structural evidence of spiral banding, it clarified the cause of unpredicted rainfall in South Texas, since the conventional observation network left the tropical cyclone undetected. Data includes surface observations (pressure, precipitation, wind, and temperature) in this storm's track and the application of the Dvorak technique, from the landfall location to Roswell, New Mexico. Offshore significant wave height information is also utilized. This research will show a high probability this system was a tropical depression, and should therefore be included in HURDAT.

Accelerating Equilibration: Application of a New Technique for Mapping Climate Sensitivity across a Wide Range of Climates

Discipline: Geoscience
Subdiscipline: Other Geoscience

Emiliia Dyrenkova*, *University of California, Berkeley* and Nicole Feldl, *University of California, Santa Cruz*

Abstract: Equilibrium climate sensitivity (ECS), defined as the global average surface warming at equilibrium following a doubling of CO_2 concentration, is a widely used metric for quantifying projections of climate change. A curious behavior has been observed in climate models at very high concentrations of CO_2: the ECS exhibits a pronounced maximum at sea-surface temperatures (SSTs) around 300-320 K and CO_2 levels exceeding 1120 ppm. However, equilibration of a model with prescribed CO_2 concentration takes many years of model time, which limits the number of simulations that can be run and provides coarse data that can miss important details. To overcome this computational challenge, we will run a global aquaplanet simulation employing an equilibration technique previously applied only to small domain models in the literature. First, the model will be run to equilibrium with pre-industrial CO_2 levels. Then, instead of the conventional approach whereby CO_2 is increased and SST equilibrates, we will prescribe an increase in SST and equilibrate the CO_2 concentration. This will allow us to map out ECS for a wide range of climates, thus evaluating the existence, position, and magnitude of the peak in a model with different physics. Prior work has hypothesized that the peak in ECS is due to an SST-dependent change in the cloud feedback, however, the mechanism remains unclear. Faster computation in a global model has the potential to identify the controls on the phenomenon and further our understanding of the influence of CO_2 on clouds in a much warmer world.

Optimizing Observational Arrays in the Tropical Pacific By Estimating Correlation Lengths

Discipline: Geoscience
Subdiscipline: Other Geoscience

Winnie Chu*, *Harvey Mudd College* and Matthew Mazloff, *Scripps Institution of Oceanography, UC San Diego*

Abstract: Accurate observations of biogeochemical variables in the ocean are critical to monitoring the effects of climate problems. With limited resources, we want to maximize the coverage of sensor measurements by estimating the distances over which an observation correlates with its surrounding area. In our research we quantify these correlation lengths for carbon and oxygen in the Tropical Pacific Ocean using realistic model statistics of the region. Our results are correlation scales which inform the locations for sensor deployment that best capture large-scale biogeochemical variability.

Detection of the Dcpa Gene in Sediment Samples in Puerto Rico

Discipline: Geoscience
Subdiscipline: Other Geoscience

Axwel Deliz* and Elizabeth Padilla-Crespo, *Interamerican University of Puerto Rico, Aguadilla Campus*

Abstract: Due to its widespread use, improper handling and recalcitrant nature, chlorinated solvents are toxic & ubiquitous contaminants. In the past, 1,2-Dichloropropane (1-2,D) was used as a soil fumigant, and industrial solvent. 1-2,D is toxic causing damage to the liver and kidney; potential carcinogen. The EPA set a Maximum Contaminant Level (MCL) of 5 ppb for 1,2-D in drinking water. Two *Dehalococcoides (Dhc)* strains, RC and KS, have been implicated in 1,2-D-to-propene dechlorination. The *dcpA* gene encodes the reductive dehalogenase responsible for transforming 1,2-Dichloropropane to then non-toxic propene. Fresh water and sediment from the west coast of Puerto Rico, with no previous knowledge of exposure to 1,2-D were sampled. Following, DNA was extracted and interrogated with primers targeting the *dcpA* gene. PCR results showed the presence of the *dcpA* gene at various of the collected samples. Further research aims to shed light on RDase gene dissemination and the adaptation of dehalospiringpopulations in tropical sediments, aquatic, and subsurface environments.

Presence and Succession of Cable Bacteria at Hydrate Ridge, NE Pacific Ocean

Discipline: Geoscience
Subdiscipline: Other Geoscience

Claire Andrade*; Cheng Li and Clare Reimers, *Oregon State University*

Abstract: Cable bacteria and *Beggiatoa* are filamentous microbes that oxidize sulfide and have been shown to exhibit a seasonal succession in coastal sediments, intercepting fluxes of free sulfide to the water column. Hydrate Ridge (HR) is a permanently hypoxic offshore location with methane seeps along the Cascadia convergent margin where *Beggiatoa* mats naturally occur while traces of cable bacteria have not been reported. In the present study, we are using sediment cultivation, microelectrode profiling, fluorescence in situ hybridization (FISH), and 16s rRNA gene sequencing to investigate the presence and emergence of cable bacteria in HR sediment. Our results to date indicate that after 3 weeks of cultivation in oxygenated seawater, geochemical signatures of cable bacteria can be observed in HR sediment while colonies of *Beggiatoa* were still present on the sediment surface. Bacterial filaments belonging to the family of Desulfobulbaceae became observable by FISH. These observations suggest that cable bacteria are present in the microbial community of HR sediment, and as in coastal environments they may emerge if concentrations of electron acceptor increase. We are in the process of repeating these experiments with fresh HR sediments and analyzing 16s sequencing results from a suite of HR and other offshore samples. The combined outcome will show if cable bacteria are much more widespread throughout the ocean than previously thought.

Investigating How Continental Geometry and Land Surface Properties Control Relative Humidity over Land

Discipline: Geoscience
Subdiscipline: Other Geoscience

Kylie Kinne*, *University of California Los Angeles* and Nicholas Lutsko, *Scripps Institution of Oceanography*

Abstract: Climate model simulations of warmer climates show strong decreases in relative humidity over land, which has important implications for future changes in heat stress and land habitability -- changes which have the potential to dramatically alter human comfort, activity, and productivity. Well-established theories exist for what sets changes in relative humidity over land in the tropics and subtropics, but these theories break down at midlatitudes. In particular, the influences of continental geometry and land surface properties on relative humidity at mid-latitudes are not well understood. We address these issues using an idealized atmospheric model coupled to a simple bucket land model. By varying the shape of a mid-latitude continent, the depth of the land bucket, and the “evaporative resistance” of the land, we are able to clarify the relationships between land surface properties and relative humidity over land. The simplicity of the model allows us to provide straightforward interpretations of the results, which can be applied to understand relative humidity changes in observations and climate models.

Attenuation of Groundwater-Derived Nitrogen Flux within the Yucatan Peninsula Karst Subterranean Estuary

Discipline: Geoscience
Subdiscipline: Other Geoscience

Stephen Galindo*, *Humboldt State University* and Meagan Gonneea, *United States Geological Survey*

Abstract: Highly permeable karst subterranean estuaries (KSE) contain aquifers with high dissolved chemical load, representing a major source of terrestrially-derived nutrient and trace element transport to the coast via subterranean groundwater discharge (SGD). Our study focuses on inorganic nitrogen cycling in the Yucatan KSE, where high amounts (79.48 ± 27.62 μmol/L) of dissolved inorganic nitrogen (DIN) in the groundwater are ultimately discharged into the ocean through coastal springs and diffuse discharge. During transport, terrestrial groundwater mixes with recirculated marine groundwater and as a result is subjected to changes in salinity and dissolved oxygen content. This mixing results in chemical gradients that influence nitrogen speciation and concentration. Water samples were collected from cenotes (sinkholes in the limestone), springs, and offshore transects in 2012-2014. Nitrogen removal occurred during mixing between terrestrial groundwater and marine water within the subterranean estuary and was 30% for the west coast, 54% for the north, and 42% for the east. Based on previous estimates of SGD and DIN concentrations, and accounting for nitrogen removal, we calculated a DIN flux to the Yucatan coast. For the west coast, the DIN-flux is 3,450 ± 1,330, the north coast is 5,522 ± 1,981, and the east coast is 2,917 ± 1,911 metric tons/year. Understanding the biogeochemical processes that alter nitrogen concentrations in oxic/anoxic waters within the KSEs is critical to estimating N-fluxes associated with groundwater discharge.

Effects of Genetic Variation and Disturbance Legacy of Trembling Aspen on Soil Microbial Function

Discipline: Geoscience

Subdiscipline: Other Geoscience

Olivia Lopez[*1]; Chase Kasmerchak[1]; Erika Marin-Spiotta[2]; Richard Lindroth[1]; Eric Kruger[1] and Nick Pomplun[1], *(1)University of Wisconsin-Madison, (2)University of Wisconsin, Madison and Earth Science Women's Network*

Abstract: Forest fragmentation has altered the genetic diversity of plants, both among and within species, by generating selective pressure or random changes in the frequency of different genotypes. Plant community composition plays an important role in ecosystem functions mediated by soil microorganisms, but little is known about how genetic variation *within* species affects these processes. This research examines how genetic variation in *Populus tremuloides* influences soil microbial activity and nutrient cycling in a forest in southern Wisconsin. At our site, 14 genotypes are represented within 18 populations. Half of the sites were subjected to a thinning treatment to mimic an intermediate disturbance. Results show that thinned stands had ≈12-20% greater rates of nitrogen mineralization and nitrification than unthinned stands (both $p < 0.05$), although there was considerable variation among plots within the same treatment. A short 11-day laboratory litter addition experiment showed that thinned stands had 22-27% greater cumulative microbial respiration, with greater CO_2 respired per gram of soil per day when high CT litter was added, although neither are statistically significant. Soil-only jars with no added litter showed the opposite, with unthinned soils respiring more than twice as much CO_2 as thinned soils ($p < 0.05$). We expect a longer laboratory experiment and an upcoming 18-month field experiment to reveal effects of litter chemistry (high vs low CTs and C:N ratios) and soil disturbance legacy (thinned vs unthinned) on litter decomposition. Our results will provide insight on how ecosystem disturbance affects genetic diversity, microbially-mediated functions, and carbon storage in soils.

Anthropogenic Influences on Extreme Precipitation Events over the San Francisco Bay Area in a High-Resolution Regional Climate Model

Discipline: Geoscience
Subdiscipline: Other Geoscience

Flor Maciel[*1]; Christina Patricola[2]; Emily Bercos-Hickey[3] and Michael Wehner[3], *(1)University of California, Santa Cruz, (2)Iowa State University, (3)Lawrence Berkeley National Laboratory*

Abstract: The San Francisco Bay Area has a high population density and a large public infrastructure that need to be protected from natural hazards. As anthropogenic climate change continues to unfold, it is imperative that city agencies have reliable projections that estimate how impactful weather events may change in the future. Precipitation is one such hazard that is expected to change in a warmer climate. Specifically, the extreme precipitation from atmospheric rivers and extratropical cyclones is of key interest. Here we investigated how the intensity of five historical storm events that impacted the San Francisco Bay Area could change if similar events occurred in future climates. We used the Weather Research and Forecasting (WRF) model to simulate the storms in the historical climate in which they occurred, and under future climate conditions (the Representative Concentration Pathway 8.5 emissions scenario at the middle and end of the 21st century). We examine future changes in regional storm-total precipitation and the probability of extreme 3-hourly precipitation rates. This research provides quantitative estimates of how climate change can affect extreme precipitation in the future.

Testing Hypotheses for the Role of Climate Change in Hominin Evolution Using the Geochemistry of Carbonates from the East African Rift System

Discipline: Geoscience
Subdiscipline: Other Geoscience

Cameron Brown[*1]; Deepshikha Upadhyay[2] and Aradhna Tripati[2], *(1)Pennsylvania State University, (2)University of California, Los Angeles*

Abstract: A series of major hominin speciation events that took place in East Africa during the Pliocene-Pleistocene epochs have been linked to landscape evolution. Previous studies examining the role of climatic and environmental pressures on hominin evolution have used either discontinuous outcrops exposed proximal to, or marine sediments distal from, hominid fossil sites. These sediments have been used to develop stable carbon and oxygen isotope (13C, 18O) proxy-based reconstructions of ancient environments, showing evidence for a series of changes including a transition from woodland to savannah-dominated environments. This work has prompted researchers to hypothesize that speciation events coincided with cooling of the African climate and local aridification during times of glacial intensification. It is speculated that local environmental pressures led to an increase in brain size, breakthroughs in stone technology, and the migration of Homo sapiens out of Africa. However, recent clumped isotope reconstructions from soil carbonates (Passey et al., 2010) have challenged this hypothesis, depicting relatively high and stable temperatures during the past 4 My. To find resolution between these competing hypotheses, we are examining paleosols and lake sediments near hominin fossil sites, including recently recovered drill cores that provide access to an unweathered and continuous archive of past environmental change. Isotopic data (13C, 18O, and Delta-47) are used to constrain past changes in vegetation, hydrology, and temperature.

Tumor Genomics As a Route to Characterizing Multiple Myeloma

Discipline: Health
Subdiscipline: Medicine

Taylor Aucutt*[1]; Nicola Camp[2] and Rosalie Waller[1], *(1)University of Utah, (2)Huntsman Cancer Institute*

Abstract: Multiple myeloma (MM), a plasma cell cancer, is one of the more common hematological malignancies and is increasing by 0.8%/yr. Treatments have improved but most patients do not survive past 5 years after diagnosis. It is currently unclear why certain people get MM, although genetic risk factors have been proposed and a few discovered. The molecular make-up of the malignant MM cells is highly variable from patient to patient, thus making it difficult to model and treat. This presentation illustrates a novel method for modeling gene expression and characterizing the malignant MM cells. RNA extracted from malignant (CD138+) cells was used for whole transcriptome sequencing (gene expression in malignant cells). Transcriptome sequencing provided expression for about 58,000 genes. Multi-dimensional reduction was used on the 58,000 genes, resulting in 30 variables or principal components (PC). Values for each PC vary across patients allowing us to better characterize the patient's MM and describe the complexity of each tumor. Initial analysis show that the principal components can be used to predict patient prognosis, due to the association between principal components and current clinical prognosis methods. Although still in the early stages, this novel characterization method shows excellent potential as a useful tool for clinical management. In the future we will consider response to treatment in the hopes that this characterization of tumors will help tailor treatments to patients. Before translation into the clinic, however, further research will be needed to replicate our findings and determine the full scope for this novel technique.

Guinea Pig Model of Mild Hyperandrogenemia during Puberty: Potential Cause of Polycystic Ovarian Syndrome (PCOS)

Discipline: Health
Subdiscipline: Medicine

Juriana Examaray Barboza Sagrero* and Cecily Vauna Bishop, *Oregon State University*

Abstract: Abstract: Polycystic Ovary Syndrome (PCOS) is an idiopathic disorder prevalent in ~5-10% of reproductive-aged women. In PCOS women who become pregnant, many experience complications including increased susceptibility of having a miscarriage, high blood pressure, and gestational diabetes, among others. Additionally, exposure to PCOS may have transgenerational impacts: offspring may be at increased risk of overall poor health in adulthood. In previous studies, rhesus monkeys exposed to mildly elevated testosterone (T) with and without a high fat diet (HFD) developed many PCOS-like symptoms; however, transgenerational studies in macaques are challenging due to longer generational intervals (5+ years). We hypothesize the guinea pig sow is a good surrogate for primates and will show a similar PCOS-like phenotype. All experiments will begin in August 2020. We will obtain Hartley Guinea Pigs prior to puberty. Subcutaneous implants will be placed containing either cholesterol (n=4) or T (n=4) between 1 and 4 months of age. Serum T levels and weight will be assessed weekly, and females will be monitored for signs of estrus daily. At 4 months of age, body composition will be assessed by DEXA scanning, and all females will undergo necropsy. We expect T-treated females to have deviations in length of estrus cycles and mild metabolic dysfunction, similar to studies in rhesus monkeys. The proposed model can be used in future studies combining T and/or HFD exposure during pregnancy to determine transgenerational impacts on offspring. Furthermore, this model can be used to test interventions that may be beneficial for women seeking to conceive.

Effect of Platelet-Rich Plasma on Endometrial Cytokine Expression

Discipline: Health
Subdiscipline: Medicine

Victor O Perez* and Michelle Anne Kutzler, *Oregon State University*

Abstract: Current treatments for reproductive problems in beef cattle involve hormones and antibiotics which are expensive and often ineffective. Our objective was to test effectiveness of intrauterine platelet rich plasma (PRP) on endometrial pro-inflammatory cytokine (IL-6, IL-8, TNFa) expression. Twelve Angus-crossbred heifers calved under supervision. Nine heifers calved normally (eutocia) and three heifers needed assistance (dystocia). The eutocia heifers were divided into groups to receive intrauterine treatments: platelet rich plasma (PRP), platelet poor plasma (PPP), and saline-treated eutocia (EUT). The dystocia heifers were also treated with saline (DYS). Endometrial cells were collected from cervix at 2- and 4-weeks post-calving. Intrauterine treatment was administered once after samples were collected 2-weeks post-calving. Total RNA was isolated from endometrial cells using a standard phenol-chloroform protocol. Complementary DNA (cDNA) was prepared from the total RNA using a commercial kit. Forward and reverse primers for IL-6, IL-8, and TNFa as well as the housekeeping gene (β-actin) were used for real-time polymerase chain reactions to determine relative gene expression. Paired Student's t tests were used to compare the relative expression of each group to saline-treated controls. Due to the small sample size in each group, there was no significant effect of any treatment (PRP, PPP) or dystocia on expression of IL-8 ($p=0.984$, $p=0.313$, $p=0.593$, respectively), IL-6 ($p=0.324$, $p=0.593$, $p=0.816$), or TNFa ($p=0.398$, $p=0.752$, $p=0.825$). The use of (PRP) as a treatment for reproductive problems and reduction of pro-inflammatory cytokines could provide producers with an alternative to traditional antibiotic or hormonal treatments.

Ivabradine Improves Heart Rate and Quality of Life in Hyperadrenergic Pots: First Randomized Clinical Trial

Discipline: Health
Subdiscipline: Medicine

Pam Taub; Adena Zadourian; Hannah Lo; Cameron Ormiston[*]; Shahrokh Golshan and Jonathan Hsu, *University of California, San Diego*

Abstract: Postural Orthostatic Tachycardia Syndrome (POTS) is a multifactorial disorder that primarily impacts young women and significantly reduces their quality of life (QOL). Although non-pharmacological and pharmacological therapies exist, current treatments fail to provide significant relief. We investigated the effect of ivabradine (selective blocker of the Ifunny channel in the sinoatrial node) on heart rate (HR), quality of life (QOL), and plasma norepinephrine (NE) levels in patients with hyperadrenergic POTS defined by plasma NE>600pg/mL and abnormal tilt table test. 22 patients with hyperadrenergic POTS completed a randomized, double-blinded, placebo-controlled, crossover trial with ivabradine. Patients were randomized to start either ivabradine or placebo for 1-month, and then were crossed over to the other treatment for 1-month. HR, QOL, and plasma NE levels were measured at baseline and at the end of each treatment month. The average age was 33.9±11.7 years, 95.5% were female (n=21), and 86.4% were white (n=23). There was a significant reduction in HR between placebo and ivabradine ($p<0.001$). Patients reported significant improvements in QOL with the RAND 36-Item Health Survey 1.0 for physical functioning ($p=0.019$) and social functioning ($p=0.016$). There was a strong trend in supine and standing NE levels ($p=0.056$). Patients did not experience any significant side-effects such as bradycardia or hypotension with ivabradine. In this first randomized, double-blinded, placebo-controlled crossover trial, ivabradine was shown to be safe and significantly improved HR, QOL, and NE in patients with the hyperadrenergic subtype of POTS. With this significant HR reduction, patients with POTS had improvement in functional status.

Clinically Relevant Multi-Drug Resistant Plasmid Found in Environmental *Escherichia coli* Isolate from the Hudson River, NY

Discipline: Health
Subdiscipline: Medicine

Ricardo Canela[*]; Iván Muñoz-Gutiérrez and Luis Mota-Bravo, *University of California, Irvine*

Abstract: Antibiotic resistance is a health crisis currently impacting the world. Drug resistant infections are threatening to surpass cancer and diabetes as the leading cause of death by the year 2050. Strains of *Escherichia coli* are known to cause serious intestinal, blood and urinary tract infections in humans. We hypothesize that an environmentally isolated strain of *E. coli* from a metropolitan area could possess antibiotic resistance genes. The objective of this study is to characterize the antibiotic resistance genes and mobile genetic elements capable of horizontal gene transfer (HGT) within *E. coli* isolate SW6760 isolated from the Hudson River in New York. We tested 24 clinically relevant antibiotics on isolate SW6760 using a disk diffusion test and created an in-silico assembly of its plasmids for annotation and gene analysis. The results revealed a large plasmid of 135kbp that contained nine antibiotic resistance genes: *aadA5, aph (3'')-Ib, aph(6)-Id, blaTEM-1B, mph(A), sul1, sul2, tet(A),* and *dfrA17*. These genes confer resistance to five commonly administered antibiotics: Ampicillin, Streptomycin, Sulfisoxazole, Tetracycline, Trimethoprim, and an intermediate resistance to Cefazolin. Conjugation tests reveal a set of IncF conjugative genes present on this plasmid which confirms the mechanisms for HGT. This study shows that environmental strains of *E. coli* have the same drug resistant genes as clinical isolates, potentially contributing to the ongoing global health crisis.

Developing a Clinical Trial from the Ground up

Discipline: Health
Subdiscipline: Other Health

LeCario Benashley[*] and Jennifer Bea, *University of Arizona*

Abstract: In research, much time is dedicated to the discussion of a study's intervention and its subsequent results, but hardly any time is given to detail the equally important steps which had to happen before a study and its results could even manifest. This project seeks to highlight those many necessary steps. That journey will be demonstrated using the study titled "PrEvention of Falls among OLdeR Multiethnic cANcEr Patients receiving chemotherapy" (PErFORM ANEW). The trial is a complex multicomponent project which aims to reduce the number of falls in the most at-risk population. It offers to be the perfect case-study to illustrate the people needed, the approvals required, the protocols to be incepted, the materials to be created, and the overall work necessary for a research idea to be ethically implemented and successful in its aims.

The Role of Preschool Educators' Competencies on Children's Early Literacy Development

Discipline: Health
Subdiscipline: Other Health

Aaliyeh Ayub[*] and Vickie Yu, *California State University Northridge*

Abstract: Numerous studies have supported the importance of teaching literacy skills during the first few years of formal education. However, fewer research studies have been conducted examining the benefits of introducing early literacy skills before children enter kindergarten. Introducing these skills before allows all children, regardless of socioeconomic status, to reduce the literacy gap between themselves and their peers prior to beginning kindergarten. Although beneficial for the students, studies show that preschool educators have limited knowledge about phonological and phonemic awareness skills, that are known to be crucial in literacy development. Without this knowledge, how are they expected to teach and

correct phonological awareness tasks to emergent readers? The aim of this study is to understand preschool educators' level of understanding of early literacy skills and methods to implement these skills. We designed a survey study to identify the phonological and phonemic awareness skills of preschool educators in the Southern California region, as well as any other extralinguistic factors that may potentially affect their knowledge. As data collection is still on-going, we expect to find that many early educators do not possess sufficient knowledge of phonological awareness in order to aid the development of early literacy skills for young readers.

Characterizing the Distribution of Ticks and Tick-Borne Pathogens in Yolo County

Discipline: Health
Subdiscipline: Other Health

Paola Vidal-Espinoza*; Laura Backus and Janet Foley, *University of California, Davis*

Abstract: The presence of ticks that carry and transmit disease to humans and animals is of significant concern in California. It is known that both the ticks that carry human pathogens and tick borne pathogens occur in Yolo County, and that humans are exposed to ticks through outdoor recreational and work activities, but the risk to people is not well known in this area. Therefore, the goal of this research is to characterize the risk of tick-borne pathogens to humans in Yolo County. This will be accomplished by collecting ticks, testing them for pathogens, and mapping the geographic results. We will identify five different sites to collect ticks throughout Yolo county and flagging each location at least twice. We will map the results using ArcMap GIS software. Ticks that are collected will then be identified to species by morphologic identification. After identification, pathogen testing will be conducted on ticks for rickettsial bacterial and *Francisella tularansis* using real-time PCR. By surveilling the area and mapping the geographic distribution of pathogens, we can assess tick-borne disease risk in a suburban and peri-agricultural landscape. The resulting data will allow healthcare providers and public health officials to identify cases early and assess the risk to the public in a highly-populated area, and be able to better evaluate the risks of harmful pathogens from tick bites.

Klebsiella Oxytoca with a Class 1 Integron Carrying Antibiotic Resistance Gene Cassettes Found in the Environment

Discipline: Health
Subdiscipline: Other Health

Ashley Urrutia*[1]; Amelie Garenaux[2] and Luis Mota-Bravo[2], *(1)University of California Irvine, (2)University of California, Irvine*

Abstract: Antibiotic resistant bacteria are becoming a major clinical problem worldwide. To better understand the nature and dissemination of antibiotic resistant bacteria, it is important to identify the sources of antibiotic resistance genes (ARGs) and the means to mobilize them. Plasmids, integrons, and transposons are mobile genetic elements (MGEs) known to contribute to the dissemination of ARGs. We hypothesized that environmental bacteria, specifically *Klebsiella oxytoca,* can constitute a source of ARGs through the MGEs they carry. The objective of this work was to characterize the plasmids found in an antibiotic resistant *K. oxytoca*, obtained from San Diego Creek, CA. The isolate was collected on a selective medium and identified by MALDI-TOF. The resistance profile of the isolate was determined by Disk Diffusion Tests. Plasmid DNA was then isolated with Qiagen MidiPrep, sequenced with Oxford Nanopore and Illumina, assembled with Unicycler, and compared with sequences from the NCBI database using BLAST. The isolate was determined to contain four plasmids. One plasmid, Plasmid 3, carried ARG's coding for resistance to aminoglycosides, sulfonamide, and trimethoprim on a class 1 integron. Comparative analysis showed that the insertion of the class 1 integron might have occurred via a Tn402-like transposon. Similar plasmids were found in isolates from different species collected in the United States, Japan, and China from agricultural and clinical settings. This is the first report of an environmental *K. oxytoca* carrying this integron region on a plasmid, highlighting the importance of environmental bacteria as a source of mobilized antimicrobial resistance genes.

Associations between Socioeconomic-Related Factors and Awareness of Genetic Testing for Cancer Risk Among Black Women

Discipline: Health
Subdiscipline: Public Health

Brittany Gardner*, *National Institutes of Health/National Cancer Institute*; Tasia Isbell, *University of Texas Health Science Center at Houston* and Nadine Barrett, *Duke University School of Medicine/Duke Cancer Institute/Duke Clinical Translational Science Institute*

Abstract: Genetic tests are powerful tools for determining cancer risk. Yet, its uptake into standard clinical practice remains low, especially among minority and underserved populations. This study aims to evaluate the associations between insurance coverage, income insecurity, and genetic testing for cancer risk awareness among Black women.

The NCI-funded community assessment entitled Project PLACE (Population Level Approaches to Cancer Elimination) assessed awareness of genetic testing for cancer risk using one item (yes/no). Perception of income insecurity was measured by how well respondents perceived their present income level to be meeting their financial needs and health insurance status was measured using one item (yes/no).

We examined the independent associations between income insecurity and health insurance status, and awareness of genetic testing using two-sided chi-square tests.

Of the 95 respondents, 46.3% were not aware of genetic testing; with higher awareness among those reporting living comfortably on their present income (39.2%). Income insecurity was inversely associated with awareness of genetic testing (*p*=0.04). Health insurance status was not significantly associated with awareness of genetic testing (*p*=0.09).p

Awareness of genetic testing remains low and socioeconomic factors may influence genetic testing awareness. This may contribute to lower rates of genetic testing among minorities and underserved populations. As genetic testing becomes more available and necessary for cancer treatment, it will be important to understand the role of income insecurity, regardless of insurance status or income level. Future interventions should strive to make evidence-based cancer prevention methods more accessible to a broader demographic of patients.

Impact of Individual HIV Status on HIV/AIDS Related Stigma in Lesotho

Discipline: Health
Subdiscipline: Public Health

Aparna Manocha* and Ndola Prata, *University of California, Berkeley*

Abstract: Lesotho's HIV/AIDS prevalence rate of 23.6% is the second highest in the world and poses a serious threat. HIV stigma and fear of discrimination are pervasive in the country, resulting in major barriers to prevention, testing, and health services. The impact on access to healthcare results in a need to understand which populations are most affected by stigmatization and where to target programs. We investigated the role that an individual's HIV status has on stigma held with the purpose of assessing which sub-populations express the most stigmatizing views. We hypothesized that HIV-positive individuals possessed less HIV-related stigma. We utilized questionnaire data collected by the 2014 Demographic Health Survey. Three questions were utilized to reflect stigma, including willingness to care for a relative with HIV, buying vegetables from an infected vendor and allowing a teacher with HIV to continue. Multivariate regression controlled for sociodemographic characteristics including age, education, wealth index, religion, type of residence and marital status revealed a significant, positive relationship between positive HIV status and no bias for the teacher and vegetable vendor questions (p=0.003; p=0.000). Educational attainment was found to mediate the relationship between HIV status and stigma as higher education increased the odds ratio for having less bias for all 3 variables (p=0.000). Our results demonstrate *negative* associations of HIV stigma with positive status, education, wealth, age, marriage and religion. The significant disparities of where stigma exists demonstrates the need to develop educational interventions and strategies to reduce bias in the targeted populations identified by this study.

The Influence Climate Change Will Have on the Vectorial Capacity of the *Aedes Aegypti* Mosquito in South America: A Systematic Map

Discipline: Health
Subdiscipline: Public Health

Liliana Diaz* and Richard Dozal-Lockwood, MPH PhD, *Portland State University*

Abstract: Tropical infectious diseases such as dengue, chikungunya, and Zika affect millions of people annually in all regions of the world, and remain one of the major threats to global public health. The disease burden propagated by these arboviruses has rapidly increased in recent decades due to the range expansion of their shared vector, the *Aedes aegypti* mosquito. Given that the Intergovernmental Panel on Climate Change (IPCC) predicted a global increase in temperatures of 1.4-5.8°C over the next century, understanding how that will affect the vectorial capacity of the *Aedes aegypti* is an essential strategy for public health planning.

This paper will examine findings from a systematic map on the current state of research on this increasingly important influence on infectious disease in South America. The objectives are to: (1) assess the geographical regions represented and (2) identify potential gaps in the existing literature concerning South America.

In an effort to perform an exhaustive search, the databases Medline, PubMed, Academic Search Premier, Fuente Académica, MedicLatina, Environment Complete, Gale in Context: Environmental Studies, Health Reference Center Academic, and Agricultural & Environmental Science will be searched for studies published between Jan 1, 1980 and March 6, 2020 that evaluate the relationship between temperature and *Aedes aegypti* populations.

The resulting literature that meets the criteria for inclusion will then undergo an inductive qualitative analysis for systematic data extraction. Subsequently, they will then be categorized according to geographical region for comparison, in order to identify potential dearth of research on South America.

Using Student Narratives and Ethnographic Approaches to Investigate Factors Influencing the Dietary Behaviors of Latinx College Students

Discipline: Health
Subdiscipline: Public Health

Jesus Chavez* and Alana LeBron, *University of California, Irvine*

Abstract: The social ecological model of health acknowledges that individual behaviors are made under the influence of different social determinants. These determinants can create long-term eating behaviors that can determine whether chronic, non-communicable diseases appear later in life. Previous research has also demonstrated that the transition between adolescence and adulthood, which for many occurs during college, is a significant period that shapes food choices and habits. The objective of this study was to uncover what factors play a prominent role in the decisions made by Latinx college students regarding food and diet. Twenty UCI undergraduate Latinx students were recruited to participate in this qualitative study that used semi-structured interviews and ethnography. These two methods were developed using both an inductive and deductive approach, searching for and analyzing codes from transcripts and food journals and creating codes based on already known influential factors, respectively speaking. Major themes discovered were that the prioritization of school and work created barriers to eating nutritiously. Additionally, the physical, economic, and social context students live under promoted the consumption of an unhealthy diet. However, when participants did opt to acquire healthier options, they did so by sacrificing variety and/or traditional, cultural dishes. This study illustrates that in order to improve the eating patterns of Latinx college students, interventions must be sensitive to both the Latinx and the college student identity. It also invites the question of how food environments can be modified to acknowledge and support these identities so that healthier decisions are more easily made.

Poor Melanoma Survival in Asian Americans Points Toward the Need for a Targeted Educational Intervention

Discipline: Health
Subdiscipline: Public Health

Clarice Ho*[1]; James Zheng[2] and Susana Ortiz[2], *(1)University of California, Berkeley, (2)University of California, San Francisco*

Abstract: Melanoma incidence is increasing in the United States and it is the deadliest form of skin cancer. While rarer in Asian Americans and Pacific Islanders (API), this population has poorer survival and prognosis after diagnosis in comparison to Caucasian populations. We predicted that this was the case due to a difference in demographic and tumor characteristics. To identify the causes of poor melanoma survival among API patients, we conducted a retrospective multivariate analysis of API and Caucasian cohorts from the Surveillance, Epidemiology, and End Result database.

Our Cox-proportional hazards models demonstrated that API had poorer overall and melanoma-specific survival compared to Caucasians. API were at a significantly higher risk for melanoma-specific mortality, with a hazard ratio of 1.24 (p-value: 0.014), while presenting with deeper tumors and later stages of disease. We concluded that survival differences between API and Caucasians can be attributed to differences in demographic and tumor characteristics, while also discovering independent risk factors associated with increased melanoma-specific mortality for the entire cohort, such as low county median income.

Our results point to a need for increased melanoma awareness and education in the API community, encouraging earlier diagnosis and preventative practices. We plan to conduct a clinical study to determine the efficacy and retention of tailored health education efforts in an API population. We will use self-management practices such as reported skin exams and sun-protective techniques as a measure after administering a brochure and an educational presentation that is adapted to the socio-cultural dynamics of the population.

Barriers and Facilitators to Healthy Eating in Black Women Attending an HBCU

Discipline: Health
Subdiscipline: Public Health

Asha McElroy*[1]; Ramine Alexander[1]; Jeannette Wade[1]; Sharon Parker[1] and Cheryl Giscombe-Woods[2], *(1)North Carolina Agricultural and Technical State University, (2)The University of North Carolina at Chapel Hill*

Abstract: Black women have the highest rates of obesity or being overweight compared to any other group in the United States, which can lead to chronic illnesses. A primary contributor to obesity in black women are cultural factors such as the expectation of being a “Strong Black Women”, which can negatively influence black women's health and eating habits. The strong black woman stereotype states that they internalize this concept of having to be strong, suppress their emotions, resist being vulnerable and prioritizing care for others in order to uphold an image. Previous studies done on college students have studied barriers and facilitators to diet, however, little is known about the barriers and facilitators to healthy eating in black women attending an HBCU. Therefore, the purpose of this study is to explore the socio-cultural barriers and facilitators to healthy eating in black women. Three focus groups were conducted with black women (n=17) attending an HBCU between the ages of 18-25. Participants answered questions related to obesity, mental and physical health and what it is like to be strong. Several themes emerged related to barriers and facilitators to healthy eating. Barriers identified were cost, access to healthy food, and life-related stress. Facilitators identified were social support, cooking, and nutrition-related knowledge. Preliminary data from this study will be used to design a culturally salient nutrition intervention that incorporates sociocultural factors that impact diet in black women ages 18-25.

“This Is My Choice. This Is My Life:” How Mexican and U.S. American Culture Affects the Reproductive Health Decisions of Female Adolescents Living in the San Diego/Mexico Border Region

Discipline: Health
Subdiscipline: Public Health

Vivian Maldonado[*]; Ruvani Fonseka and Dr. Jay Silverman, *University of California, San Diego*

Abstract: Latinas in the U.S. are at highest risk for adolescent pregnancy (46.3 births per 1000) with those of Mexican origin at highest risk. ARCHES (Addressing Reproductive Coercion in Health Settings) is a brief intervention to address reproductive coercion (behaviors that directly interfere with female attempts to use contraception) and intimate partner violence within contraceptive counseling. This qualitative study aims to understand the role of binational Mexican and U.S. American culture on female adolescents living in the San Diego/Mexico border region and their reproductive health decisions. Qualitative data has been collected to understand the perspectives of adolescents and health providers of San Ysidro Health Clinic. Transcripts are being analyzed using the constant comparative method to understand reproductive health decision making factors among female adolescents. Preliminary data shows that a consistent theme expressed by adolescent female patients is that strict parents and their conservative “Mexican” beliefs about contraception are a barrier to FP services access/use, although many of these adolescents maintain different, more empowering beliefs than their parents, and have found ways to access/use contraceptives despite parental disapproval. Despite her mother’s disapproval of teen contraception use, one participant said she got birth control in secret because “this is something I’m doing for me.” Several adolescents interviewed have been successful in advocating for their reproductive health rights, while others struggled with navigating conflicting cultural messages and expressing body empowerment. The findings from this study can contribute to our understanding of how culture permeates borders and influences the health outcomes of vulnerable populations.

Role of Gender in Perspectives of Discrimination, Stigma, and Attitudes Relative to Cervical Cancer in Rural Sénégal

Discipline: Health
Subdiscipline: Public Health

Natalia Ongtengco[*1]; Andrew Dykens[1]; Hamidou Thiam[2]; Zola Collins[3]; Elly Lou De Jesus[3]; Caryn Peterson[1]; Tianxiu Wang[3]; Ellen Hendrix[3]; Youssoupha Ndiaye[4]; Babacar Gueye[5]; Omar Gassama[6]; Abdoul Kasse[7]; Adama Faye[8]; Jennifer Smith[9] and Marian Fitzgibbon[3], *(1)University of Illinois at Chicago, (2)Region medical de kedougou Bureau régional de la formation, de la supervision et de la recherche, (3)Institute for Health Research and Policy, University of Illinois at Chicago, (4)Division of Planning, Research and Statistics, Sénégal Ministry of Health and Social Action, (5)Sénégal Ministry of Health and Social Action, Center for Disease Control, Division of Noncommunicable Diseases, (6)ervice of Obstetrics and Gynecology, University of Cheikh Anta Diop, (7)Cancer Institute, University of Cheikh Anta Diop, (8)Institute of Health and Development, University of Cheikh Anta Diop, (9)School of Public Health, University of North Carolina*

Abstract: Cervical cancer is the leading cause of female cancer deaths in Sénégal and ranks fourth globally. Gendered perceptions and behaviors play a significant role in women’s health. Our study analyzed gender differences on perceptions of gender roles, discrimination, cancer attitudes, cancer stigma, and influences in healthcare decisions to inform cervical cancer prevention work. We conducted a cross-sectional survey of 158 participants, 101 women and 57 men (ages 30–59) across nine non-probability-sampled communities in the rural region of Kédougou, Sénégal, from October 2018 through February 2019. Bivariate analysis was conducted to assess gender differences across all variables. We found significant gender differences regarding the perception of a woman’s role ($P < 0.001$) and a man’s role ($P = 0.007$) and in the everyday discrimination questions of “decreased respect by spouse” ($P < 0.001$). Regarding cancer stigma, among women, 18.00% disagreed while among men, 3.6% disagreed that “If I had cancer, I would want my family to know that I have it.” When making decisions about one’s healthcare, women are more likely than men to trust social contacts such as their spouse (46.5% vs 5.3%, $p < 0.001$) while men are more likely than women to trust health workers such as a nurse (50.9% vs 18.8%, $p < 0.001$). Furthermore, both men and women were more likely to state that men have the final decision regarding the healthcare decisions of women ($p < 0.001$). Our data reveal cancer stigma and structural disadvantages for women. Social and behavior change communication interventions are needed.

ተስፋ መቁረጥ (To lose hope): the Precarity of Hope and Healing in Ethiopia’s Medically Plural Health System

Discipline: Health
Subdiscipline: Public Health

Meron Girma[*] and Rachel Chapman, *University of Washington, Seattle*

Abstract: Formal healthcare in Ethiopia is provided through public, private and non-governmental organization (NGO) sectors. In Addis Ababa, public and private sectors provide most communities’ medical care. Recently, Ethiopia launched an initiative to increase health coverage, yet underutilization of both sectors continues. This study gathered ethnographic interviews and hospital observations to identify causes of public and private healthcare underutilization. Analysis of patient and provider narratives revealed patterned *itineraries of underutilization*, and clear differences in service delivery and quality between the private and public sectors. Both sectors face accessibility issues that negatively affect patient and provider experiences. Public hospitals are congested, and underfunded, and private hospitals are understaffed and expensive, but both sectors face constant shortages of medical equipment and drug stocks. The complexity and gaps in the current healthcare system leave healthcare providers overburdened and patients feeling neglected, uncertain and frustrated. Health-seeker trajectories among health options in Ethiopia's medically-plural system are characterized by prolonged searches and costly treatment dead ends, without any healing or even end to suffering and ultimately, complete hopelessness. A conceptual framework is proposed to explain why the quest for healing generates hopelessness for health seekers and providers. While providers combat hopelessness with referrals to other sites of care, health seekers navigate precarity of the public sector through an economy of affection - a wide range of community relationships of mutuality, and collectivity. This labor has fostered development of third spaces for community organizing and spiritual enlightenment, where suffering is addressed, healing occurs and lost hope is regenerated.

Addressing Urban-Rural Health Disparities through Park Trail Improvements

Discipline: Health
Subdiscipline: Public Health

Margaret Lee*; Sally Davis, Ph.D; Cameron Solomon, Ph.D and Richard Kozoll, MD, MPH, *University of New Mexico*

Abstract: Rural communities often battle disproportionately high rates of chronic diseases such as obesity, diabetes, cancer compared to their urban and suburban counterparts. This urban-rural health disparity may be attributed to less physical activity which reduces risk of such illnesses, in rural residents. Current research on the implementation of scientifically backed physical activity recommendations in rural areas is incomplete despite glaring urban-rural health discrepancies. It is therefore essential to develop and identify successful aspects of an evidence-based model that promote physical activity on a community-level in rural populations. Putting knowledge into practice, the Park Trail was built and enhanced in the Village of Cuba, New Mexico to encourage walking amongst residents. Infrared sensors placed throughout the trail recorded pedestrian traffic, along with the time and date each observation was made, before and after the paving of the trail in July 2019. Data from the electronic counter indicated an immediate rise in the usage of the trail. As part of a larger longitudinal project, VIVA-Step Into Cuba, data taken from the sensors is visualized and analyzed through the programming language, R, to study the relationship between the paving of the trail and the increase in trail usage. Our group establishes a positive correlation between the paving and rise in patrons, suggesting that increased availability and enhancements of venues for physical activity encourages rural residents to be more active. Confirmation of a positive relationship through statistical analysis would have great implications for a physical activity implementation model in a rural community.

Reducing Health Disparity in the American Indian Population: A Paradigm Change with the Use of Home Based Kidney Care

Discipline: Health
Subdiscipline: Public Health

SIERRA KISTLER*, *Boise State University* and Vallabh O Shah, *University of New Mexico*

Abstract: Kidney failure represents one of the largest healthcare costs in America today. In fact, Medicare spending for people with Chronic Kidney Disease(CKD) was over $84 billion in 2017. In the U.S. the prevalence of CKD is particularly high in American Indians including Zuni Indians where kidney failure rates are ~20 times higher than in the general population. Also concerning, the progression of CKD is significantly faster in these populations than in their white counterparts. To help mitigate this disparity a new approach to care referred to as Home Based Kidney Care (HBKC) was implemented in Zuni Pueblo New Mexico. HBKC relies on the use of community health workers trained to provide point of care technology in patients' homes. The program places a large emphasis on patient preference and encourages patients to take on an active role in their care. Preliminary findings suggest that this model of care is more effective at lowering patients BMI and HbA1c levels when compared to usual care. In an effort to understand other effects of this program, nutritional aspects related to the progression of CKD were studied in a randomized controlled study consisting of 125 Zuni Indians. Trends between groups suggest phenotypic changes such as decrease in BMI and HbA1c are related to better nutritional outcomes such as fat, carb, and kcal intake, as well as patients' glycemic load. The plan for future research includes statistical modeling to control for confounding variables to better understand the relationship between phenotypic changes and nutritional aspects.

Pro-Vaping Bots and Advertisements Shift the E-Cig Twitter Conversation

Discipline: Health
Subdiscipline: Public Health

David Keating, Ph.D. and Jay Doshi*, *University of New Mexico*

Abstract: Electronic cigarettes are associated with devastating health effects, yet e-cig use has increased in recent years. Possible exposure to pro-vaping information on social media could influence individuals towards using e-cigs, so we were motivated to explore the source, sentiments, and functional attitudes of Tweets regarding electronic cigarettes in name of public health.

We utilized Twitter Keyword Search API to collect 7789 e-cig related tweets between 06/08/20 and 06/15/20. A random sample of 500 original tweets was independently and manually coded. We defined minimum intercoder reliability between two coders as a Kappa statistic ≥ 0.7 for each variable.

Utilizing the bot-o-meter tool, we identified that 35% of tweets were published by social bots. We found that nearly half of bot tweets were advertisements, contributing to advertisements making up 23% of the coded tweets. Moreover, 29% of bot account tweets expressed positive sentiments, increasing the overall abundance of positive sentiments by 8%.

Furthermore, bots published 64% of tweets that displayed the social-adjustive function, which are tweets that regard socializing and/or personal relationships, despite their mere 35% abundance. While other functional attitudes maintained their abundance-based distribution. For instance, the most common function for both account types was the utilitarian function, tweets that associate with personal feelings and effects, and bot accounts made up 41% of tweets containing the function.

These results suggest that, although most e-cig related tweets have neutral sentiments, bot accounts artificially increase the available positive sentiments of e-cigarettes on Twitter. Therefore, bot accounts could be influencing individuals towards electronic cigarettes.

Financial Stress, Food Insecurity, and Fast Food Consumption in Latinx College Students

Discipline: Health
Subdiscipline: Public Health

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Abstract: College student health is an important public health issue. Transitioning to college can intensify students' financial stress and food insecurity (Baker & Montalto, 2019). Financial stress and/or food insecurity may lead to eating habits (e.g., fast food consumption) that increase risk for chronic disease, further exacerbating health problems into adulthood (Sogari et al., 2018). Latinx college students are especially at-risk of financial stress. The hypotheses were: (1) food insecurity would be positively related to fast food consumption by Latinx college students, and (2) financial stress would be positively related to food insecurity, and directly and indirectly related to fast food consumption. Self-report data were collected (via online surveys) at three California State Universities in Los Angeles County (all Hispanic-Serving Institutions). Participants were 1402 Latinx undergraduates (77.9% female). As hypothesized, path analyses indicated (1) food insecurity was directly related to fast food consumption (*Beta*=.07, *p*=.019) and (2) financial stress was directly related to food insecurity (*Beta*=.50, *p*<.001) and fast food consumption (*Beta*=.07, *p*=.789); indicating financial stress was directly and indirectly related (through food insecurity) to fast food consumption. When analyses were run separately for genders, the relationship between financial stress and fast food consumption was stronger for men (*Beta*=.15, *p*=.028) than women (*Beta*=.02, *p*=.185), while the relationship between food insecurity and fast food consumption was stronger for women (*Beta*=.10, *p*=.007) than men (*Beta*=.15, *p*=.028). It is important to address financial stress and food insecurity in Latinx college students through resources and education so students have access to better food choices.

Differential Impacts of COVID-19 on Dine College Employees' Wellbeing

Discipline: Health
Subdiscipline: Public Health

Krishanya Smith*; Shelby Kinlichee; Amber Kee and Mark Bauer, *Dine College*

Abstract: Dine College (DC), the Navajo Nation tribal college, rerouted from face-to-face to a fully online instruction method due to COVID-19. Unreliable internet access has created barriers for education delivery as DC campuses closed and employees' responsibilities transitioned online. The study investigated how the transition to remote teaching due to COVID-19 has impacted the wellbeing of DC employees. In particular, we measured associations between anxiety and wellness indicators including physical activity, nutrition, and sleep.

DC employees, 18 years old and older, were recruited using a convenience sampling method. An online survey was emailed to employees via DC listserv. The survey consisted of 34 questions, 11 of which were personal well-being questions. Descriptive analysis, chi square testing, and qualitative analysis were conducted.

Preliminary results from 28 surveys showed 71% (n=20) have experienced anxiety from the effects of COVID-19 and 46.43% (n=13) reported difficulty falling asleep. 67% (n=19) engaged in physical activity 3-4 days or more a week. Most employees who experienced anxiety engaged in physical activity 3-4 days or more a week. 17.66% (n=5) reported having fair nutritional health. A third of those who experienced anxiety reported better than fair nutritional health.

Study findings may be used by DC to create guidelines to better support employee wellbeing. Findings suggest employees are facing issues with anxiety and sleep deprivation, and physical activity may be an effective strategy to help cope with anxiety. DC should consider offering online health education seminars to enhance nutritional health and physical activity.

Effects of COVID-19 Social Distancing Policy on Work Efficiency Among Tribal College Employees

Discipline: Health
Subdiscipline: Public Health

Shelby Kinlichee*; Krishanya Smith; Amber Kee and Mark Bauer, *Dine College*

Abstract: COVID-19 social distancing policies have forced many tribal colleges to transition from in-person to remote teaching. Dine College (DC), located on the Navajo Nation, made this transition and faced internet connection issues that have impacted DC employees and students. The research question for this study asked how COVID-19 social distancing and stress affected DC employees' work efficiency.

DC employees who had internet access were recruited using convenience sampling. A 39-question survey was emailed through the DC listserv. The survey included 12 questions guided by themes from the *CDC Quality of Work life Questionnaire.* These questions asked about work productivity and efficiency, and targeted employees' technological knowledge prior to COVID-19 and if DC's response measures to support remote online teaching were sufficient.

Preliminary results from 38 participants showed 62% (n=38) of employees experienced more stress during social distancing than before the pandemic occurred. Before COVID-19, 42% (n=35) of employees had excellent technological skills i.e. internet troubleshooting. During the pandemic, DC provided zoom tutorials and information technology (IT) support, which 50% (n=32) of employees indicated were beneficial. Descriptive analysis, qualitative analysis, Chi-square testing, and multivariant analysis were conducted.

Findings from the study will provide DC with resilience-based recommendations for continued efforts to cope with COVID-19 and contribute to the literature surrounding COVID-19 and tribal colleges. Findings suggest DC employees had increased work-related stress and faced many challenges related to remote online teaching. Additional measures can be taken by DC to increase employee and institutional efficiency.

Impact of COVID-19 on the Mental Health of Parents or Legal Guardians of Children on the Navajo Nation

Discipline: Health

Subdiscipline: Public Health

Faye Sorrell* and Mark Bauer, *Dine College*

Abstract: Mental health includes the emotional, psychological, and social well-being affecting how a person thinks, feels, and acts. This study investigates the life impact of COVID-19 on the mental health among Navajo families. It explores the perception of stress, and how life experiences are seen as stressful or worrisome, among Navajo parents and guardians. Social support was also measured to show how friends/families help each other and communicate in a time of need. We hypothesized parents/guardians who had someone communicate with would be less stressed than those who lacked the type of social support. An additional hypothesis is caregivers who worked during the pandemic were likely to feel worried they were exposing their families to COVID-19 compared to those who did not work. Parents and guardians who resided on the Navajo Nation were recruited using a snowball sampling method among individuals on social media with a flyer displaying the project criteria and its purpose. An online survey consisted of 36 questions asking for demographics, perceived stress, social support, and recommendations. The results were analyzed using descriptive analysis and chi-square testing were conducted. The preliminary results from 31 surveys showed 83% of caregivers provided financial or supportive care for children and 86% were able to talk to someone compared to 14% who said they could not; 29 participants indicated they worried about exposing their families. The Navajo Nation lacks mental health care outlets on the Navajo Nation and this study would help with in-person or online mental health program development.

Covid-19 Impact on the Mental Health of Caregivers on the Navajo Nation

Discipline: Health

Subdiscipline: Public Health

Kyann Dedman-Cisco* and Mark Bauer, *Dine College*

Abstract: American Indians experience high rates of mental health issues which may be exacerbated by the COVID-19 pandemic. The Navajo Nation is among the most severely affected areas in the US impacted by COVID-19. Many Navajos live in multi-generational homes with caregivers who have a role in providing care to children, elderly, and chronically ill/disabled individuals. The aim of this study was to assess the impact of COVID-19 on the mental health of Navajo Nation caregivers by understanding caregiver burden.

Caregivers, 18 years old and older, who lived on the Navajo Nation were recruited using a snowball sampling method. A 36-item online survey asked questions on demographics, anxiety, worry, perceived stress, caregiver burden, and social support. The link to the survey was shared through Facebook, email, and flyers. Descriptive analysis, chi-square testing, and qualitative analysis were conducted.

Preliminary results from 33 survey responses showed the majority of participants frequently worried about COVID-19 in the past month (61.3%) and believed they were at risk of contracting COVID-19 (64.5%). Employed caregivers were more likely to experience stress, between providing care and meeting responsibilities for family or work, than unemployed caregivers.

Findings from this study can help caregiver programs better prepare for future pandemics. Findings suggest that caregivers with additional responsibilities are more susceptible to mental health issues. The Navajo Nation needs to offer more programs and resources to alleviate mental health issues for caregivers, especially for those who are employed and have multiple roles and responsibilities.

Morningness/Eveningness, Diet and Adiposity in Latino Children

Discipline: Health
Subdiscipline: Public Health

Gisselle Moreno* and Selena Nguyen-Rodriguez, *California State University of Long Beach*

Abstract: Chronotype refers to biological differences in individual sleep-wake patterns and alertness which is characterized along a continuum between morningness and eveningness. Compared to morning types, evening chronotype has been associated with unhealthy dietary behaviors which can increase obesity risk. While childhood obesity disproportionately affects Latino youth, few studies have examined the interrelationships among chronotype, dietary behaviors and obesity in Latino children. Identifying the impact of morningness/eveningness on nutrient intake in Latino children may inform dietary strategies that can improve obesity prevention efforts for Latino children. This study examined whether morningness/eveningness was related to fat and sugar intake and adiposity indicators in Latino pre-adolescents. Pearson correlations were conducted on data from self-report surveys, 24-hour diet recalls, and anthropometric measures of 100 Latino children (10-12 years) living in Long Beach and surrounding cities. Results indicated no significant correlation between morningness/eveningness and macronutrient intake of fat (p=.258) or sugar (p=.163), nor with BMI percentile (p=.461) or percent body fat (p=.282). Our results are contrary to previous literature that supports an association between chronotype and dietary intake. While 24-hour diet recalls are known as valid measures of dietary intake, ability to recall and estimate amounts may have reduced accuracy of dietary data. To obtain a more accurate reporting of dietary intake, future studies should include proxy-assisted recalls, portion size training, or objectively measured dietary intake in a lab setting. Calculating midpoint of objectively measured sleep may also be beneficial to enhance chronotype assessment.

Understanding the Mental Health Impacts Regarding the Navajo Nation Facemask Policy.

Discipline: Health
Subdiscipline: Public Health

Karianne Jones* and Carmella Kahn, *Dine College*

Abstract: COVID-19 has severely impacted the Navajo Nation. To address the rising numbers of cases, the tribal government enacted several policies intended to reduce viral exposure. The purpose of this study is to understand the mental health impacts of the facemask policy, implemented on April 17, 2020, by analyzing the knowledge, behaviors, and resources of facemask usage among Navajo Nation community members. Associations between mental health outcomes and type of facemask, sense of safety, and other behavior choices were measured.

Participants who are adults 18 years old and older, who reside in the Navajo Nation, and self-identify as American Indian were recruited using snowball and convenience sampling. A mixed-methods approach was used to conduct an online survey, a focus group, photovoice, and a key informant interview. Recruitment flyers were posted on Facebook and interviewees were contacted through phone or email. Descriptive analysis, qualitative analysis, and chi-square testing were conducted.

The preliminary results from eight eligible responses showed 63% (n=5) of the participants preferred surgical masks over homemade masks. 75% (n=6) of participants experienced no anxiety and 88% (n=6) strongly agreed that facemask usage by others in public made them feel safer. The study is not closed, additional responses will be included in final results.

Findings from the study can help develop recommendation policies. Findings suggest that usage of facemask in public settings increases a sense of safety and lowers anxiety. The Navajo Nation needs to continue the facemask policy and offer resources to support access to facemasks to promote mental health.

The Impact of a Food Desert on Obesity in Health Zone 1 Compared to Its Neighboring Health Zones of Duval County, Florida.

Discipline: Health
Subdiscipline: Public Health

Annik Segree*; Aileen Miller and Dr. Brian Seymour, *Edward Waters College*

Abstract: Obesity is a major health risk in the USA and it disproportionately affects the African American communities due to food insecurities. Duval County, Florida is divided into 6 Health Zones by public health officials. Health Zone 1 (HZN1) is situated in a food desert and its population is predominantly of African American descent. We conducted a study in Duval County in which we hypothesized that the obesity and cardiovascular disease rates in HZN1 is greater than those of the other HZNs which we referred to as the control group in this cross-sectional study. We used questionnaires to collect data from a total of 120 residents of which 60 were from HZN1. We also collected data to calculate participants' body mass index (BMI). Individuals were classified as normal weight ($18.5 \geq \text{BMI} < 25.0$ kg/m^2), overweight ($25.0 \geq \text{BMI} < 30.0$ kg/m^2) or obese ($\text{BMI} \geq 30.0$kg/m^2) using the World Health Organization criteria. Using the single tail, two sample Z-test, it was found that there was no significant difference in BMI between residents of HZN1 and residents of the control group as 41% of both groups were obese. However, HZN1 self-reported more health issues, particularly hypertension ($Z = 3.64$, p-value < 0.001), than the control group. We concluded that obesity is prevalent in both HZN1 and its neighboring Health Zones in Duval County however health related symptoms were more prevalent in HZN1.

Time Waveforms of Amazon River Dolphin (Inia Geoffrensis) in Peruvian Amazon

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Yvan Pierre* and Marie Trone, *Valencia College*

Abstract: Documentation of Amazon River dolphin (Inia geoffrensis) activity is difficult due to the opaque water in which they commonly inhabit in conjunction with their morphology and shallow-surfacing behavior. Furthermore, obtaining quality audio recordings of these animals is also challenging given their preference for shallow habitats characterized by currents carrying copious quantities of debris, changing bottom topography, and dynamic hydrologic cycles. Recently the IUCN changed the status from data deficient to endangered due to unsustainable fishing practices. However, the quantity of animals found in the wild is still unknown. The goal of this research is to develop methods to acoustically count Amazon River dolphins in their natural habitat. An understanding of the dynamic time waveform is needed to accomplish this goal. To measure the waveforms, a hydrophone array was set-up that was able to find their position and location and pinpoint not only distance from the boat but give an estimated number of how many were in an area at a time. Through this research, it shows a new way to discover the remaining populations of these animals, as well as possible improvements to sonar technology and a better understanding of high-amplitude pulses that are made, and so further investigation is warranted.

Postcranial Skeletal Ontogeny in the California Condor (*Gymnogyps californianus*)

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Sorilis Ruiz-Escobar*, *University of Florida* and Helen James, *Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution*

Abstract: Determining the age at death of animals whose remains are found in paleontological and archaeological sites can provide information about the former breeding ranges of the species represented and seasonality of site use. Bone surface textures can serve as a size-independent method of aging avian skeletal remains. To develop this method, we studied postcranial bone growth and maturation of bone surface textures in the skeleton of the California condor (*Gymnogyps californianus*) using a series of carcasses of known age at death. Our study aimed to determine (1) if growth patterns of the wing and leg bones differed, (2) at what age can a young bird no longer be distinguished from an adult, and (3) how skeletal maturity relates to milestones in the bird's locomotory development. We measured the length of the coracoid, humerus, ulna, carpometacarpus, first phalanx of the major digit, femur, tibiotarsus, and tarsometatarsus in 42 specimens. Fourteen specimens, ranging in age from 9 to 5124 days old, were selected as a representative growth series and used to study the texture of the measured bones, the sternum, and the synsacrum. We found that a hatch-year bird can be identified by the texture of the long bones until 212 days (8 months), but the sternum retains immature texture until 1.5 years old. It appears that jumping and flying (required for fledging) behaviors are not performed until the leg (for jumping) and wing (for flying) are at or near adult size, although bone surface textures may not yet be adult.

Effects of Oral Selenium-Supplementation during Different Trimesters of Pregnancy in Beef Cows on Complement-Mediated Killing of Bacteria

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Ian Thompson-Hernandez*; Brian Dolan and Jean Hall, *Oregon State University*

Abstract: The Pacific Northwest is among those regions with the lowest concentration of Selenium in soils. Plants grown on those soils and animals consuming forages from those soils therefore have reduced concentrations of Se as well. Previous work in sheep and cattle has shown that Se supplementation above current USDA recommendations improves body condition scores and certain immune responses. We hypothesized that increasing whole-blood Se concentrations would enhance complement-mediated killing of bacteria in plasma of pregnant beef cows. Pregnant cows were assigned to one of four groups at conception (control, and groups 1, 2, and 3 corresponding to trimester of Se-treatment). Plasma samples collected after corresponding treatment periods were inoculated with a predetermined concentration of *Vibrio coralliitycus*, a novel bacterium, to assess complement-mediated bacterial killing. Bacterial growth is measured using an endpoint of 0.200 optical density (approximately 10h) and compared against a standard curve of bacteria alone. This procedure assesses the percent reduction of bacteria during a 30-minute killing period. Our preliminary data from a similar study shows that medium and high levels of Se supplementation (27.6 and 7.5 mgSe/cow per day) significantly improve complement-mediated immunity. By studying the effects of supplementation with Se-yeast during different trimesters of pregnancy in cows, we hope to expand our understanding as to the best time to supplement pregnant cows with oral Se to maximize their complement-mediated immunity. This research could also help inform the USDA on Se requirements for pregnant cows.

Skeletal Muscle Differentiation Relies on the Association of Specific Subunits of the SWI/SNF Complex

Discipline: Life Sciences

Subdiscipline: Biochemistry

Kexin Zhang[*1]; Teresita Padilla-Benavides[1] and Anthony N. Imbalzano[2], *(1)Wesleyan Univeristy, (2)University of Massachusetts Medical School*

Abstract: Normal development and differentiation depend on the activation of new programs of gene expression and promote the establishment of specific cell lineages. This process involves the activation of transcriptionally silent genes in repressive chromatin structures. We hypothesize that transcriptional regulators and chromatin remodeler enzymes allow genomic DNA to be accessible to the transcriptional machinery in a lineage-specific manner. The mammalian SWI/SNF is an ATP-powered, multi-subunit enzyme complex that remodels nucleosome structure, facilitating the expression of lineage-specific genes. Our lab utilizes cultured C2C12 myoblasts, as a model for studying the principles of tissue-specific gene expression and differentiation.

The SWI/SNF chromatin remodeling enzymes are essential in myogenesis. Different combinations of SWI/SNF subunits may play distinct roles in gene expression. We hypothesize that cooperation between various assemblies of the complex may result in specific functions. Three variants of SWI/SNF complexes have been defined, based on the differential association of the subunits. These are BAF, pBAF, and non-canonical BAF (ncBAF). We are investigating whether a specific assembly of the SWI/SNF enzymes mediates myogenesis. To address this question, we used shRNA to knock-down the expression of specific SWI/SNF subunits in C2C12 myoblasts, and analyzed the effects on skeletal muscle differentiation. We found that the BAF and potentially the ncBAF complexes are required for myogenesis, as deletion of representative subunits from these two complexes impaired differentiation and, in some cases, lead to cell death. This work established the basis to understand how does the diversity of mSWI/SNF enzyme complex arrangements impact cell differentiation and function.

Characterization of *Escherichia coli* Rec N Wild-Type and Variant Proteins in Vitro

Discipline: Life Sciences
Subdiscipline: Biochemistry

Helen Gomez[*] and Shelley Lusetti, *New Mexico State University*

Abstract: DNA double stranded breaks (DSBs) are detrimental DNA lesions as their defective repair causes chromosomal instability which can lead to diseases in humans and antibiotic resistance in bacteria. The bacterial RecN protein is essential in the DSB repair pathway as it stimulates RecA-dependent homologous recombination by hydrolyzing ATP. This current study is aimed to investigate the role of the *E. coli* protein product of *recN* mutants conferring resistance to ionizing radiation. We have purified a soluble fraction of wild-type *E. coli* RecN achieving stabilization through liquid chromatography. We determined that maintaining a presence of sucrose is fundamental for RecN solubility during cell lysing which establishes our basis for the purification process of the protein product of *recN* mutants. We will observe the activity of RecN through ATP hydrolysis, ATP-dependent DNA binding, and RecA mediated strand exchange assays. My project involves cloning these mutations into a protein expression vector and comparing the repair activities of the variant enzymes to the wild-type RecN protein. Understanding how a modification in RecN is leading to ionizing radiation resistance helps further studies define the key role of RecN in bacterial repair pathways.

Development of Apolipoprotein AI Chimera for Targeted Drug Delivery to Breast Cancer Cells

Discipline: Life Sciences
Subdiscipline: Biochemistry

Robert Mejia[*]; Daanish Kulkarni and Vasanthy Narayanaswami, *California State University, Long Beach*

Abstract: A current challenge in drug delivery for cancer treatment is the ability to effectively target specific diseased cell types without toxic effects on healthy cells. Our objective is to generate a platform for targeted drug delivery employing self-assembling nanodiscs comprised of phospholipids and apolipoprotein-AI (apoAI). ApoAI is a protein located on high density lipoproteins, which facilitates selective uptake of cholesterylester by binding scavenger receptor class-B type-1 (SR-B1). We hypothesize that a chimeric protein of apoAI with MT1-AF7p (apoAI-AF7p), a peptide ligand that binds membrane metalloproteinase 14 (MMP14), will enhance the targeting capability of nanodiscs to tumor cells. MMP14 is a protein responsible for metastasis in many cancer cells. We designed a construct of apoAI with a hexa-His-tag at the N-terminal and MT1-AF7p at the C-terminal end and sub-cloned it into a pET20b(+) expression vector. Recombinant wild-type (WT) apoAI and apoAI-AF7p proteins were over-expressed in E. coli, purified by affinity chromatography and confirmed by immunoblotting and LC-MS. Preliminary secondary structural characterization by circular dichroism spectroscopy revealed that the chimera retains the overall fold and alpha-helical content of WT apoAI. Preliminary functional analysis indicated that the chimera retained lipid binding ability comparable to that of WT apoAI. In subsequent studies, we propose to assess the tertiary fold by fluorescence spectroscopy and determine cellular targeting of nanodiscs generated with apoAI-AF7p using MDA-MB-231 cells, a model for triple negative metastatic breast cancer with high expression levels of MMP14 and SRB1. The chimeric apoAI-AF7p nanodiscs bear tremendous potential for targeted drug delivery to MDA cells.

Determining Detergent Dependence of Cytolysin a Oligomeric State through Native Mass Spectrometry

Discipline: Life Sciences

Subdiscipline: Biochemistry

Lejla Biberic*; Amber Rolland and James Prell, *University of Oregon, Department of Chemistry and Biochemistry*

Abstract: Membrane proteins, including pore-forming toxins (PFTs), play important roles in human health. PFTs are promising for nanopore sequencing and drug delivery, but to maximize success in these applications, it is important to know the size of the pore and thus the oligomeric state (number of identical subunits). The flexibility of alpha-PFT transmembrane helices may allow their oligomeric state to vary in different environments. Elucidating the relationship between oligomeric state and detergent environment is thus important for PFT bionanotechnology applications. Here, we studied how native oligomeric states of Cytolysin A (ClyA), an alpha-PFT found in pathogenic strains of *Escherichia coli*, varied in different detergent environments using native mass spectrometry (MS).

Native MS enables preservation of noncovalent complexes and accurate measurement of the complex mass. Together with a known monomer mass, this allows unambiguous determination of oligomeric state. ClyA was incubated with various detergents and screened for complex formation using Blue Native PAGE. Preliminary native MS results show that ClyA forms various oligomeric complexes ranging from octameric to dodecameric in n-dodecylβ-D-maltoside and octaethylene glycol monododecyl ether. ClyA forms no identifiable pore complexes in n-octyl-β-D-glucoside, in contrast to previous reports, while n-tetradecylphosphocholine heavily adducts to and stabilizes ClyA monomers only. Combining these experimental results with computational modeling enables further investigation into the relationship between detergent properties and oligomeric state. These findings will not only advance the fields of MS and structural biology but also provide new insight for PFT applications in bionanotechnology through manipulation of desired oligomeric state and pore size.

Evaluating Keratin 5 Expression in Breast Epithelial Cells: Overcoming a Potential Artifact

Discipline: Life Sciences
Subdiscipline: Biochemistry

Selina Montoya*; William C. Hines and Katelyn Alvarez, *University of New Mexico*

Abstract: Keratins are a family of intermediate filament proteins whose expression is limited to epithelial cell types. Immunological staining for specific keratins is common in clinical laboratories, where staining is used identify tissue of a tumor’s origin. Keratin 5 (K5) has largely been recognized as marker of myoepithelial cells, however there is some disagreement in the literature of whether other cells may also express this protein, with claims that luminal cells express K5. We find that K5 is one of the highest expressed transcripts in myoepithelial cells and is expressed at a level that is roughly 163-fold higher then luminal cells, which themselves express K5 at a level lower than fibroblasts and most other stromal cell types. The near absent expression of K5 in luminal cells conflicts with tissue immunostaining, where we detect abundant K5 protein in luminal cells. These discrepant results have led us to question the specificity of these commonly applied K5 antibodies. Our hypothesis is that the K5 antibodies are detecting other proteins in luminal cells that produce a false signal. To investigate, we have measured protein levels in primary cultured luminal and myoepithelial cells using mass spectrometry. We found K5 was exclusively expressed in myoepithelial cells, which is consistent with K5 transcript levels measured by RNA-sequencing, leading us to conclude that luminal staining by K5 antibody is an artifact. To be certain, we have knocked out K5 in primary cultures of myoepithelial cells. These data will be presented and discussed.

Expanding the Use of Tyrosine Phenol Lyase in the Enzymatic Synthesis of Unnatural Amino Acids

Discipline: Life Sciences
Subdiscipline: Biochemistry

Jubilee Munozvilla*, *California State University, Long Beach* and Jason Schwans, *California State University Long Beach*

Abstract: The use of enzymes in the synthesis of pharmaceuticals and biochemical tools offers an attractive approach to generate complex structures in high yields. Tyrosine phenol lyase (TPL), an enzyme biologically involved in the degradation of tyrosine, has been used to synthesize substituted tyrosines for biochemical studies. Expanding the scope of substrates to naphthol-based compounds offers an attractive approach to enzymatically synthesize complex molecules to then construct potential pharmaceuticals. Using *Citrobacter freundii* TPL we enzymatically synthesized the naphthol-analog of tyrosine, but in low yield. Our hypothesis is weak binding of the larger substrate led to the low yield. To test this hypothesis, we mutated several bulky residues near the substrate-binding site (M288, M397, F448) to open space for substrate binding. Plasmids were generated using site-directed mutagenesis and sequenced to confirm the mutation. The constructs were recombinantly expressed in *E. coli*, purified by affinity and ion-exchange chromatography, and analyzed by kinetics studies. Initial results indicate that multiple mutants are active and we are currently determining the effects of different substrates on enzyme activity. Further, we are surveying reaction conditions using high-performance liquid chromatography (HPLC) to evaluate the yields and number of products formed. While a goal of this study is aimed at the more efficient production of tyrosine derivatives, a larger goal is to better understand the features important for substrate binding in enzymatic reactions. This understanding may aid in the development of enzymes with a broad range of substrates efficiently converted to products in the biochemical generation of complex molecules.

Analyzing Conformational Changes of Steroid Response Activator RNA (SRA-RNA) Bound to Sharp Suppressor Protein Using Circular Dichroism (CD)

Discipline: Life Sciences
Subdiscipline: Biochemistry

Bryan Okosun* and Thomas Leeper, *Kennesaw State University*

Abstract: The Steroid Receptor Activator (SRA)-RNA is a common target in many diseases including various types of cancer and is important for the diagnosis and treatment. SRA-RNA is used for a response to steroid hormones by tumor cells. However, the activity is hindered by RNA binding proteins such as the SMRT/HDAC1-Associated Repressor Protein (SHARP). The activity of SHARP is not well understood yet. Nonetheless, this protein binds to the STR7 domain of SRA-RNA and suppresses the activity while forming a ribonucleoprotein complex. We hypothesize that this binding protein will result in a conformational change in the SRA-RNA structure.

In this experiment, SHARP2 was purified along with STR7 RNA. A ribonucleoprotein complex was formed and Circular Dichroism was then used to analyze the interactions within the complex and the thermodynamic parameters. Unbound STR7 RNA and unbound SHARP2 was compared to an SRA-RNA SHARP2 Ribonucleoprotein complex. This study is important because SHARP function will be understood more to improve therapeutic cancer treatments.

Evaluating Expression Constructs of the Human Astrovirus Virginia 1 Spike Protein

Discipline: Life Sciences
Subdiscipline: Biochemistry

Kevin Delgado-Cunningham*; Jordan Ford; Lena Meyer and Rebecca DuBois, *Department of Biomolecular Engineering, University of California, Santa Cruz*

Abstract: Human astrovirus Virginia 1 (VA1) has been associated with encephalitis in immunocompromised patients. The VA1 capsid is expected to include a receptor-binding protein (spike) derived from a C-terminal domain of the capsid polyprotein. Similarly to the spike protein of the classical human astroviruses, the VA1 spike is expected to bind and elicit neutralizing antibodies. Antigenic studies using recombinantly produced VA1 spike may enable the development of a subunit vaccine based on the spike protein. We thus seek to identify a stable expression construct within the C-terminal region of the human astrovirus VA1 capsid protein. A series of expression constructs is being screened for stability after recombinant production. Solubility-enhancement-tagged constructs are expressed in *E. coli*, and select constructs are expressed in *Spodoptera frugiperda* Sf9 insect cells using the baculovirus method. Purifications are carried out using TALON metal affinity chromatography followed by gel filtration chromatography. Constructs which, after purification is complete, show negligible aggregation by gel filtration chromatography and remain soluble are considered stable. Initial purifications of solubility-enhancement-tagged constructs have provided microgram yields at modest purities. Expressions in Sf9 cells have begun. It is expected that milligram yields will be achieved for a subset of the constructs tested, and that buffer conditions compatible with stability will be identified. Such yields would enable structural and immunogenic studies of the VA1 spike. Identification of a stable expression construct will provide evidence of a spike domain in the capsid protein of human astrovirus VA1, and support the development of a VA1 subunit vaccine.

Virus-like Particles (VLPs) As a Vaccine Platform

Discipline: Life Sciences
Subdiscipline: Biochemistry

Erich Sohn* and Dr. Naomi Lee, *Northern Arizona University*

Abstract: Virus-like particles (VLPs) are composed of self-assembling viral structural proteins that resemble viruses but do not contain a viral genome. Therefore, VLPs are non-infectious themselves and may provide an efficient platform for vaccine development. VLPs increase the efficacy of poorly immunogenetic antigens, increase vaccine stability, and allow for a more versatile display of antigens. In this project, we produced VLPs from the MS2 bacteriophage in *E. Coli*. W used standard molecular biology techniques to transform MS2 single-chain dimer plasmid (pDSP62) through electroporation of electrocompetent C41 cells. Transformed cells containing an antibiotic resistant for kanamycin grew colonies on an agar plate. Addition of IPTG induced cells to synthesize VLPs. We then lysed the cells to isolate and confirm VLP formation using agarose gel electrophoresis by detecting the presence of RNA encased in the VLPs, indicating successful VLP production. Unfortunately, agarose gels did not indicate successful VLP formation, at this time. However, Sodium Dodecyl Sulfate–polyacrylamide (SDS) gel electrophoresis confirmed expression of the MS2 coat protein. Therefore, next steps are to continue troubleshooting VLP synthesis then purify crude VLP samples via gravity column. Upon successful VLP synthesis, qualitative VLP concentration will be determined using SDS gel electrophoresis. Future studies will focus on chemical conjugation of nucleoside adjuvants via the tyrosine side chain using Diels-Alder chemistry. In conclusion, VLPs could serve as an effective vaccine platform due to their non-infectious nature and their ability to increase antigen immunogenicity.

Structural and Functional Analysis of Apolipoprotein E3 Modification By a Lipid Peroxidation Product, 4-Hydroxynonenal

Discipline: Life Sciences

Subdiscipline: Biochemistry

Abbas Abdulhasan*[1]; Muhammad Imam Uddin Abeer[1] and Vasanthy Narayanaswami[2], *(1)University of California, Long Beach, (2)California State University, Long Beach*

Abstract: Post-mortem tissues from brains of Alzheimer's disease (AD) patients show higher levels of 4-hydroxynonenal (4-HNE) modified proteins, with 4-HNE arising as a result of oxidative stress and lipid peroxidation. The overall goal of our study is to understand the effect of 4-HNE modification on the structure and function of apolipoprotein E3 (apoE3) and apoE4, which play a critical role in brain cholesterol homeostasis. Individuals carrying the *APOE* ε4 allele are at a higher risk of developing AD in a gene-dose dependent manner. In the present study, we report the biophysical and functional analyses of 4-HNE modification of apoE3 and apoE4. Recombinant apoE3 and apoE4 were modified by 4-HNE, followed by Western blot, mass spectrometric analyses, circular dichroism (CD) spectroscopy and lipid binding assay. Western blot with 4-HNE specific antibody confirmed modification of apoE3 and apoE4, with a major band at ~36 kDa, while mass spectrometric data revealed modification of K72 and K75. CS spectra revealed that 4-HNE-modified apoE3 and apoE4 were highly helical (~60%) comparable to that of unmodified proteins (~58%). Modification significantly impaired the ability of apoE to bind lipids, with the calculated t½ (time required for initial absorbance to decrease by 50%) for apoE3 being 165.6 min, while that for 4-HNE-apoE3 was 516.8 min. Similarly, the $t_{1/2}$ for apoE4 was 4.95 min, while that for 4-HNE-apoE4 was 16.3 min. In conclusion, assessing the differences in the susceptibility to age-related oxidative modifications aid in understanding the molecular basis for the role of apoE4 as a risk factor for AD.

UV Light Increases Arginine Methylation of Histone H4 By PRMT1

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alejandra Leal*, *California State University, Los Angeles* and Cecilia Zurita-Lopez, *California State University, Los Angeles, Department of Chemistry and Biochemistry*

Abstract: UV irradiation can lead to cancer by directly damaging DNA or by altering the activity of enzymes that modify histone proteins. Histone proteins contain amino-terminal tails that become post-translationally modified, leading to changes in gene expression. This project investigates the effect of UVB light (280-315nm) on the formation of asymmetric dimethylation at arginine residue 3 in histone H4 (H4R3adma) catalyzed by the enzyme PRMT1. We hypothesize that when exposed to UV light, the enzymatic activity of PRMT1 will increase causing greater formation of H4R3adma. Methylation reactions were carried out in vitro using recombinant bacterially expressed GST-PRMT1 constructs and commercially purchased full-length histone H4 protein. The reactions were carried out in the presence or absence of UVB light at 37°C for 1 hour. While the effects of UVB light on H4R3adma by PRMT1 have yet to be validated, preliminary evidence suggests that UVB exposure causes an increase in automethylation of PRMT1 as well as an increase in H4R3adma product. In addition, the development of an assay using histone H4 extracted from mammalian cells exposed to UVB is also underway. A greater understanding of transcriptional regulation and UVB damage response pathways will be gained by investigating UV irradiation on H4R3adma by PRMT1.

Preparation of Apolipoprotein C III Peptide Antigens for Display on Virus like Particles to Combat Cardiovascular Disease

Discipline: Life Sciences
Subdiscipline: Biochemistry

Nicholas Lopez* and Dr. Naomi Lee, *Northern Arizona University*

Abstract: Cardiovascular disease (CVD) is the leading cause of death for men, women, and people of most racial and ethnic groups in the world. Common risk factors for CVD include elevated serum levels of low-density lipoprotein cholesterol (LDL-C) and triglycerides (TG). Research has shown that Apolipoprotein C III (ApoC3) plays an important role in the metabolism of TGs by inhibiting both the hepatic clearance of TGs and the enzyme lipoprotein lipase which hydrolyzes TGs into free fatty acids for uptake by muscular tissue. Changes in gene expression of ApoC3 can drastically affect TG levels as seen in ApoC3 knockout mice that are hypotriglyceridemic and overexpression of ApoC3 that leads to hypertriglyceridemia. This makes therapeutics that reduce ApoC3 levels a potential target for vaccine development. We will synthesize potential ApoC3 peptide antigens using solid phase peptide synthesis and characterization of the peptides will be conducted using MALDI-TOF MS, HPLC, and Circular Dichroism spectroscopy. Using chemical biology tools, we will increase the alpha helical content of ApoC3 peptide antigens to best mimic the alpha helical character of human ApoC3. Eventually the ApoC3 peptide antigens will be conjugated to virus like particle vaccine platforms and mice will be challenged to better understand the role of immunization on the murine antibody response and the effects on serum levels of LDL-C and TGs.

Characterization of Two Acid Phosphatases from *Acinetobacter Baumannii*

Discipline: Life Sciences
Subdiscipline: Biochemistry

Phuong Cao*; Elizabeth Moreno-Smiley; Jieh-Juen Yu; Bernard Arulanandam and James Chambers, *University of Texas at San Antonio*

Abstract: Bacterial phosphatases constitute a diverse, ubiquitous group of enzymes that hydrolyze various phosphoester substrates. Emergent multi-drug resistant *Acinetobacter baumannii* is one of the major causes of hospital-acquired infections. Since acid phosphatases (EC 3.1.3.2) have been implicated as virulence factors involved in bacterial homeostasis and stress response for stationary phase survival, the purpose of these study was to characterize this enzyme in *A. baumannii*. BLAST genomic analysis revealed a well-studied acid phosphatase SurE (255aa, 28.2 kDa) and its ortholog, AcpA (322aa, 34.6 kDa), which additionally contains a signal peptide for potential secretion. Utilizing the pET expression system, A poly His-tag gene construct was expressed in *E. coli*, recombinant proteins rSurE and rAcpA were purified by Ni-affinity chromatography. The presence of the constructs was confirmed using zymogram PAGE analysis; both proteins were enzymatically active at pH 6.5. Their physicochemical properties were compared by measuring hydrolase activity dependence on various divalent metal ions at different pH values using *p*-nitrophenylphosphate (*p*NPP) as substrate. rSurE exhibited highest activity in the presence of Mn^{2+} followed by Co^{2+}, Mg^{2+} and Ni^{2+}. In contrast, rAcpA required Ni^{2+}, Mg^{2+}, or Co^{2+} followed by Mn^{2+} for optimal activity. Both enzymes exhibited hydrolytic activity at a broad pH range (5.5-7.5). Kinetic analysis of 4-MUP hydrolysis by rAcpA revealed K_m and V_{max} values of 164 μM and 5,800 nmoles/minute, respectively. Although both acid phosphatases hydrolyze artificial substrates (4-MUP and PNPP), future studies will examine the native endogenous substrate and function for these two enzymes. Understanding this organism may enhance future medical interventions.

Self-Assembling Peptide-Based Vaccines for HIV

Discipline: Life Sciences
Subdiscipline: Biochemistry

Jasmyn Genchev*; Jasmyn Genchev and Dr. Naomi Lee, *Northern Arizona University*

Abstract: Self-assembling peptides spontaneously assemble into unique beta-sheet fibrils due to interactions between the alternating hydrophilic and hydrophobic properties within their amino acid sequences. Self-assembling peptides can produce strong antibody responses against peptide antigens displayed along the fibril. The purpose of this research is to novel HIV vaccines using a self-assembling peptide, Ac-QQKFQFQFEQQ-NH_2 (Q11), to create an immune response. Q11 was previously shown as a potential vaccine platform. However, at this time, self-assembling peptides were not utilized to develop HIV vaccines. Thus, we will use Q11 fibrils displaying the HIV antigen to induce a B-cell response when administered to mice. However, to induce T-cells, the PADRE peptide will also be displayed on the fibrils. Standard Fmoc solid phase peptide synthesis will be used to synthesize all peptides. The Q11 fibrils displaying the HIV antigen and PADRE peptides will be co-assembled at varying concentrations of antigen. A detailed analysis of peptides and fibrils will be conducted using MALDI-TOF, HPLC, TEM, and circular dichroism. The project was started in January 2019. Thus, data will primarily include peptide synthesis results. So far, successful peptides of Q11, HIV-linker, and Q11HIV have been synthesized. Future studies include the synthesis of the PADRE peptide, examination of the synthesized fibrils using TEM and vaccinating mice to test for an immune response via ELISA assays (AY 2020). In conclusion, this project aims to develop novel and robust vaccine candidate against HIV using a combination of self-assembling peptides, HIV antigens, and the PADRE epitope.

A Divergent Heme-Oxygenase Enzyme Activates Organelle Transcription in Malaria Parasites

Discipline: Life Sciences
Subdiscipline: Biochemistry

Celine Slam*; Amanda Mixon and Paul Sigala, *University of Utah*

Abstract: Malaria is a devasting disease with around 500,000 deaths annually. Severe malaria is caused by single-cell, eukaryotic *Plasmodium falciparum* parasites that infect and grow inside human red blood cells (RBCs). Parasites have developed unique adaptations to survive within the heme-rich environment of RBCs, including many unusual proteins with unknown functions. We have identified a divergent heme-oxygenase homolog (PfHO) in the *P. falciparum* genome that binds heme but has lost heme-oxygenase activity. PfHO is targeted to the parasite apicoplast, a chloroplast-like organelle with a small genome that houses core metabolic pathways. Prior data shows that *in vitro* PfHO binds DNA in a heme-dependent manner and is essential for the apicoplast to transcribe its genome into RNA. We propose that PfHO binds heme that accumulates due to parasite digestion of hemoglobin, causing PfHO to dissociate from DNA and thereby turn off apicoplast transcription in mature parasites. Other organisms similarly contain pseudo-HOs though their function is unclear. Higher-plants retain a divergent HO of unknown function that lacks tight heme-binding and is plastid-localized like PfHO. We are analyzing the phylogenic relationship between these divergent plant HOs, PfHO, and other *Plasmodium* homologs by sequence analysis, remote homolog algorithms, and structural comparison of PfHO to known HOs to identify earlier protein ancestors more closely related to the divergent parasite and plant HO homologs. These phylogenetic studies will elucidate sequence changes that underpin the evolutionary divergence in PfHO function away from a canonical role as a heme-degrading enzyme towards its novel function in regulating apicoplast transcription.

Expression and Purification of human Brain and Muscle ARNT-Like 1 Protein (hBMAL1) for Structural and Functional Studies

Discipline: Life Sciences

Subdiscipline: Biochemistry

Paulina Rios*; Brenda Moreno and Chuan Xiao, *University of Texas at El Paso*

Abstract: The circadian rhythm is an internal biological clock that approximately lasts 24 hours. It is fundamental for the survival of organisms because it coordinates their internal physiology with the external environment. This synchronization is responsible for temporal homeostasis, food intake, and metabolism, to mention a few. The circadian oscillator is dependent on transcriptional and translational feedback loops (TTFL), where Circadian Locomotor Output Cycle Kaput (CLOCK) and Brain and Muscle ARNT-Like 1 (BMAL1) form a heterodimer and act as transcription factors to promote the transcription and translation of Period (PER) and Cryptochrome (CRY). After accumulation, PER/CRY complexes function as repressors to inhibit the function of CLOCK/BMAL1. Constant disruption of Circadian rhythm due to environmental stress or genetic factors has been correlated to health problems like sleep disorders, neurological diseases, and higher risks of certain types of cancer. Researchers hypothesize that new therapeutical strategies could be developed by understanding the atomic structure of the circadian proteins and their complexes. This project aims to conduct structural and functional studies of full-length hBMAL1 to obtain further information on its role in the circadian rhythm. To achieve this objective, high purity recombinant hBMAl1 is needed. Herein, large volumes of *E. coli* strains were expressed and purified using different chromatography techniques (affinity and size exclusion). Next, purified hBMAL1 will be characterized by biochemical and biophysical methods to determine its structure. The results will contribute to the biochemistry knowledge on the mechanism of circadian rhythms.

Real-Time Characterization of Cell Membrane Disruption By α-Synuclein Oligomers in Parkinson's Disease

Discipline: Life Sciences
Subdiscipline: Biochemistry

Jacob Parres-Gold*[1]; Andy Chieng[1]; Stephanie Wong Su[1] and Yixian Wang[2], *(1)California State University, Los Angeles, (2)California State University of Los Angeles*

Abstract: Aggregation of the natively unfolded protein α-synuclein (α-Syn) has been widely correlated to the neuronal death associated with Parkinson’s disease. Mutations and protein overaccumulation can promote the aggregation of α-Syn into oligomers and fibrils. Recent work has suggested that α-Syn oligomers can permeabilize the neuronal membrane, promoting calcium influx and cell death. However, characterizing this permeabilization has proven difficult, and, as such, most previous works have only studied the disruption of artificial lipid bilayers. This work uses scanning ion conductance microscopy (SICM) to image, in real time and without using chemical probes, the topographies of live SH-SY5Y neuroblastoma cells after exposure to α-Syn oligomers. Substantial changes to the membrane morphology were observed, with micrometer-scale hills and troughs observed at lower α-Syn concentrations (1.00 μM) and large, transient pores observed at higher α-Syn concentrations (6.0 μM). These findings suggest that α-Syn oligomers may permeabilize the neuronal membrane by destabilizing the lipid bilayer and opening transient pores. Future projects will aim to understand better the protein/membrane interactions driving this disruption, with the goal of identifying therapeutic targets for treatments of Parkinson’s disease.

Investigating the Role of L66 in the Internal Motions of TrkB

Discipline: Life Sciences
Subdiscipline: Biochemistry

Karin Crowhurst and Akemi Hinzer*, *California State University, Northridge*

Abstract: Human neuroreceptor TrkB interacts with four neurotrophins to activate signaling pathways that maintain neuronal health. To understand the binding selectivity this protein displays, we have been using nuclear magnetic resonance (NMR) spectroscopy to perform dynamics experiments examining possible allosteric changes. Previously work had indicated the lysine in position 66 to be of interest due to notable dynamics in the biologically relevant timescale. In a prior iteration of this experiment we had mutated the lysine to an alanine, but found the mutation to be overly disruptive. Therefore, the experiment was repeated using a lysine to tryptophan mutation in hope the more conservative exchange would better preserve the structure of the wildtype protein. We have recorded a ^{1}H-^{15}N correlation spectrum to confirm proper structure, and while the spectra align more closely with the wild type, the L66W mutation proved to be disruptive as well. Analyzing the data gathered from the R_2 R_1 experiments will help to show these effects as well as the internal movements of TrkB.

Recombinant Expression of the Macro-H2A Histone Macrodomain and Analysis of Complex Formation with the VRK1 Kinase By Size-Exclusion Chromatography

Discipline: Life Sciences
Subdiscipline: Biochemistry

Dalal Azzam* and Gabrielle Budziszewski, *University of North Carolina at Chapel Hill*

Abstract: Cancerous cells stimulate the production of cell cycle proteins that promote or improperly regulate the cell cycle, allowing unrestricted cell growth and division. VRK1, an understudied nuclear kinase, has been found to be upregulated in

cancers including gliomas and breast cancer. Studies suggest that cancer cells take advantage of increased VRK1 levels to promote tumor growth. VRK1 has been observed to form a complex with the macro-H2A histone variant during the cell cycle, which mechanistically regulates VRK1's ability to phosphorylate the histone H3 tail during the cell cycle. We sought to understand the mechanistic details of the interaction between the macro-H2A histone and VRK1 proteins using protein crystallography and biochemical techniques. We cloned and expressed the macro-H2A macrodomain in E. coli and purified the expressed protein by cobalt metal affinity FPLC and ion-exchange chromatography. We attempted to purify the VRK1-H2A macrodomain complex by size-exclusion chromatography to generate high-quality, homogeneous protein complexes to screen for crystallization conditions using commercial screening materials. Size-exclusion chromatography experiments to isolate the complex have been unsuccessful so far, suggesting that VRK1 and H2A macrodomain may interact transiently and do not form stable complexes suitable for crystallography. In future work, we will mutate the putative interaction interface between the H2A macrodomain and VRK1 to determine which residues are important for inhibiting VRK1 function and hypothesize how this inhibition is carried out. We anticipate this work will clarify how macro-H2A inhibits VRK1 during the cell cycle and how imperative this inhibition is to the functioning of living cells.

Determining E3 Ligase and E3 Ligase Recruiter Activity in Proteolysis Targeting Chimera Induced Degradation Using a Cell-Based Bioluminescence Assay

Discipline: Life Sciences
Subdiscipline: Biochemistry

Ronnesha Johnson*; Isaac Marquez; Sean Toenjes; F. Javier Piedrafita and Jeffrey Gustafson, *San Diego State University*

Abstract: PROTACs (proteolysis targeting chimera) are small dual-ligand molecules that together target a POI (protein of interest) for degradation. One end of the PROTAC specifically binds to the POI while the other recruits an E3 ligase to form a complex. When this complex forms, the E3 ligase ubiquitinates the POI, targeting it for degradation by the proteasome. This recent chemical biology strategy stimulated design of numerous PROTACs targeting previously deemed undruggable targets. However there are only three E3 ligase binders used in the current PROTACs, limiting the potential scope of this application. We propose a method of discovering novel E3 ligase binders through development of a cell based assay to determine degradation activity of E3 ligase recruiters.

To develop this assay we first transfected HEK293T cells with a known promoter and a NanoLuc luciferase gene reporter with HaloTag7(HT7-Nanoluc) fusion protein, for the cells to deliberately express HT7-NanoLuc. The expression of Nanoluc indicates the amount of protein being expressed by the cells. In this system, Nanoluc serves as the POI, whereby the HaloPROTAC molecule possesses an alkyl-chloro motif that binds and targets HaloTag7 fused to Nanoluc for its degradation. This cell-based assay serves as a platform to test the efficacy of a new library of PROTACS with varied E3 ligase binders by quantifying luminescence where reduced levels luminescence equates to an effective PROTAC.

If successful, this approach will identify new E3 ligases and their respective binders which can lead to novel, distinct PROTACs and revolutionize targeted therapies.

Incorporating Substrate Features in Fmoc Amino Acids to Develop More Potent and Specific Butyrylcholinesterase Inhibitors for the Potential Treatment of Alzheimer's Disease

Discipline: Life Sciences
Subdiscipline: Biochemistry

Nicole Paz-Bracamonte*, *California State University, Long Beach* and Jason Schwans, *California State University Long Beach*

Abstract: Alzheimer's Disease (AD) is a chronic neurodegenerative disease leading to irreversible memory loss and is the most common form of dementia. While a cure for AD is not available, approaches including cholinesterase inhibitors are under investigation to mitigate the effects of this disease. For the two major classes of cholinesterases, acetylcholinesterase (AChE) and butyrylcholinesterase (BChE), studies showed that BChE activity increased in individuals with AD while AChE activity was similar. The increased BChE activity is suggested to deplete available acetylcholine, and this depletion may contribute to dementia. We identified Fmoc-amino acids as BChE inhibitors, and Fmoc-Lys-O^- was one of the most potent inhibitors. The structural similarities of the Fmoc-Lys-O^- cationic ammonium group and trimethylammonium group of the enzyme's substrate, acetylcholine, may contribute to Fmoc-Lys-O^- as an effective inhibitor. Building on this result, we hypothesized that methylation of the Lysine side chain may mimic the substrate and lead to better inhibitors. We first synthesized a dimethylamino analog of Lysine, characterized the product by NMR, and used kinetics assays monitored by UV-Vis spectroscopy to determine inhibition constants (K_I values). The K_I value for Fmoc-Lys$(CH_3)_2$-O^- was four-fold lower than Fmoc-Lys-O^- (40 μM versus 150 μM, respectively), indicating the dimethylamino compound is a better inhibitor. The results support the hypothesis that adding substrate features lead to a more potent BChE inhibitor. Additional studies indicated that the compound selectively targets BChE relative to AChE. Currently, we are synthesizing the trimethyl ammonium compound to further test the model that the methyl groups contribute favorably to binding.

Imbalanced Muscle Lipid Metabolism in Lew.1WR1 Rats Results in Increased Mass and Reduced Insulin Sensitivity

Discipline: Life Sciences

Subdiscipline: Biochemistry

Sidney Martin*; Sharifa Love-Rutledge; Genoah Collins; Quiana Vidal; Laura Catherine Wright and Luis Mercado, *University of Alabama in Huntsville*

Abstract: Prediabetes and metabolic syndrome are increasing in prevalence globally. FAT10 is a ubiquitin-like protein related to increased obesity, kidney disease, several cancers, and type 1 diabetes susceptibility. The young T1D susceptible LEW.1WR1 rat overexpresses FAT10 and has higher fasting concentrations of blood insulin. Our lab is interested in understanding if and why the LEW.1WR1 rat would be more susceptible to a prediabetic phenotype (glucose intolerance/insulin resistant). We hypothesized that LEW.1WR1 rats would have an increased level of fatty tissue, and develop markers of insulin resistance. In this 12-week study, LEW.1WR1 and LEW/SsNHsd rats (n = 24) were either fed a control diet or a high-fat diet. During the study, the control rat became increasingly more glucose intolerant. At harvest, we isolated fasted muscle samples for gene expression analysis using quantitative real-time polymerase chain reaction to better understand the relative expression differences of lipid metabolism genes in the rat groups. The lipolytic genes like INSIG-1 were downregulated while the lipogenic genes like FASN were upregulated in both rat groups. The results suggest that there was more lipid being produced, causing the control LEW.1WR1 rats to increase in muscle lipid content. We concluded that the increase in mass and glucose intolerance was due to an imbalance of lipogenic and lipolytic gene expression, which are markers of reduced insulin sensitivity. These results shed light on the FAT10 mechanism, laying the foundation for future work on prediabetes.

Bacterial Membrane Depolarization and Permeability Studies and Surface Plasmon Resonance Microscopy Measurements to Investigate the Mechanism of Innate Antimicrobial Effector Molecules Against *Staphylococcus Epidermidis*

Discipline: Life Sciences
Subdiscipline: Biochemistry

MARIA KALA*; Edith Porter; Yixian Wang; Chris Cardona and Dara Banh-Thai, *California State University of Los Angeles*

Abstract: Due to bacterial resistance against antibiotics increasing worldwide, there is a need for new approaches in the antimicrobial drug design. Cholesteryl esters with antibacterial activity have emerged as novel effector molecules of the innate immune system and our lab seeks to understand their mode of action in conjunction with well-established antimicrobial peptides (AMPs) to guide future drug development for multidrug resistant bacteria. The objective of this study was to adopt a fluorescence-based assay to measure bacterial membrane potential and permeability with DiBAC4(3) and propidium iodide (PI), respective and to establish conditions for SPRm binding studies with a multidrug resistant *Staphylococcus epidermidis* strain associated with healthcare infections as bacterial target (SE). We found a dose dependent increase of DiBAC4(3) and propidium iodide fluorescence immediately after addition of the AMP protegrin 1 (PG-1) with maximal increases observed for 5 mg/mL PG-1 (up to over 10-fold) in agreement with its known membrane targeted pore forming activity. In contrast, the ionophore gramicidin effected primarily a dose dependent increase of DiBAC4(3) fluorescence consistent with its primarily membrane depolarizing activity. However, cholesteryl linoleate containing liposomes produced also increased DiBAC4(3) fluorescence likely due to their hydrophobicity coupled with a lack of polarization mimicking dead bacteria. For SPRm, SE was immobilized to gold chips and we were able to determine a preliminary dissociation constant for human lysozyme (K_D 5.074 x10^{-6}M). Our next step will be to employ SPRm for binding studies with antimicrobial cholesteryl esters and antimicrobial peptides. This research may inform future drug development.

Aptamer-Modified Microelectrode Biosensors for Neurotransmitter Detection Using Methylene Blue Redox Label

Discipline: Life Sciences
Subdiscipline: Biochemistry

Lyza Martinez*, *Ana G. Mendez University* and Lisandro Cunci, *Universidad Ana G. Mendez*

Abstract: A biosensor is a device that can determine the concentration or presence of chemicals, such as neurotransmitters, which share information from one neuron to another. Methylene blue (MB) is a synthetic dye that stains to negatively charged cell components like nucleic acids, aptamers, and certain excitatory neurotransmitters. This research focuses on the modification of the surface of carbon fiber and platinum microelectrodes using methylene blue label to improve the sensitivity and selectivity of neurotransmitters, specifically to the detection of dopamine (DA) and epinephrine (EPI). Fast Scan Cyclic Voltammetry (FSCV) allows us to measure neurotransmitters because of selective electrochemical detection based on voltage-dependent oxidation and reduction processes. Electrochemical Impedance Spectroscopy (EIS) is a technique that can give data about adsorption properties of molecules that stick to the surface of the electrode. Developing new modification protocols using techniques such as FSCV and EIS will enable the detection of biomolecules with and without redox reaction simultaneously. The idea to improve the microelectrode's system will allow us to be more selective of the biomolecule that we want to detect. To perform this, we tried to modify microelectrodes with MB to try and see if there is better interaction of the Neuropeptide Y (NPY) with the surface of the microelectrode.

What Is the Functional Role of Organelle Zinc Finger 1 in the Plant C-to-U RNA Editing Complex?

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alfredo Jimenez-Salinas* and Michael Lloyd Hayes, *California State University, Los Angeles*

Abstract: Higher plants utilize protein complexes to precisely edit hundreds of RNA transcripts in organelles. The mechanistic model of RNA editing involves a C-to-U deamination reaction facilitated through the interaction of the RNA with a protein complex. Complex models have been proposed, but the minimal editosome capable of catalyzing C-to-U changes and the functions of many of the protein components have not been revealed. This research focuses on describing the functional role of one critical protein component belonging to the RAN-binding protein 2 type zinc fingers protein family, Organelle Zinc finger 1 (OZ1). Zinc finger proteins have been associated with RNA binding; though RNA binding and site recognition in these editosomes is known to occur via PPR proteins, OZ1 may be interacting with a scaffold RNA sequence. Recombinant OZ1 from *Arabidopsis thaliana* was used to analyze zinc coordination and RNA binding of this zinc finger protein. ICP-MS and ESI-MS analyses of a truncated variant of OZ1, only the sequence containing its two zinc finger domains (OZ1zf), indicate that OZ1 does in fact coordinate with zinc ions. Electrophoretic mobility shift assays (EMSAs) examined RNA binding to the sequence around an editing site. Further experimentation might bring us a step closer to manipulating this precise editing machine for use in biotechnology.

Computational Study of Triclosan Binding on the Androgen Receptor

Discipline: Life Sciences
Subdiscipline: Biochemistry

Jose Delgado* and Evangelia Kotsikorou, *University of Texas Rio Grande Valley*

Abstract: Endocrine disrupting chemicals (EDC) can disrupt hormone function and gene expression. EDCs are capable of endocrine disruption is by acting on nuclear receptors such as the androgen receptor (AR). This can be observed in the crystal structures of AR, where an array of diphenyl molecules were crystallized in the shallow binding pocket known as binding function 3 (BF 3). Triclosan, an antibacterial agent, is a diphenyl molecule that has recently been identified as an endocrine disruptor. Studies have shown that the presence of triclosan prompts the release of the pre-bound dihydrotestosterone, the endogenous ligand of AR, from its steroid pocket. It is thought that triclosan allosterically regulates the AR by binding to and interacting with the BF 3 site. In this study, we used computational methods to analyze the binding of triclosan to BF 3. Different modules of the molecular modeling software Schrodinger were used to carry out all calculations. An analysis of the conformational space of triclosan was carried out using Macromodel and Jaguar. Potential binding pockets were identified using SiteMap, and triclosan was docked to BF 3 using Glide. It fits in the BF 3 similarly to the diphenyl compounds seen in the crystal structures. Analysis of the interactions between triclosan and the BF 3 site were measured using Macromodel. Preliminary results show that triclosan favorably interacts with the BF 3 site mainly due to hydrophobic interactions with most of the binding pocket residues. Hydrogen bonding interactions with two glutamic acids help orient triclosan in the pocket.

Using Citizen Science through Video Game Puzzles to Improve RNA Secondary Structure Modeling

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alexandra Strom*[1]; Hannah Wayment-Steele[2] and Rhiju Das[2], *(1)San Diego State University, (2)Stanford University*

Abstract: Studying RNA secondary structure and folding is critical to understanding the biological functions that they perform and synthesis of new RNA medicine. Structure prediction is an elusive method that becomes increasingly imperative in synthesis and research of RNAs. Although many secondary structure packages have been developed, the most widely-used packages have been demonstrated to have low accuracy for real-world prediction tasks. We have previously demonstrated improved accuracy with a model that was trained using machine learning on high-throughput structural data obtained from Eterna, the online RNA design video game. Here, we further explore machine-learning-based RNA models by determining what attributes of structural data are most crucial for improving their accuracy. We characterized chemical mapping data spanning nine years of citizen-scientist-driven experiments from more than 400 participants on Eterna. We found that the sequence and structure space of player-designed sequences was highly diverse based on many metrics. We trained multitask-learning models using differing splits of the Eterna Cloud Lab data to determine what attributes of structural data most improve model accuracy. This work lays a critical foundation for improving RNA modeling and prediction, two necessary methods for development of RNA-based technologies including vaccines and other therapeutics.

Synthesis and Enzymatic Bypass Studies of N^6-Deoxyadenosine-DNA Peptide Crosslinks

Discipline: Life Sciences
Subdiscipline: Biochemistry

Gabriela Gonzalez-Vasquez*; Pratibha P. Ghodke; Hui Wang; Carl A. Sedgeman; Kevin M. Johnson and F. Peter Guengerich, *Vanderbilt University*

Abstract: DNA-protein crosslinks (DPCs) are DNA lesions formed by covalent binding of proteins to DNA. If left unrepaired, due to their very bulky natures, they can stall replication forks and result in genome instability. The DNA-dependent metalloprotease SPRTN and the proteasome have both been suggested to be involved in the repair by cleaving large DPCs to DNA-peptide crosslinks (DpCs). 1,2-Dibromoethane (DBE) is a known carcinogen that can crosslink the repair protein AGT (O^6-alkylguanine DNA-alkyltransferase) to the N6 position of deoxyadenosine (dA) in DNA. AGT-N^6-dA-DNA DpC was synthesized using a 15 mer peptide to investigate its effect on DNA replication *in vitro* by human translesion synthesis (TLS) DNA polymerases η, ι, and κ. The DpC was bypassed by human TLS polymerase η, ι and κ at different rates. Polymerase η incorporated all four nucleotides across the lesion, and polymerases ι and κ only incorporated the correct nucleotide. Further kinetic and LC-MS/MS analysis of primer extension products were done to determine the efficiencies and fidelity of nucleotide incorporation by each TLS polymerase. The catalytic efficiency of incorporation of the correct nucleotide opposite to the adduct by polymerase k decreased in more than 10^3 fold, while polymerase η and ι in 12.2 fold and 1.1 fold, respectively. These results reveal the importance of AGT-N^6-dA-DNA DpC lesion on replication by TLS DNA polymerases and their mutagenic potential.

Catalytic Activity of Tumor Relevant Mutant Isocitrate Dehydrogenase 1 (IDH1)

Discipline: Life Sciences
Subdiscipline: Biochemistry

Nalani Coleman[*]; Danielle Caliger; Ella Thornberg; Lucas Luna and Christal Sohl, *San Diego State University*

Abstract: Isocitrate dehydrogenase 1 (IDH1) is found commonly mutated in grade II and III gliomas and secondary glioblastomas. Normally, IDH1 catalyzes the conversion of isocitrate and NADP$^+$ to α-ketoglutarate and NADPH. However, in mutated form, IDH1 catalyzes α-ketoglutarate and NADPH into NADP$^+$ and D-2-hydroxyglutarate, an oncometabolite. D-2-hydroxyglutarate is toxic to cells and drives a number of pro-tumorigenic pathways. To understand the molecular mechanisms of how mutated IDH1 can lead to brain cancer, we created point mutations in IDH1 to understand the effects on enzyme activity. We hypothesized that point mutations will affect the catalytic efficiency of mutant IDH1. Site-directed mutagenesis was used to generate mutations at residue 132, the most common site of mutations in cancer patients. Wild type (WT) IDH1 and mutant IDH1 were heterologously expressed in bacteria. Following purification of IDH1 mutants using affinity column chromatography, steady-state kinetic assays were used to compare the catalytic activity of WT versus mutant IDH1. By elucidating the types of mutations at R132 that facilitate D2HG production, we can have a better understanding of how IDH1 mutations affect prognosis and therapeutic response.

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First Report of Trimethoprim Resistance *dfrA8* Gene in Environmental Isolate of *Klebsiella Variicola*

Discipline: Life Sciences
Subdiscipline: Biochemistry

Sheila Gonzalez-Ramos[*1]; Andrei Tatarenkov[1] and Luis Mota-Bravo[2], *(1)University of California, Irvine, (2)University of California, Irvine MSP program*

Abstract: Genes that confer resistance to the antibiotic trimethoprim are diverse and often found as gene cassettes in class I and II integrons, except the dihydrofolate reductase resistance gene *dfrA8*. We hypothesized that the *dfrA8* gene is mobilized by distinct mobile genetic elements and disseminated across species via conjugation and transposition. A water sample of bacteria was collected from the Hudson River in New York and one isolate was identified as *Klebsiella variicola* by MALDI-TOF. Disk Diffusion Test (DDT) was performed to establish antibiotic resistance phenotype. Plasmids were extracted, sequenced, and assembled. The bioinformatic analysis detected the *dfrA8* gene flanked by two *IS26* elements in the IncR plasmid of 67 Kbp. DDT showed antibiotic resistance to Sulfisoxazole and Trimethoprim, encoded by *sul2* and *dfrA8*, respectively. Comparative analysis was performed using the BLAST tool from NCBI and CGE databases. Only 21 instances of the *dfrA8* gene were found in plasmids of *Enterobacter*, *Salmonella*, *Shigella*, and *Escherichia coli*. Surprisingly, three *E. coli* strains housed the *dfrA8* gene in their chromosomal DNA. Findings suggest that the *dfrA8* gene has been moved by IS26 elements and introduced into plasmids with different replicons such as IncFII, IncFIB, IncHI2, IncHI1B, IncHI2A, and IncX1, as well as chromosomes. This study is the first report of *K. variicola* carrying the *dfrA8* gene. The propagation of the *dfrA8* gene among diverse taxa, including pathogenic strains from clinical samples, provides a useful model to study dispersal of resistance genes posing a threat to human health.

Development of an Online Database for Bacterial Microcompartment Research

Discipline: Life Sciences
Subdiscipline: Biochemistry

Kaylie Bair[*]; Jessica Ochoa and Prof. Todd Yeates, *University of California, Los Angeles*

Abstract: Bacterial microcompartments, or MCPs, function as proteinaceous metabolic organelles within bacterial cells. Previously, there was no organized resource where information about microcompartments was readily accessible or available for scientific research. We have created an online database with information about microcompartment proteins and other large protein assemblies. The database offers information and utilities for both advanced and novice researchers. The resources we have created can be used to support a broad range of research investigations on structural, functional and genomic aspects of MCPs and other large protein assemblies. The database was created using a variety of technologies. The web interface was created using PHP and HTML. The interactive tools, including our interactive 3D structure viewer, were built using Python and JavaScript. In addition, the models and downloads presented were generated using PyMol. The database is currently operational and houses over 120 unique biological structures, each with their own downloadable amino acid and nucleotide sequences. In addition, the database also contains an interactive 3D structure viewer and downloadable PyMol files for each entry. In the coming months we hope to develop secondary website features including a genome browser and the capability to generate 3D printable files.

Degradation of Biodegradable Plastics in Soil Environment.

Discipline: Life Sciences
Subdiscipline: Biology (general)

Huy Huynh*, *University of Houston, Downtown* and Poonam Gulati, *University of Houston-Downtown*

Abstract: Due to excessive use and disposal of plastics, there is an alarming amount of plastic waste in landfills and in the waters. The plastic that ends up in the oceans creates great difficulties such as choking and entanglement for the marine animals. Annually, 300 million tons of synthetic plastics accumulate in the whole environment across the globe, and the decomposition of synthetic plastic can take up to 1,000 years. Previously, we studied the microbial residents of different plastics placed in saltwater in Galveston. We also studied skimmer analysis of the plastics and found no changes. Therefore, we are now studying biodegradable plastic, which is designed to degrade faster, in the soil environment. The polylactic acid plastic samples were all cut to 4.5-centimeter diameter and placed in the soil. Every three weeks, one set of samples were removed. The microbial biofilms were scraped off, centrifuged and frozen as pellets. These will be sent for DNA analysis to obtain the identity of the bacteria that may be contributing to the degradation of the plastics. The plastic samples are being analyzed using thermal analysis and infrared spectroscopy.

Assessing Changes in Vocal Learning Processes over Time in a Biological Invader

Discipline: Life Sciences
Subdiscipline: Biology (general)

Valeria Perez*; Grace Smith-Vidaurre and Timothy Wright, *New Mexico State University*

Abstract: Vocal learning has evolved repeatedly throughout evolutionary history. Although vocal learning is a social process, little is known about how social dynamics influence vocal learning. Biological invaders that are capable of vocal learning are useful systems to test this idea, because invasion leads to fluctuations in population size. If vocal learning is altered by the invasion process, then we would expect changes in patterns of acoustic similarity in an invasive population over time. Monk parakeets (*Myiopsitta monachus*), small parrots native to South America, have established invasive populations around the world through repeated introductions via the pet trade. Parakeets in Uruguay, part of their native range, exhibit strong individual signatures but low acoustic similarity within nesting sites. Here, we addressed whether the invasion process has altered vocal learning processes as established populations in the invasive range reach sizes comparable to the native range. If so, we predicted that invasive populations will display modifications in patterns of acoustic similarity over time within nesting sites. We compared acoustic similarity patterns in Austin, TX, where parakeets were recorded in 2004, 2011, and 2019. We used three methods of measuring acoustic similarity at the individual and site social scales: visual inspection, spectrographic cross-correlation, and supervised machine learning. The strength and statistical significance of acoustic convergence over social scales was evaluated using Mantel tests. Our preliminary results for 2011 and 2019 indicate that invasive parakeets in Austin exhibit strong individual signatures and low convergence of shared calls within nesting sites in both of these two years.

Epidemiological Factors Contributing to the Infection of Parasitic Jellyfish (*Polypodium hydriforme*) in Oklahoma Paddlefish (*Polyodon spathula*)

Discipline: Life Sciences
Subdiscipline: Biology (general)

Katie Easter* and Mark Paulissen, *Northeastern State University*

Abstract: *Polypodium hydriforme* is a parasitic freshwater jellyfish that infects the oocytes of acipenseriform fishes, like sturgeon and paddlefish, that inhabit the Midwestern river systems of the United States. In the past, sturgeon have been the prime supplier of commercially sold caviar but overfishing by humans has caused a fast decline in these populations making *P. hydriforme* more difficult to study in sturgeon. The eggs of Oklahoma's largest game fish (*Polyodon spathula*), have been used as popular substitute for caviar since Oklahoma supports a stable population of Paddlefish. Batches of paddlefish *(Polyodon spathula)* eggs, called roe, were collected at the Paddlefish Research Center and assessed for infection. Assessments were used to examine possible connections between parasite and host by comparing characteristics of

females whose roe was infected with *P. hydriforme* to characteristics of the uninfected females. Epidemiological data collected on each female included quality of roe, catch location, total roe weight, roe screened weight, roe fat weight, fish weight and length. Findings suggest that there were no differences in fish length, fish weight, total roe weight and quality of roe between females with infected and uninfected roe. However, it was determined that roe screened weight was higher in infected individuals and roe fat weight was significantly lower in infected individuals.

The Role of Ephrin Downstream Signaling in the Process of Newt Lens Regeneration

Discipline: Life Sciences
Subdiscipline: Biology (general)

Alyssa Miller* and Katia Del Rio-Tsonis, *Miami University*

Abstract: Newts are capable of regenerating many organs including their lungs, brain, heart, and many eye parts. Our lab focuses on the newts' ability to regenerate their lens. Following a removal of the lens, cells from the dorsal iris lose their identity as an iris and transform into a lens- a completely separate cell type. Interestingly, the ventral iris is unable to regenerate a lens. Our lab investigates the molecular mechanisms that govern the differences between the regeneration-competent dorsal iris and its morphologically indistinguishable counterpart, the ventral iris. Using gene analysis, Ephrins, a family of proteins, were identified as differentially expressed between the irises. Eastern newts had their lens surgically removed and a soluble Ephrin inhibiter was injected into the eye. After 30 days, immunohistochemical analyses were performed. Select conditions were repeated *ex vivo*. It was found that ventral lens regeneration was induced *in vivo* following the inhibition of Ephrin receptors. Similar results were observed *in vitro* using separated dorsal and ventral iris segments. Additionally, western blots have been optimized using newt tissue and are being used to analyze the activation or inhibition of the downstream cascade of Ephrins following their inhibition. These results represent the first time that inhibition of a specific target unlocked the regenerative potential of the ventral iris *in vivo*. By inducing regeneration in a tissue that was previously thought to be incapable of doing so, we can continue to piece together the puzzle of regeneration in higher vertebrates which could hold great clinical and therapeutic significance.

Does the Invaginated Eye of the Disco Clam Use Opsin-Based Phototransduction to Detect Light

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jennifer Ortiz*; Kyle McElroy and Jeanne Serb, *Iowa State University*

Abstract: Animals use a variety of morphologically diverse eyes to perform a wide range of tasks, such as navigation, interaction with other individuals, and detection of environmental cues. In marine bivalve molluscs alone, there are five types of eye structures: cap eyespot, pigmented cup, compound, mirror, and invaginated. For most animal eyes, it is known that opsins are the light-sensitive proteins, but we do not have a concrete understanding of how bivalve vision works on the molecular level. In this study, we obtained raw RNA sequences for three different limid species with invaginated eyes (*Ctenoides ales, C. mitis,* and *C. scaber*), and assembled transcriptomes for each species. We identified opsin genes using known opsins from the scallop, *Argopecten irradians*. All candidate opsins were analyzed phylogenetically to determine their relationship with other bivalve opsins. The opsin gene tree indicates that limid opsins have undergone a lineage-specific diversification such that many of these opsins are paralogous, rather than orthologous. We identified conserved motifs within the opsin genes to try to further understand possible opsin structure and function.

Caenorhabditis Elegans Strains Respond Differently to Various Nematicidal Chalcones

Discipline: Life Sciences
Subdiscipline: Biology (general)

Daisy Xiong*; Sophie Jimenez and Alejandro Calderon, *California State University, Fresno*

Abstract: Plant Parasitic Nematodes (PPNs) cause billions of dollars in monetary losses in the agricultural industry each year. Most nematicide agents are a type of pesticide that are harmful to humans and the environment, not to mention, PPNs are becoming more resistant to many nematicides. Thus, a new, more environmentally friendly form of pesticide is needed to control nematodes in agriculture to prevent economic losses. Previous research discovered that certain organic chalcones (**17**, **25**, and **30**), derived from the parent molecule 1,3-diphenyl-2-propen-1-one, are 100% effective against the model nematode *Caenorhabditis elegans* at concentrations of 10-5 M. Previous research, in an attempt to understand the action mechanism of the chalcones, also isolated mutant nematodes that are resistant to Chalcone **17** and Chalcone **30**.

In the current study, we conducted experiments to study the lifespan of four different strains of *C. elegans*, a GFP standard strain used to identify and isolate the mutants, the N2 Wild Type Bristol strain, and the two chalcone mutant strains (Ch17-m and Ch30-m). Our interest is to develop a more robust and reliable assay to identify differences in various *C. elegans* strains, including chalcone mutant strains. Our results indicated that the GFP Standard Strain used to generate the mutants has a similar lifespan as the N2 strain. When analyzing the GFP standard strain for this experiment, Chalcone **17** was more effective than Chalcone **30** in killing nematodes. While in the N2 Wild Type experiment, Chalcone **30** more effectively killed the *C. elegans* nematodes than Chalcone **17**.

DNA Methylation Significance in Ectomycorrhizal Fungi *Rhizopogon Vinicolor* and *R. Vesiculoses C*olonizing Douglas-fir (*Pseudotsuga menziesii*)

Discipline: Life Sciences
Subdiscipline: Biology (general)

Ana Chavez[*], *California State University, Fresno* and Alija Mujic, *California State University Fresno*

Abstract: DNA methylation is an important factor in understanding epigenetic gene regulation in symbiotic species. Epigenetics is a crucial approach to develop modern medicinal treatments and diagnosis for severe diseases like cancer. In this study, Ectomycorrhizal fungi that form symbiotic relationships with tree species and beneficial for forest ecosystems will be observed. Fungi fruiting bodies are thought to produce antibacterial properties useful for antibiotic development and medicinal treatment. Fungi in the genus *Rhizopogon*, in this project specifically, *Rhizopogon vesiculosus* and *Rhizopogon vinicolor,* are host-specific sister species that colonize *Pseudotsuga menziesii* (Douglas-fir) in different ways. To investigate downregulation and upregulation in *R. vesiculosus* and *R. vinicolor* in colonizing *P. menziesii,* whole-genome bisulfite methylation sequencing will be used. DNA methylation patterns observed in *Rhizopogon* fungi will be compared to metatranscriptomes of fungal and host-tree interaction to investigate the role of DNA methylation in the regulation of symbiosis. Symbiosis gene interactions are important because they play a major role in increasing the rates of survival between species. DNA methylation studies are a novel way to provide valuable information about the symbiotic relationships between *R. vesiculosus* and *R. vinicolor* on *P. menzie*sii.

Understanding the Association Among Environment, Microbiome, and Golden Retriever Health.

Discipline: Life Sciences
Subdiscipline: Biology (general)

Kayla Medina[*] and Christopher Miller, *University of Colorado Denver*

Abstract: Golden Retrievers across the United States suffer from increased adverse health outcomes due to obesity. However, there has been limited study of the link between environmental factors such as diet and microbiome, and how that might affect dogs who suffer from an adverse health outcome. Given the fact that there is a strong association between microbiome composition and body condition in humans and mouse models, we hypothesized that there is a relationship among diet, microbiome, and adverse health outcomes in dogs. To begin to explore this hypothesis, we utilized high throughput 16S rRNA gene sequencing methods. Using a Course Based Undergraduate Research Experience in General Biology labs, we have characterized the microbiome composition of 400 Golden Retriever fecal samples with replication. Our work is one of the largest samplings to date to characterize the common microbes found in a single dog breed, and lays the groundwork for understanding associations among variation in microbiome composition and environmental factors.

PRMT7 Methylates PGC-1α in a Temperature Dependent Manner

Discipline: Life Sciences
Subdiscipline: Biology (general)

Meryl Ann Mendoza[*1]; Janielle Cuala[2]; Immaculeta Osuji[2]; Mariel Mendoza[3]; Benjamin A. Garcia[3] and Cecilia Zurita-Lopez[2], *(1)California State University, Los Angeles, (2)California State University, Los Angeles, Department of Chemistry and Biochemistry, (3)University of Pennsylvania*

Abstract: Like phosphorylation, arginine methylation is a modification found in proteins that can alter their function, allowing them to be part of many cellular processes. PRMT7 is a member of a family of nine mammalian protein arginine methyltransferases (PRMTs). To date, it is also the only member of the PRMT family with greater activity at temperatures below 37˚C. We set out to determine whether peroxisome proliferator-activated receptor γ coactivator 1α (PGC-1α, human isoform 2, NP_037393.1), is a substrate for PRMT7. PGC-1α is a protein that is strongly induced by cold exposure and who regulates metabolic processes such as mitochondrial biogenesis, gluconeogenesis, and respiration. We performed *in vitro* methylation reactions using purified recombinant mammalian PRMT7 enzyme at various temperatures (37˚C, 30˚C, 21˚C, 18˚C, 16˚C, and 4˚C). Full length, truncated portions, as well as a fragment of PGC-1α corresponding to amino acid residues 481-798 (the C-terminus) were used as substrates. The methylation reactions were resolved by gel electrophoresis and detected via fluorography. Methylation was also verified by mass spectrometry. Results show that PRMT7 and PRMT1 (used as a control) both differ in their choice of methylated arginine residues in PGC-1α and more importantly, that temperature affects the extent of methylation. Since the activity of PGC-1α is dependent on temperature, this work, which enables us to map out the methylation in PGC-1α allows us to better understand its function at various temperatures.

The Therapeutic Impacts of Exogenous Estradiol on Wound Healing in Larval Zebrafish

Discipline: Life Sciences
Subdiscipline: Biology (general)

Edith De La Torre[*]; Sara Dresler and Matthew Salanga, *Northern Arizona University*

Abstract: Estrogen is a hormone naturally found inside the body produced by ovaries, adipose tissue, and the adrenal glands. A form of estrogen known as Estradiol (E2) is critical during the inflammatory process of wound healing.

Additionally, literature suggests that E2 may be a potential therapeutic agent for chronic wounds. Essentially, a higher E2 dosage will result in an increase in tail regeneration. In these studies, an E2 dose curve was conducted to find the optimal dose of E2 that provides optimal wound healing for chronic wounds using *Danio rerio* (Zebrafish). Zebrafish were used because they are a literature accepted model system, and their dermal tissue expresses the same genes as humans. Larvae were placed in four treatments of E2 (0 nM, 0.1 nM, 1.0 nM and 10 nM) with a sample size of 16 fish per treatment. These fish were dechorionated at 24 hours post fertilization (hpf) and placed in their respective treatment for 24 hours. Wounding and imaging commenced at 48hpf. At 72 hours post amputation (hpa), any surviving fish had their tails imaged and tail areas were measured using ImageJ. The difference in tail areas (From 0hpa to 72hpa) was measured and an upward trend appeared in the raw data. A power analysis showed that the sample size was not large enough to be statistically significant. This suggests that, once the sample size doubles, the data may show a stronger relationship between higher E2 doses and increased wound healing, and that E2 could be a therapeutic candidate.

Individual Consistency in the Contact Call of an Urban, Invasive Parrot, the Rosy-Faced Lovebird

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jonathan Brooks*; Dominique Hellmich and Timothy Wright, *New Mexico State University*

Abstract: Individual consistency in the structure of vocalizations is necessary for the formation and maintenance of both individual vocal signatures and population-level vocal dialects. Though there is significant evidence of individuals using consistent vocalizations across very short timescales (e.g. hours, days), there is little empirical support that similar patterns persist across longer timescales (e.g. years) in wild populations. Our aim was to examine whether the individuals of an introduced, urban parrot population maintained consistent call structures over time. For our study, the contact calls of marked individuals were sampled at a breeding colony in Tempe, AZ from May to July in 2019 and 2020. Spectrographic cross-correlation and principal components analysis were used to visually assess individual call structure similarity. A partial mantel test was then used to determine whether call structure remained consistent within individuals between our sampling points. Our results indicate that the lovebirds do maintain consistent, individually distinct contact calls over both short and long periods of time.

Quantitative Analysis on the Deletion of Self-Reactive T Cells Against Dendritic Cell-Producing Endogenous Sp-Mhcs

Discipline: Life Sciences
Subdiscipline: Biology (general)

Hui (Charlotte) Wang*[1]; James Moore[2]; Hasan Ahmed[1] and Rustom Antia[1], *(1)Emory University, (2)Fred Hutchinson Cancer Research Center*

Abstract: During T cell development, T cells are clonally deleted by negative selection in the thymus in order to provide tolerance against self-reactive lymphocytes. The large number of possible self-peptide MHCs (spMHCs) and the relatively short period for negative selection in the thymus impose a quantitative constraint on the efficiency of clonal deletion against self-reactive lymphocytes. It is, however, particularly important to delete T cells specific for dendritic cell endogenous sp-MHCs -- this is because DCs play a central role in the activation of T cells and the generation of immune responses. Since DCs in the thymus have very similar patterns of gene expression as DCs in the periphery, Matzinger has hypothesized that it may be possible to reliably delete all T cells specific for DC-endogenous sp-MHC (DC-self). Here we use quantitative models to explore Matzingers hypothesis. We begin with a simple model where the rules for stimulation of a T cell in the thymus is the same as that in the periphery. In this scenario, we find that it may be difficult to reliably delete T cells specific for rare DC-self antigens. We then explore how differences in both the threshold and dynamics of T cell activation in the thymus vs. the periphery may allow us to reliably avoid stimulation of T cells against DC-self. Our results suggest that the complex pattern of T cell priming in secondary lymphoid organs may arise, at least in part, to prevent the stimulation of autoimmune T cells responses to DC-self.

Seasonal Impacts on the Fat and Population Cycles of Invasive *Gambusia Affinis* (western Mosquitofish)

Discipline: Life Sciences
Subdiscipline: Biology (general)

Courtney Moulton* and David Reznick, *University of California, Riverside*

Abstract: The lifecycles of *Gambusia affinis* (Mosquitofish) have been studied in their native range (eastern United States), where seasonality is prominent, and winters are pronounced. Populations introduced to Southern California face subdued seasonality, and it is unclear how they have adapted. We are studying the seasonal lifecycle, including the fat cycling, of the nonnative population of *G. affinis* in the Santa Ana River. The results can lead to a better assessment of how this invasive population utilizes its resources and impacts the River's ecosystem, and the native species in it. We predict that this population will have a longer reproductive season and either a reduced or no fat cycle. Our study involves the collection of 30 Mosquitofish each month over the span of a year. Upon collection, the fish are euthanized, preserved, and brought to the lab for processing. Each specimen's percent of body fat is estimated, and the pregnant females dissected, and their embryos staged. These data are used to determine how nonnative populations have adjusted to the region's mild climate;

their fat cycling will distinguish the amount of time the population overwinters for and how this has influenced the span of their reproductive season. We are also studying the male annual cycle. In native populations, males delay maturation to store fat and overwinter, which leads to seasonal fluctuations in the numbers of immature and mature males. By estimating the numbers of mature and immature males from each collection, we will determine if this trend exists in Southern California's populations.

Aspire, Learn, Mentor, Achieve (ALMA) Science Academy and Mentorship Pipeline: Can an Informal Science Program Prepare Students for STEM Careers of the 21st Century?

Discipline: Life Sciences
Subdiscipline: Biology (general)

Vanessa Gaeta-Garcia[*1]; Luisa Espericueta[1]; Martha Romero BS[1]; Jose Rea MA[1] and Dr. Frank Zaldivar PhD[2], *(1)University of California, Irvine, (2)Department of Pediatrics, University of California, Irvine*

Abstract: The Aspire, Learn, Mentor, Achieve (ALMA) Science Academy program focuses on (1) exposing elementary-age students to hands-on STEM education and (2) the development of mentorship throughout elementary school, middle school, high school, and graduate and professional students. A review of the educational literature indicates that early exposure to STEM prior to 4th grade develops a curiosity in STEM. The ALMA Science Academy starts with its summer camp focusing on environmental pollution and its effects on human health. It is followed by 22 interactive labs on separate Saturdays during the academic year, exposing our students to biology, medicine, engineering, 3D printing, and coding. Our mentors develop a peer to peer mentor pipeline that follows them throughout their academic career. We recruit 70 elementary school students using teacher recommendation and parents are required to attend 3 workshops on educational development. A pre- and post-test gauges student learning of material presented. 90% of the enrolled students complete the program and grasp the lesson content and increase their knowledge about science. The students also reported an increase in pursuing science careers in the future. The ALMA Science Academy and mentorship program show that students of color are extremely interested in science and demonstrate value to early educational STEM exposure. In the overall spectrum, early exposure to biology gives students tools that they can utilize to continue their academic development as well as sparks an interest in science which they can follow along their academic journey.

The Functional Anatomy of Tail Regeneration in the California Alligator Lizard, *Elgaria Multicarinata*

Discipline: Life Sciences
Subdiscipline: Biology (general)

Carla Beatriz Campos[*]; Clint E. Collins, PhD and Marisa G. Correa, *California State University, Sacramento*

Abstract: Preventing depredation, or being consumed by a predator, is vital for future reproductive opportunities and survivorship. Therefore, organisms have evolved a diverse repertoire of adaptations to escape predators. Caudal autotomy, or tail self-amputation, and regeneration are striking, coupled adaptations supporting lizard survival and evolutionary diversification. We studied the organization of muscles and support structures in original and replacement tails of California alligator lizards (*Elgaria multicarinata*). We hypothesized regenerated tails exhibit structures that maintain movement capacity. We requisitioned samples of original (n=4) and regenerated (n=4) tails from the California Academy of Science Herpetology Collection and scanned them using a MicroCT scanner. Then, we dipped specimens in a custom-modified iodine solution to render the muscle tissue radio-opaque, and rescanned to visualize muscle tissue. Scans were analyzed and segmented in Amira 3D visualization software. Preliminary results indicate cartilaginous rods replace bony vertebrae and protective osteoderms (bony scales) appear smaller and less dense than originals. Muscles appear less organized and smaller. We anticipate that this new model species will show similar structure patterns and organization compared to previous studies. Yet muscle sizes should be relatively larger in this species, which uses its tail to move and balance. Results vary due to confounding factors in regeneration phase and environment. This study characterized the secondarily-simplified, regenerated structures by quantifying differences in bone, muscle, and cartilage of original and regenerated tails. Our results enhance our knowledge of appendage regeneration in vertebrates and provide a new model for biomedical and clinical applications including prosthetics and biomimicry.

Airborne Fungi Degrade Haloalkane

Discipline: Life Sciences
Subdiscipline: Biology (general)

Stiphany Blanco-Laureano[*] and José Pérez-Jiménez, *Universidad Ana G. Méndez, Recinto de Gurabo*

Abstract: Halides (haloalkanes) are persistent organic pollutants in water, sediments, and soil. Chlorinated and brominated halides are colorless, flammable and toxic liquid compounds. They are commonly found in pesticides, herbicides and industrial solvents. Exposure to these toxic compounds pollutants is probable. Since these pollutants tend to accumulate due to their low bioavailability, which leads to reduced degradation, and therefore toxicity. For this reason, biodegradation must be considered, because it is more viable and economical way to transforming them into less harmful or non-hazardous compounds. Recently, an aerobic degradation pathway of bromoalkane was described for the yeast *Yarrowia lipolytica* 3589. Until now, this only yeast reported that can degrade it. Our objective is isolate putative fungi capable of degrading chlorobutane and bromobutane. 1-bromobutane and 1-chlorobutane were added independently to mineral media as the only carbon source on agar plates. These plates were randomly exposed to air from different places in Puerto Rico and incubated at room temperature. After approximately ten days, small fungal colonies were observed for three sites in the mineral media amended with 1-chlorobutane (~5%). The microscopic examination revealed isolates that presented fine mycelia septa and conidiophore arrangements resembling different strains of *Penicillium* and *Aspergillus.* ITS sequence resulted on *Cladosporium*, *Fusarium*, *Curvularia*, and *Scopulariopsis* strains. Also, initial tests demonstrate the degradation of the halogenated compound, fluorobenzene. Neotropical ecosystems have provided fungi with diverse capabilities that can be useful in the remediation of contaminated sites and preserving public health.

Probing the Role of the PBRM1 Bah Domains through Mutational Analysis

Discipline: Life Sciences
Subdiscipline: Biology (general)

Paloma Ruiz[*]; Christopher Petell; Jessica Skela; Brenda Temple and Brian Strahl, *University of North Carolina at Chapel Hill*

Abstract: The genome consists of DNA wrapped around histone proteins, creating nucleosomes that form chromatin. Post-translational modifications of nucleosomes affect gene expression and chromatin function through recruitment of effector proteins containing specialized “reader” domains. While many reader domains have been investigated for their histone binding specificities, the function of several readers are still unknown. We investigate a reader protein, PBRM1, that has multiple chromatin binding domains including six bromodomains and two bromo-adjacent homology (BAH) domains. PBRM1 is involved in transcriptional regulation, mutations in it result in aberrant chromatin remodeling that detrimentally alters gene expression profiles. We aim to characterize, for the first time, the functional and biological impact of PBRM1 BAH domains by disrupting their ability to bind to chromatin.

We first used computational methods to model each domain interacting with a histone peptide. From this, we defined residues that were potentially critical to binding and chose four per domain to mutate based on their structural relevance. After purifying these mutant domains, we used Nano-DSF, which monitors protein stability based on its denaturation temperature, to determine if the conformation of the mutants were perturbed. Next, we used peptide pulldown assays to find if the mutants showed histone binding defects. We selected one mutant for each BAH domain based on stability and binding defects to insert in a cell line. From this, we hope to determine the functional roles of the PBRM1 BAH domains, as well as any subsequent impacts in the transcriptome and cellular phenotypes.

Studies on the Relationship between Eg5 and MUSA1 during Xenopus Laevis Somitogenesis

Discipline: Life Sciences
Subdiscipline: Biology (general)

Maria Alejandra Torres-Colon[*] and Edwin Traverso Avilés, *University of Puerto Rico at Humacao*

Abstract: Muscle mass atrophy leads to a loss of motor function and physical disability. In vertebrates, muscle fibers arise from mesodermal transitory blocks known as somites. The maturation of somites is tightly regulated by mechanisms that maintain a balance between protein synthesis and degradation. Studies in adult mice show that the muscle ubiquitin ligase of SCF complex in atrophy called MUSA1 acts as a negative regulator during muscle mass growth. MUSA1 is an F-Box protein that targets substrates for degradation by ubiquitinylation. However, the role of MUSA1 in the african frog *Xenopus laevis* is unknown. Our downregulation experiments of MUSA1 in *X. laevis* produce an abnormal growth of somites and disruption of the intersomitic boundaries, seen by immunostaining of morpholino injected embryos. To fully understand the function of MUSA1 as an F-Box protein is important to identify its specific substrates. Others have shown by mass spectrometry that MUSA1 has a critical role in the correct formation of the mitotic spindle during mice mammopoiesis, by targeting the bipolar mitotic kinesin Eg5. In this study, we sought to test Eg5 as a substrate of MUSA1 during early muscle development in *X. laevis*. We found through immunostaining that both the MUSA1 and EG5 proteins are present in the somitic tissue at the tadpole stages. We are currently evaluating by western blotting Eg5 abundance in samples of somites dissected from MUSA1 morpholino injected embryos. Our studies may reveal a possible substrate-enzyme interaction between Eg5 and MUSA1, which might be critical for correct early muscle development.

Identifying New FGFR Signaling Components in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Biology (general)

Melissa Garcia-Montes de Oca[*1]; Michael Stern[2]; Victoria Puccini de Castro[1]; Omar Payan Parra[1]; Mariya Stefinko[1]; Cindy Voisine[1]; Te-Wen Lo[3] and Jessica Palalay[2], *(1)Northeastern Illinois University, (2)Biology, Northeastern Illinois University, (3)Ithaca College*

Abstract: Fibroblast growth factor receptors (FGFRs) are cell-surface receptor tyrosine-kinases (RTKs) that phosphorylate specific intracellular tyrosine residues to trigger downstream responses such as cell proliferation, migration, and differentiation. The study of the EGL-15 FGFR in the nematode *C. elegans* has long been used to understand principles of RTK signaling, since defects in the processes mediated by EGL-15 result in striking phenotypes that provide powerful genetic tools. One such process is the regulation of fluid homeostasis. Hyperactivation of EGL-15 causes excessive accumulation of clear fluid inside the worm’s body (the Clr phenotype). The isolation of Suppressor Of Clr (*soc*) mutants has led to the identification of many of the core components of EGL-15 signaling, such as the Grb2/SEM-5 adaptor protein that links RTK signaling to the RAS/MAPK pathway. Although SEM-5 is required for EGL-15 signaling, a mutation that truncates EGL-15 and eliminates its SEM-5 binding sites does not confer a Soc phenotype. These data suggest the existence of an alternate pathway that links EGL-15 to SEM-5/Grb2. To identify components of this alternate pathway, we repeated the screen for Soc mutants in this *egl-15* mutant background. Of 25 mutations analyzed, 11 define two new *soc* genes, *soc-3* and *soc-4,* whose molecular identities were recently determined by a whole-genome sequencing approach. *soc-3* encodes a protein with structural features consistent with it acting within an alternate pathway that can couple EGL-15 to SEM-5/Grb2. Future experiments will test this hypothesis and probe the roles of these new FGFR signaling components.

Metabolomics Studies Reveal Altered Gut Metabolites in Metabolic Syndrome Mice That Disrupt *Pparg* Gene Expression

Discipline: Life Sciences
Subdiscipline: Biology (general)

Eduardo Peralta-Herrera* and Eliseo F. Castillo, *Division of Gastroenterology and Hepatology, Department of Internal Medicine, University of New Mexico School of Medicine*

Abstract: Metabolic syndrome (MetS) is a cluster of conditions including high blood pressure, high blood sugar, abdominal obesity, and abnormal cholesterol levels that increases an individual's risk to heart disease, stroke, diabetes, and non-alcoholic fatty liver disease. MetS affects about one-third of the US population and one-fourth of the world population. Currently, there are no medications to treat MetS, so identifying contributing etiological factors for future therapeutic targets is critical. The goal of this study was to determine the functional role of the gastrointestinal (GI) tract in MetS. Therefore, we examined the GI tract of healthy controls (C57BL/6J) to mice with MetS (MS Nash). MS Nash mice were obese, had more peritoneal fat, fatty livers, and longer colons. Further examination of the MS Nash colon revealed decreased Peroxisome proliferator-activated receptor gamma (*Pparg*) gene expression, a major gene that maintains intestinal homeostasis through fatty acid oxidation (FAO), maintenance of the microbiota and dampening of inflammatory pathways. Metabolomic analysis of colonic samples revealed significant differences in concentrations of metabolites allantoin and phosphorylcholine, which can be produced by bacterial species in the phylum *Firmicutes* and are upstream of PPARγ, to be decreased in MS Nash mice. Additionally, we found propionic acid, a short chain fatty acid and its precursor threonine, that are involved FAO also decreased in MS Nash mice. Overall, our results show factors (*e.g.* PPARγ, FAO metabolites) that are crucial for intestinal homeostasis are dysregulated in MetS mice suggesting a dysfunctional GI tract may be a contributing etiological factor in MetS.

Annotating Contig 49 in F Element of *Drosophila Takahashii*

Discipline: Life Sciences
Subdiscipline: Biology (general)

Austin Gomez* and Siaumin Fung, *Vanguard University of Southern California*

Abstract: Two different chromatin structures can be found in eukaryotic nucleus, euchromatin and heterochromatin. Euchromatin is DNA loosely packed by histones and transcribed actively, while heterochromatin is densely packed DNA, often associated with gene silencing. The 4th chromosome in *Drosophila*, also known as the F element is heterochromatic, yet 80 genes reside in this chromosome are actively being transcribe. The goal of this project is to use comparative genomic to elucidate the regulatory motif of gene silencing by annotating genes on the 4th chromosomes and genes on the euchromatin 3rd chromosomes (control). By using genome browser, two features on contig 49 were predicted to have orthologs to *D. melanogaster*, *unc13* and *eIF4G1.* FlyBase, and BLAST are used to align our predicted genes in contig 49 to the ortholog of *Drosophila melanogaster* to create a gene model for *unc13* and *eIF4G1*. Several lines of evidence, including conservation of amino acid sequence to *D. melanogaster*, RNA-Seq data and Top-Hat splice-junction predictor were used to produce the most parsimonious annotation of the coding sequence of *unc13* and *eIF4G1* in *Drosophila takahashii*.

Histone Modifying Mutants Implicate Epigenetic Regulation in the Toxic Effects of Developmental Ethanol Exposure.

Discipline: Life Sciences
Subdiscipline: Biology (general)

Esperanza Rosas*; Madeleine Mok; Tyra Furtado; Vishek Sharma and Rachael French, *San Jose State University*

Abstract: Organisms exposed to alcohol during development can display learning disabilities, neurodegeneration, insulin resistance, and a variety of other phenotypes. In humans, these phenotypes are collectively referred to as Fetal Alcohol Spectrum Disorder (FASD). The molecular mechanisms underlying FASD are not completely understood. Previously, we found that developmental ethanol exposure (DAE) in *Drosophila* leads to slower aging, downregulation of insulin signaling, and persistent changes in gene expression. We hypothesize that DAE causes changes in epigenetic regulation of transcription, leading to long-term alteration of gene expression. To test this hypothesis, we measured the ethanol sensitivity of flies mutant for the histone modifiers *SIRT1*, *dG9a*, *LID*, *JHDM2*, and *NO66,* and found that *SIRT1, LID,* and *NO66* mutant flies were sensitive to DAE, while *dG9a* and *JHDM2* mutants were resistant. The ethanol sensitivity of these mutant

histone modifiers was tested by performing survival assays. To further understand how DAE affects the expression of these epigenetic regulators, we performed qRT-PCR. We found that DAE led to reduced expression of *dG9a*, *SIRT1*, and *LID*. Finally, we found that mutating *SIRT* and *LID* lead to altered expression of *DMNT*, the insulin receptor (*INR*), and insulin-like peptide 2 (*ILP2*). These results support our hypothesis DAE causes changes in epigenetic regulation of transcription that lead to long-term alterations of gene expression. This research will ultimately increase our understanding of the mechanisms underlying FASD and will ultimately lead to better therapies and health outcomes.

A Genetic Screen for Histone Mutations That Alter Chromatin over Active-Genes

Discipline: Life Sciences
Subdiscipline: Biology (general)

Edgardo Linares* and Grant Hartzog, *University of California, Santa Cruz*

Abstract: Transcription is a key regulated step in gene expression. In plants, animals, and fungi, DNA is stored as a DNA-protein complex called chromatin. Our goal is to better understand the role of chromatin in transcription. Chromatin is made up of multiple DNA-binding proteins called nucleosomes. Nucleosomes are composed of a core of histone proteins with 146 base pairs of DNA wrapped around them. Previous work in our lab suggests that transcription elongation factor spt5 helps RNA polymerase transcribe past nucleosomes. While working with a cold-senstive spt5 mutation that slows the rate and efficiency of elongation, we found that histone mutations could overcome the growth defects caused by this spt5 mutation. Our working model is that these histone mutations disrupt chromatin structure, allowing RNA polymerase to move along DNA assisting in spt5 elongation function. This model predicts that any mutation that disrupts chromatin will suppress our spt5 mutation. We tested this prediction by screening for histone H3 and H4 mutations that alter chromatin formation in *S. cerevisiae*, which were then tested for their ability to suppress spt5. Of our 11 histone H3 and H4 mutations, none strongly suppressed the spt5 cold-sensitive mutation. Furthermore, three mutants, 2 H4 mutations and 1 H3 showed synthetic lethality when paired with the spt5 mutation. This suggests both genes independently or dependently assist in the same essential process within the cell. Our research provides data refuting the simple model that the spt5 mutation is suppressed by chromatin disruption.

Geometric Morphometric Analysis of Foot Pad Shape of Salt Marsh Harvest Mice and Co-Occurring Rodents in the Suisun Marsh, California

Discipline: Life Sciences
Subdiscipline: Biology (general)

Dulce Robles Martinez* and Diego Sustaita, *California State University San Marcos*

Abstract: Differences in the foot morphology among rodents with differing locomotion strategies have been described in the order Rodentia. In this study we used geometric morphometric analysis to compare the foot pad configurations from digital images of the palmar and plantar surfaces of salt marsh harvest mice (SMHM) and co-occurring rodents in Suisun Marsh, California. We hypothesized that the SMHM would exhibit shorter and wider configurations of palmar and plantar pads when compared to co-occurring rodent species, because this configuration allows greater contact surface for frictional support for climbing on vertical substrates, which the SMHM uses to escape tidal inundation in its wetland habitat. Our preliminary data analyses indicated significant differences in plantar pad shapes between SMHM and California voles. However, contrary to our expectations, SMHM plantar pads were relatively narrow and elongated, whereas vole plantar pads were relatively wider and shorter. There were significant differences in palmar pad shapes among SMHM, California voles, and house mice (after accounting for size differences), such that SMHM tended to have relatively narrow shapes, whereas voles and house mice tended to have wider shapes. These results suggest that selection on foot pad morphology may differ between the fore and the hind limbs. It should be noted that sample size overall was small (n=20), and increasing sample size would further inform these conclusions.

Prevalence of Rs149483638 SNP on the IGF2 Gene and Its Correlation with Type 2 Diabetes in Hispanic Populations.

Discipline: Life Sciences
Subdiscipline: Biology (general)

Sandra Camacho*; Kevin Banco Hernandez; Alondra Maiz Zapata and Itzel Calleja, *Vanguard University of Southern California*

Abstract: Overall, American adults have a 10.5% risk of having diabetes during their lifetime but for the Hispanic American adult, the risk is over 12.5% compared to 7.5% in non-Hispanic whites. Hispanic Americans are a mixed group comprising of Mexicans, Cubans, Puerto Ricans, South and Central Americans, and other Spanish communities. This disease is very damaging and a challenge to manage for anyone. It is the seventh-largest cause of death in the United States in 2017. Detecting single nucleotide polymorphism (SNPs), in the human genome can help in determining an individual's risk of obtaining type 2 diabetes. Recent studies with SNP rs149483638 have shown that the *IGF2* gene is associated with the identification of insulin that regulates growth and metabolism in the human body. IGF2 is found in many tissues where it is synthesized and released into the periphery, with the highest levels in the liver. IGF2 facilitates ß-cell proliferation and survival in the pancreas. The alleles shown in this SNP is the C>T allele change. The goal of this research is to detect the

prevalence of SNP rs149483638 by buccal swab samples in 50 controls and 50 patients. DNA extraction followed by PCR and restriction fragment length pattern using *BstN1* enzyme will be used to detect the prevalence of this SNP and its association with Diabetes. With these results we attempt to use this SNP to detect the risk of having type 2 diabetes as a preventative method to those individuals with the higher risk.

Detection of rs1225537 SNP in the Hispanic Population of Southern California with Type II Diabetes

Discipline: Life Sciences
Subdiscipline: Biology (general)

Kevin Banco Hernandez*; Alondra Maiz Zapata; Sandra Camacho and Itzel Calleja-Macias, *Vanguard University of Southern California*

Abstract: It is estimated that about 34.2 million Americans have diabetes in 2018. Out of those 34.2 million Americans with diabetes, 7.3 million are undiagnosed, leading to greater health complications when combined with other factors. Race influences the possibility of being diagnosed with type II diabetes with Hispanics containing the highest rate of 12.5%. In Hispanics, it is the fifth leading cause of death among Hispanics in the United States due to the genetic influence. Through this, scientists study the DNA to locate and study the specific DNA sequences called single nucleotide polymorphisms, SNP, associated with type II diabetes. The SNP, rs12255372, in recent studies has been associated with type II diabetes, breast cancer, and prostate cancer. The allele involve in the risk of Diabetes is T. The purpose of the research is to investigate the prevalence of the rs12255372 SNP in Hispanics from southern California. After DNA extraction of collected buccal samples, the samples were run through a polymerase chain reaction (PCR) and confirmed by gel electrophoresis. After the amplification, the products will be digested with the restriction enzyme *MluCl*. These results will contribute to the knowledge of the prevalence of this SNP in the Hispanic population and its future medical implications.

Effects of Dimer Interface Mutants on Heat Shock Response

Discipline: Life Sciences
Subdiscipline: Biology (general)

Jade Takakuwa*; Nitika Nitika and Andrew Truman, *University of North Carolina at Charlotte*

Abstract: Heat Shock Protein 70 (Hsp70) is an evolutionarily well-conserved molecular chaperone that is critical in all organisms. Hsp70 is involved in several cellular processes such as protein folding, modulating protein-protein interactions and transport of proteins across membranes. Recent cross-linking mass spectrometry studies from our lab have shown that yeast Hsp70 (Ssa1) forms a homodimer, but the conditions under which the dimer is formed remains unknown. This study aims to determine the biological role of Hsp70 dimerization and understand the regulation of dimer formation in cells. To better understand the role of dimerization, we introduced mutations that are known to interfere with the dimer interface of Ssa1. We tested various stressors such as UV exposure, caffeine, heat shock and DNA damaging agents such as hydroxyurea and found that the dimer interface mutants exhibited phenotypical effect under high temperature. In order to accurately follow the transcriptional pathway of the heat shock response, we utilized a destabilized reporter system and found that the dimer interface mutant was defective under heat shock. Going forward we will determine the mechanisms behind temperature-dependent dimerization of Hsp70 by microscopy and further proteomics studies. Further research into the function of dimerization in heat shock response could reveal important insights into the interaction of Hsp70 with its co-chaperones and its effect on other transcriptional factors.

Investigating the Regenerative Capacity of iPSC-Derived Neurons from CAST/Eij and C57JBL/6 Mouse Strains

Discipline: Life Sciences
Subdiscipline: Biology (general)

Duane Nguyen*[1]; James Dutton[2] and Randy Daughters[1], *(1)Macalester College, (2)University of Minnesota - Twin Cities*

Abstract: Neurodegenerative diseases and central nervous system injuries have prompted extensive research in the regenerative medicine field to better understand the mechanisms and barriers to neuronal regeneration. One wild caught, inbred mouse strain, CAST/EiJ, has been shown to exhibit enhanced neuronal regeneration capacity when compared to standard laboratory stains. To begin to investigate differences in neuronal regeneration in these two mouse strains, induced pluripotent stem cells (miPSCs) derived from C57JBL/6 and CAST/EiJ, were differentiated into motor neurons (MNs) to enable assessment of neuronal regeneration after axonal injury. Through the processes of immunohistochemistry and immunofluorescent staining, we were able to identify successful neuron differentiation, along with successful motor neuron specification. Preliminary scratch assays were performed to attempt to assess neuronal regeneration and continues to be optimized.

The ultimate goal of this research is to enable a comparative test of axonal regeneration capacity between miPSC derived neurons from the two strains in support of a larger project that will use global gene expression analysis to uncover the genetic basis of differences observed.

Investigating the Correlation between Autoantibody Presence and Collagen Deposition in Lungs of Amphibole Asbestos-Exposed Mice

Discipline: Life Sciences
Subdiscipline: Biology (general)

Joselynn Castillo*; Kinta Serve and Reagan Badger, *Idaho State University*

Abstract: Asbestos are naturally occurring fibers found in rock outcroppings but also used in many commercial processes; therefore, exposures are both environmental and occupational. When inhaled, amphibole asbestos can lead to various health issues, such as cancers, autoimmune diseases, and pleural fibrosis (excess collagen deposition). Previous research in our lab has shown that anti-mesothelial cell autoantibodies (MCAAs) are produced following amphibole asbestos exposure and may be the driving force of collagen formation during fibrosis. In the present work, we are confirming the functional relationship between the presence of autoantibodies and presence of collagen deposition. We are using multiphoton microscopy to image lung samples from mice that have been exposed to different forms of amphibole asbestos (Libby amphibole or Arizona amphibole) and have shown MCAA production. We hypothesize that mice with MCAA will show higher collagen levels in their lungs. This research will allow for a better understanding of the role MCAA has in fibrosis development. This information could lead to fibrosis treatment strategies aimed at blocking MCAA function.

Characterization and Validation of Novel Transcript Isoforms Associated with U2AF1 S34F Mutations in Lung Adenocarcinoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

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Abstract: Characterization and validation of novel U2AF1 S34F -associated isoforms will provide a better understanding of the functional role of spliceosomal mutations in lung adenocarcinomas. U2AF1 S34F is one of the most recurrent splicing factor mutation in lung adenocarcinoma, which affects the binding affinity of the splicing factor to pre-mRNA, causing RNA processing alterations. Compared to its wild-type counterpart, U2AF1 S34F has been found to bind and modulate splicing introns containing CAG trinucleotides at their 3' splice junctions, causing a shift in cross-linking at 3' splice sites which is significantly associated with alternative splicing of skipped exons. However, the characteristics and functions of U2AF1 S34F -associated full-length isoforms in these genes are unknown due to the limitations of short-read data. We have used long-read nanopore cDNA sequencing to identify transcript isoforms associated with U2AF1 S34F in UPP1 , BUB3 , and TPD52L1 genes; however, given low sequencing depth, it is important to validate the results using independent methods. Here we characterize and validate U2AF1 S34F- associated transcript isoforms using RT-PCR followed by TapesStation analysis. We show that isoform usage frequencies for wild-type and U2AF1 S34F using nanopore sequencing quantification is consistent with RT-PCR followed by TapeStation quantification of isoform changes. These results will add significant insights into the understanding of the functional outcomes of U2AF1 S34F in lung adenocarcinoma and the capabilities of long-read sequencing for full-length transcript analysis.

Low Levels of Nuclear YAP Staining Is Associated with Better Overall Survival in Patients with Synovial Sarcoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Nhi Le*, *University of Houston Downtown* and Andrew Futreal, *The University of Texas MD Anderson Cancer Center*

Abstract: Synovial Sarcoma (SS) is the fourth most common type of sarcoma. Despite its rare occurrence at a 1 to 3 per million risk, 800 new cases of SS are diagnosed across the United States every year (Siegel 2007). SS is driven by the translocation of the SYT gene on chromosome 18. The yes-associated protein (YAP) is a transcriptional regulator protein that activates the transcription of genes corresponding to cell growth and suppressing apoptotic genes, its transcriptional activation can be indicated by the nuclear localization of YAP (Fullenkamp, 2016). YAP transcriptional activity was also significantly reduced after the RNAi-mediated knockdown of SS18-SSX (Fullenkamp, 2016). YAP is considered as important transcriptional regulators for cell proliferation and signal transduction in SS tumorigenesis, nuclear staining of SS tumor tissue reveals that. Since the SS18-SSX mutation correlated with SS has a direct relation with YAP activity, we hypothesize that the patient's outlook (from clinical data through various attributes such as overall survival chance and tumor subtype) and other factors (age, gender, tumor size, and types) has an inverse relation with YAP activity obtained from nuclear staining. In total, 203 samples were taken from the Department of Pathology at MD Anderson Cancer Center, in the United States. Data analysis shows that YAP activity has an inverse relation with the survival outcome of SS patients. More research should be done to improve the prediction process and treatment plan for the survival outlook of SS patients based on the YAP nuclear activity obtained.

Prospective Co-Regulatory Roles for Eif5a1/2 and Slc3a2 during Breast Cancer Progression

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Joanna Maddela*, *California State University, Northridge*; Cameron Geller, *California State Univ Northridge* and Jonathan Kelber, *California State University Northridge, Department of Biology*

Abstract: Metastatic triple-negative breast cancer has a median survival of only 10 months primarily due to a lack of targeted therapeutic options for patients. We recently demonstrated that small molecule inhibition of deoxyhypusine synthase (DHPS)-mediated eIF5A1/2 hypusination inhibits PEAK1 translation, cell viability and PEAK1-mediated TGFβ/fibronectin-driven metastasis. Given the role that intratumoral heterogeneity plays in the progression of solid tumors, we analyzed biochemical/functional connectivities between eIF5A1/2 pathway components and a literature-curated list of heterogeneity markers in relation to breast cancer patient prognosis. Interestingly, patients harboring genomic amplification of SMAD3 loci and elevated SLC3A2 mRNA expression had a greater than 3-fold decrease in survival time. Given that SLC3A2 protein expression has been previously reported to depend upon eIF5A1/2 expression, we hypothesize that SLC3A2 and eIF5A1/2 cooperatively promote tumorigenesis in triple-negative breast cancer. Here, we present data on SLC3A2 expression across different breast cancer cell lines and evidence that SLC3A2 levels can be downregulated by treating human breast cancer cells with a commercially available monoclonal SLC3A2-targeting antibody. Ongoing work aims to quantify the effect of SLC3A2 immunoneutralization on triple-negative breast cancer cell migration; TGFβ/fibronectin-driven metastasis; and eIF5A1/2 expression, hypusination and subcellular localization. This work has the potential to identify efficacious combinatorial targeted approaches to inhibit triple-negative breast cancer progression.

CD6 As a Target in the Treatment of Autoimmune Diseases and Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Peggy Randon*; David Fox; Jeffrey Ruth; Phillip Campbell and Mikel Gurrea Rubio, *University of Michigan, Ann Arbor*

Abstract:

One in eight women in the United States will develop breast cancer, with more than 42,000 fatalities expected in 2020. Immunotherapy is a promising treatment; however, current therapies engender autoimmune toxicities. This presentation reports efforts to develop novel cancer immunotherapy, which unlike currently-available checkpoint inhibitors, also suppresses autoimmunity by targeting the CD6-CD318 axis. CD318 is a cell-surface glycoprotein that correlates with cancer aggressiveness and metastatic potential. CD6 is a transmembrane glycoprotein expressed on the surface of most T cells, including natural killer (NK) cells, the body's key defense to immunological stimuli. We discovered that CD318 is a ligand for CD6, forming an immune checkpoint pathway. When the CD6-CD318 checkpoint forms, it dampens the immune response to cancer. Previous studies show that interruption of this pathway with a monoclonal anti-CD6 antibody (UMCD6) reduces CD4+ effector T cell-driven autoimmune responses. Through *in vivo,* immune-mediated tumor-killing assays, we show that UMCD6 enhances NK cells cancer-cell killing ability with more efficacy than current inhibitors. CD6 on NK and CD8+ T cells were isolated and incubated with UMCD6 or an IgG control. UMCD6 resulted in increased apoptosis (****p=7.06x10-7) and reduced survival (****p=4.71x10-5) of breast cancer cells. NK and CD8+ T cells were also isolated and incubated with UMCD6 or currently marketed checkpoint inhibitors. UMCD6 enhanced NK killing more effectively than any PD-1 inhibitor (****p<0.0001). Our results further validate the potential for effective checkpoint-inhibitor antibody treatments without the induction of autoimmune diseases.

Tetraspanin CD82 Modulation of Quiescence in Acute Myeloid Leukemia

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Christian Doyle*, *University of New Mexico* and Jennifer Gillette, *University of New Mexico, Pathology*

Abstract: Acute Myeloid Leukemia (AML) is a blood malignancy characterized by the irregular growth of myeloid lineage progenitor cells. Five-year survival rates among AML patients is below 30% due to high levels of Minimal Residual Disease—a condition thought to be mediated by quiescent 'stem-like' AML cells within the bone marrow niche. Recently, our lab demonstrated that overexpression of the tetraspanin protein CD82 enhances AML cell chemoresistance in culture and reduces its proliferative capacity once in the bone marrow microenvironment. Interestingly, overexpression of a CD82 mutant that cannot be glycosylated due to three Arg-Glu mutations (CD82OE-NGLY mutant) exhibits restored proliferative capacity. Collectively, these studies suggest a further need to study mechanisms contributing to CD82-mediated quiescence of AML cells in the bone marrow niche. To address this, we first assessed cell proliferation by quantifying DNA content in cells differentially expressing CD82 in culture, finding no significant changes in proliferation. Contrastingly, when cultured with a fibronectin matrix monolayer, we find that CD82OE cells exhibit a significant decrease in cell proliferation, whereas CD82OE-NGLY mutant cells display increased proliferation when compared to controls. To investigate the role of bone marrow stromal cell interactions on AML cell proliferation, we are currently utilizing mouse OP9 embryonic stem cells to generate both 2-dimensional and 3-dimensional co-culture systems for AML cells. Together, our studies suggest that both overexpression and glycosylation of the CD82 protein scaffold are important modulators of AML cell proliferation and future studies will be focused on elucidating specific CD82-mediated signaling pathways responsible for promoting cellular quiescence.

Matcha Tea Mediates Cancer Cell Proliferation By Inhibiting Metabolic Pathways Necessary for Adenosine Triphosphate Production

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ann Marie Flusche* and Robert Sheaff, *University of Tulsa*

Abstract: Matcha green tea is recognized for its countless health benefits. There is also some evidence that Matcha reduces mitochondrial metabolism and glycolysis, maintaining cancer cells in a quiescent state. However, the underlying molecular mechanisms behind its proposed effects remain largely unknown. Our lab has discovered that metabolic pathways in tumor survival are inhibited when Matcha is present. Matcha targets cellular metabolism by inhibiting ATP production, leading us to hypothesize that Matcha's anti-cancer activity may be due in part to inhibition of glucose metabolism. Immortalized cancer cells are glucose addicted, utilizing aerobic glycolysis (Warburg effect) to produce sufficient ATP. To test our hypothesis, we cultured HEK–293 cells (which follow the Warburg effect) and varied the growth media composition to force use of metabolic pathways. We then incubated the cells with Matcha concentrations and measured ATP production using the CellTiter-Glo Cell Viability Assay. We observed a dose-dependent decrease in ATP production when glucose media and Matcha was introduced to the cells, but we saw no effect when the cells were treated with the galactose media and Matcha. Galactose enters glycolysis only after hexokinase phosphorylation, so we were able to determine whether Matcha's inhibition occurred within this step. In the future, we plan to identify the component within Matcha that is inhibiting hexokinase as well as test our work in tissue-specific cancer cell cultures. Our results suggest that Matcha is an inhibitor of ATP production in cancer cells by targeting glucose metabolism, which may be important to understanding the anti-cancer properties of Matcha.

Effect of Green Tea Catechins on the Growth of MDA-MB 468 Breast Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Arianna Mahadeo* and Lissette Delgado, *John Jay College of Criminal Justice*

Abstract: Breast cancer is the most commonly diagnosed cancer in women. Diet is considered an important factor in breast cancer prevention and studies suggest that green tea consumption has the potential to reduce breast cancer risk. Catechins, a group of polyphenols that are found in plants, have been shown to have anti-tumor effects . Many studies have investigated EGCG, but less is known about epicatechin. We investigated the inhibition of cell proliferation in the breast cancer cell lines, MDA-MB 468 after exposure to varying concentrations of EGCG and epicatechin. Changes in proliferation were determined using the MTT assay after exposing cells for 24 and 48 hours to concentrations of catechins ranging from 1µM to 500µM. We found that after 24-hr exposure, the cells significantly decreased in growth with a lower percent of cells remaining after exposure to 500µM EGCG. Percentage of cells was higher at 1µM when compared to 500µM . However, when the cells were exposed to epicatechin in that same time period, there was no significant difference. We found that as time increased from 24 to 48 hours, EGCG significantly inhibited the growth of cancer cells at 500µM . No effect was observed for epicatechin in growth as time increased. At an exposure of 500µM epicatechin, a higher percentage of cells were alive at 24 hours when compared to 48 hours but average values among experiments were not statistically significant. Our findings suggest that EGCG is a more potent inhibitor of triple negative breast cancer cell growth than epicatechin.

Transcriptional Effects of Estrogen in the Pathogenesis of Inflammatory Breast Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Madison Snyder*[1]; Xavier Bittman[2]; Carlos Morales[2]; Vanessa Viveros[2] and Esther A. Peterson[2], *(1)Swarthmore College, (2)University of Puerto Rico - Rio Piedras*

Abstract: Triple-Negative Inflammatory Breast Cancer (TN-IBC) is one of the rarest yet deadliest forms of breast cancer. Due to its negative hormonal receptor status, TN- IBC lacks effective targeted therapeutics, leading to poor patient outcomes (ACS 2020). However, alternative cytoplasmic and membrane localized estrogen receptors (ERs) including GPR30 and the splice isoform ERα36 have been identified in TN-IBC (Oshiro et al. 2012). Studies suggest that GPR30 and ERα36 are responsive to estradiol (E2) and enhance the migration and invasion of IBC cells through estrogen non-genomic signaling. At the RNA level, the molecular changes in expression due to estrogen remain poorly understood in TN-IBC expressing these alternative receptors. Our research aims to add to our understanding of TN- IBC by characterizing the transcriptomic profile of TN-IBC cells after treatment with estrogen receptor activator (E2) and GPR30 inhibitor (G15). We hypothesize that E2 and G15 treated cells will display differential expression of genes associated with cell motility. Through total RNA isolation and subsequent RNA sequencing analysis, we identified transcriptomic changes associated with oncogenic phenotypes in TN- IBC. Subsequent gene networks were generated using String, USC Genome Browser, and Cytoscape softwares to better define the molecular signature of TN- IBC. Preliminary results suggest an upregulation of genes related to cell motility and downregulation of tumor suppressor genes in E2 treated cells. These results will aid in identifying

targets related to expression of these alternative ERs. This approach can also be applied to other cancer models to provide meaningful insights into potential therapeutic targets.

Using CRISPR to Delete the CXCL10 Gene in B-Cell Lymphoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Nicholas Rotello Kuri*, *University of Colorado Denver* and Jing Wang, *University of Colorado Anschutz Medical Campus*

Abstract: Traditional chemotherapy plans require high doses and fail to solely target cancer cells, which lead to harmful effects on the body. To avoid these side effects, the use of low dose chemotherapeutic agents to induce an increased immune response could be an effective alternative treatment. Chemotherapeutic agents have been shown to increase chemokine production, resulting in a greater CD8 T-Cell migration to the cancer. This results in an improved survival curve against cancer. The CXCL10 gene is responsible for chemokine synthesis, which results in chemotaxis of CD8 T-Cells to the tumor site. However, CXCL10 has not yet been tested with chemotherapy. We hypothesize that the expression of CXCL10 increases with chemotherapy, resulting in an increase in T-cell migration and life span against B-cell lymphomas. In order to test CXCL10's response to chemotherapy, CRISPR-Cas9 technology was used with gRNA to delete CXCL10 in B-cell lymphoma cells. First, a plasmid was created with gRNA and the Cas9 protein. Then, E. coli was transformed for cloning of the plasmid. Cells were transfected with the plasmid DNA and deletion of CXCL10 was verified by PCR. Lastly, chemokine production and T-cell migration were compared between WT and KO cells using PCR and flow cytometry. CXCL10 combined with chemotherapy is expected to show an increase in chemokine production and T-cell migration compared to KO cells, but flow cytometry and PCR data are pending. The role of CXCL10 as a target of immunotherapy is plausible and future research should measure the change in survival rates.

Functional Characterization of Multiple Myeloma GWAS Risk Variants in African American Cell Lines Via Scarless CRISPR/Cas9 Genome Editing

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Marisol Contreras*; Nicole Coggins and Luis Carvajal Carmona, *University of California Davis*

Abstract: Multiple Myeloma (MM) is malignancy of the plasma cells that accounts for 20% of all hematological cancer deaths in the US. Currently, an important health disparity exists in African Americans (AA), who are twice more likely to be diagnosed with MM compared to individuals of White ancestry. MM risk is partly determined by genetic predisposition. Genome-Wide Association Studies (GWAS) have identified16 MM loci. Two of these, rs6877329 and rs4487645 demonstrated functionality in MM development via regulation of *ELL2* and *CDC7AL* expression, however, these functions are not confirmed in AAs. Our lab combines scarless CRISPR/Cas9 homology-directed repair genome editing and Kompetitive Allele Specific PCR (KASP) to generate isogenic cell lines that model single base variants. Applying this method to rs6877329 and rs4487645 in MM.1S and MM.1R cells, MM cell lines derived from the same AA patient, we will assess allele-specific modulation of gene expression as well as measure the effects of risk status on MM cell viability and proliferation. Our study represents one of the first to generate functional data in race-appropriate models for MM GWAS risk SNPs to date and is an important step towards understanding the genetic component of MM susceptibility for improving disparities for MM in the US.

Characterizing Structural Variants in RAD51B

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Hossam Zaki* and Simona Dalin, *Broad Institute of MIT and Harvard*

Abstract: DNA Double Strand Breaks (DSBs) are fairly common, occurring about 10 times per day per cell[1]. Fortunately, there are several DNA damage repair pathways to fix these breaks and maintain genomic integrity. However, alteration of these pathways can cause genomic instability, leading to apoptosis or malignant phenotypes. It was found that in the International Cancer Genome Consortium, structural variants (SVs) were more prevalent in RAD51B than other genes involved in DSB repair. Furthermore, tumors with any mutation in RAD51B had a higher SV burden than tumors without RAD51B mutations. RAD51B has not been well characterized so we set out to assess its role in genomic instability using the PCAWG dataset. In this project, we characterized the variants of RAD51B as well as SV burden and other features of genomic instability within each tumor. Using these features we built a machine learning model to determine which variants of RAD51B are associated with features of genomic instability. Further studies will assess the role of the RAD51B variants we found to be associated with genomic instability in DSB repair. Further understanding of these variants could lead to biomarkers of tumors likely to respond to agents targeting DNA damage repair.

[1] Chang, H. H. Y., Pannunzio, N. R., Adachi, N., & Lieber, M. R. (2017). Non-homologous DNA end joining and alternative pathways to double-strand break repair. *Nature Reviews Molecular Cell Biology*, *18*(8), 495–506. https://doi.org/10.1038/nrm.2017.48

The Role of PIEZO1 and Its Network in Driving GBM Aggressiveness

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Yasine Keddari*, *University of California, Merced* and Sara Piccirillo, *University of New Mexico*

Abstract: Glioblastoma (GBM) is the most fatal form of primary brain tumor in adults, with median survival time ranging from only 12 to 15 months. GBM's heterogeneous nature has made it difficult for researchers to find effective treatments that can prolong patient survival. The existence of multiple GBM subtypes (Mesenchymal, Classical, Neural and Proneural) highlights this heterogeneity; of the four subtypes, Mesenchymal tumors are said to have the worst prognosis. These subtypes manifest themselves as a result of specific driver gene alterations. A potential contributor to the severity of GBM is PIEZO1, a mechanosensor that increases tumor stiffness through a feedforward mechanism that is mediated by a network of genes that control key cellular processes, including Extracellular Matrix Remodeling. To determine whether there is a correlation between GBM subtype and expression of genes in the PIEZO1 network, we analyzed GBM patient gene-expression data that was available through The Cancer Genome Atlas Initiative portal. We grouped GBM patients with primary tumors and classified them based on GBM subtype. We then compared the relative expression levels of PIEZO1-related genes in each subtype, and performed statistical analysis using one-way ANOVA. Data was graphed and analyzed using GraphPad Prism 8.00. Our preliminary data suggests that the PIEZO1 network is significantly overexpressed in the Mesenchymal subtype. In particular, we observed that specific genes, such as SCNN1G, SCNN1A, PLOD1, PLAU, SCAMP2 and SCL4A7 are Mesenchymal-specific. This suggests that increased tumor stiffness contributes to worse prognoses in GBM patients, through promotion of the Mesenchymal subtype.

Effect of the Cio-Cmdx Nanoparticles in the Cytokine's Expression of Macrophages

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Shakira Crespo*, *University of Puerto Rico at Mayagüez* and Maribella Domenech, *University of Puerto Rico at Mayaguez*

Abstract: The use of magnetic nanoparticles as therapeutics has emerged as a complementary approach to enhance cell death and drug sensitivity in tumors. Monocytes and macrophages are part of the tumor microenvironment and can infiltrate the tumor tissue delivering cytokines as well as nanoparticles sequestered from peritoneal a bloodstreams fluid. The transport of nanoparticles in macrophages can enhance their cytotoxic effects by increasing the local tissue dosage and/or modulating macrophage secretory profile. The impact of nanoparticles in the phenotype and secretory profile of monocytes and macrophages is unknown but is important to understand nanoparticle therapy efficacy. This project examines the effect of cIO-CMDX nanoparticle concentration on the viability, phenotype, and cytokine profile of THP-1 human monocytes. The nanoparticles are composed of iron oxide (IO) and coated with carboxymethyldextran (CMDx). Monocytes and macrophages polarized to M1 and M2 phenotype were treated with nanoparticles at a concentration of 0.1 and 0.6 mg/ml for 2 hours. Cell viability and secretory profile of 27 human cytokines were examined at 48 hours post-treatment. The cell viability for M1 and M2 were not affected by cIO-CMDx and maintained above 50-70%. The expression of IL-12, IL-7, and IP-10 were different in M1 and M2 treated with nanoparticles. In M2 cells, the expression of IL-12, IL-7, and IP-10 had six-, four- and two-fold change increase respectively. M1 phenotype expression of IL-12 and IL-7 had two- and four-fold change increase, while IP-10 expression reduced 80% compared to control. Concluding that nanoparticles can modulate cytokine expression profiles of macrophages.

UHRF1 Downregulation By Palbociclib Decreases Invasion in Osteosarcoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Kelsey N. Salcido* and Claudia A. Benavente, *University of California, Irvine*

Abstract: Osteosarcoma, the most common bone cancer, has seen little therapeutic advances in the last 30 years. Mutations at the *RB1* gene are associated with increased mortality, metastasis, and poor chemotherapy response. However, the precise mechanism(s) through which this occurs is unknown. Our lab identified the epigenetic regulator ubiquitin-like with RING finger domain 1 (UHRF1) as a protein overexpressed in osteosarcoma and transcriptionally repressed by RB. We hypothesized that UHRF1 overexpression contributes to osteosarcoma tumor progression. Using CRISPR-Cas9 gene editing, UHRF1 knock-out (KO) cells were generated and through proliferation and migration assays, we observed decreased proliferation and migration in UHRF1 KO osteosarcoma cell lines compared to non-targeting controls. Thus, we found that UHRF1 overexpression in human osteosarcoma cell lines positively regulates proliferation and migration. Interestingly, studies have shown that palbociclib, a CDK4/6 inhibitor currently in clinical trials as second line treatment for advanced sarcomas with CDK4 overexpression, decreases proliferation and migration in osteosarcoma cells. However, the mechanism of action by which palbociclib decreases migration remains unknown. We postulated that palbociclib decreases migration in osteosarcoma cells by decreasing levels of UHRF1. Thus, we treated SJSA-1 cells (CDK4-amplified) UHRF1-KO and controls cells with palbociclib. Our results showed a decrease in the UHRF1 protein expression that correlated with the decrease in migration following treatment with palbociclib in control SJSA-1 osteosarcomas.

Removal of UHRF1 in SJSA-1 UHRF1-KO rendered the cells insensitive to the effect of palbociclib. This allows us to preliminarily conclude that palbociclib decreases migration in osteosarcoma cells through the decrease of UHRF1 levels.

The ER Stress Factor XBP1s Modifies Tdp-43 Toxicity in Drosophila Model

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Joshua Lopez-Scarim*; Lorena De Mena; Deepak Chhangani and Diego Rincon-Limas, *University of Florida*

Abstract: Abnormal distribution, modification, and aggregation of TAR DNA-binding protein 43 (TDP-43) are the hallmarks of multiple neurodegenerative disorders, including amyotrophic lateral sclerosis (ALS). While mechanisms associated with TDP-43 pathogenesis are poorly understood, recent evidence suggests that endoplasmic reticulum (ER) stress contributes to TDP-43 toxicity. For instance, in transgenic rat neurons, a mutant version of TDP-43 (TDP-43^{M337V}) induces nuclear depletion of transcription factor X-box Binding Protein 1 spliced (XBP1s). This factor is a key member of the IRE1-mediated unfolded protein response (UPR), which mediates refolding and degradation of misfolded proteins. Therefore, we investigated the protective role of XBP1s in transgenic flies expressing human WT and mutant TDP-43 proteins. First, we demonstrated that overexpression of XBP1s suppresses TDP-43 toxicity in the fly eye. In contrast, knock-down of endogenous XBP1 transcripts in the adult eye enhances TDP-43 toxicity in both TDP-43^{WT} and TDP-43^{M337V}. To understand the mechanisms behind our observed rescue, we found that XBP1s overexpression does not affect the total levels of TDP-43 protein. Further experimentation to evaluate how XBP1s affects TDP-43 distribution and/or aggregation may hold key to understand its neuroprotective properties. Lastly, we observed that, at early age, TDP-43 failed to activate ER stress response in our models. We believe that our preliminary results contribute to a better understanding of the mechanisms underlying TDP-43 proteinopathies and underscore the potential therapeutic activity of XBP1s against TDP-43 insults.

Science Communication and RNA Interference in the Model Eukaryote *Tetrahymena Thermophila*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Maya Matsumoto* and Suzanne Lee, *Western Washington University*

Abstract: RNA interference (RNAi) pathways function in many eukaryotes as a defense mechanism against viruses and to repress gene expression through small (s)RNA-guided actions. An RNAi pathway in *Tetrahymena thermophila* produces ~23-24 nucleotide (nt) sRNAs, but its biological function remains unclear. *T. thermophila* is an interesting model organism in which to investigate this pathway, RNAi, as it evolved from an early branching lineage of eukaryotes and therefore has the potential to reveal broadly conserved mechanisms and lineage-specific diversification.

Our research is uncovering evidence of a role for the ~23-24 nt sRNA pathway in genome maintenance and integrity, as sRNA biogenesis knockouts and a large proportion of knockout cells exhibited enlarged extranuclear DNA bodies ("chromatin extrusion bodies") and elevated protein markers of DNA damage. This presentation will report on efforts to communicate the research being carried out on this pathway through the construction of a website and production of visuals. My goal is to create visual molecular models based on our research findings and to use such visuals on our website and in publications to strengthen our ability to communicate and generate new hypotheses and findings related to the ~23-24 nt sRNA pathway.

TMEM163 (ZNT11) Protein Interacts with Distinct Znt Efflux Transporters

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Adrian Escobar*; Saima Ali and Math Cuajungco, *California State University, Fullerton*

Abstract: Our recent work showed that TMEM163 is a zinc efflux transporter that belongs to the cation diffusion facilitator (CDF) family of proteins. We propose that TMEM163 be now called ZNT11 as a new member of the Group 1 CDF family of 10 known mammalian ZNT proteins, ZNT1-ZNT10. Accordingly, we hypothesize that TMEM163/ZNT11 interacts with at least one of the ZNT proteins based on its structural and functional characteristics. We cloned cDNAs of ZNT1 and ZNT2 into mammalian expression constructs containing either Myc-DDK or HA peptide tag. Using HEK-293T cells, we used co-immunoprecipitation of either anti-HA- or anti-DDK-bound agarose beads to pull down one of the target proteins. Western blot analysis showed that TMEM163/ZNT11 physically bound ZNT1 or ZNT2 protein. To determine the functional relevance of the interaction, we performed spectrofluorometric zinc flux assays of transfected HeLa cells using two zinc-specific fluorescence dyes, Fluozin-3 (high affinity, membrane impermeable) and Newport Green (low affinity, membrane permeable). Our results confirmed that homodimers of each TMEM163/ZNT11, ZNT1 or ZNT2 protein transport zinc out of the cells, but the efflux activity of homodimer TMEM163/ZNT11 proteins varied slightly in magnitude in comparison to its heterodimer with ZNT1 or ZNT2. Overall, our investigations showed for the first time that TMEM163/ZNT11 forms functional heterodimers with ZNT1 and ZNT2 proteins. Thus, TMEM163/ZNT11 by itself, or in combination with one of these specific ZNT proteins, may play a crucial role in maintaining intracellular zinc homeostasis in specific cell types. This work is funded by NIH 2R15 NS101594.

Ksrp-Encoded Mir-3940-5p Inhibits Rictor Expression and NDRG1 Phosphorylation in Glioblastoma Cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Brittney Love[*], *University of New Mexico* and Amy Gardiner, *University of New Mexico School of Medicine*

Abstract: Glioblastoma multiforme (GBM) is the most aggressive and lethal of brain tumors. Despite treatments, which include surgery, radiotherapy, and temozolomide (TMZ), median patient survival is just 15 months. Most patients experience tumor recurrence, underscoring the importance of understanding mechanisms that promote tumor survival. To shed light on this issue, I am investigating novel molecules and pathways that regulate cell survival such as the recently discovered microRNA, miR-3940, which has tumor suppressive activity in cancer. miR-3940 is processed from an intron of KSRP, an RNA-binding protein whose expression is significantly associated with GBM patient survival. miR-3940 expression is tightly correlated with KSRP, and like KSRP, miR-3940 may have an important role in GBM. Using bioinformatic analyses, we identified Rictor, a kinase that regulates cell growth and is a component of the mTORC2 signaling complex, as a novel target of miR-3940. Rictor suppression was previously shown to increase sensitivity to TMZ, and its downstream target NDRG1 was shown to confer resistance to TMZ. We hypothesized that miR-3940 regulates Rictor expression and its downstream targets in GBM. Using established GBM cell lines, we found that Rictor mRNA and protein levels were significantly decreased following miR-3940 overexpression and significantly increased following its inhibition. Dual luciferase assays established Rictor as a direct regulatory target of miR-3940. Finally, we demonstrated that phosphorylated NDRG1 was significantly decreased following miR-3940 overexpression and significantly increased following its inhibition. Our data suggest that promoting miR-3940 expression, thereby constraining its targets, may sensitize tumors to TMZ and enhance GBM patient survival.

Culturing and Characterizing Oligotrophic Subsurface Marine Microorganisms Sorted By Flow Cytometry

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Erica Duncan[*1]; Megan Mullis[2] and Brandi Reese[1], *(1)Texas A&M University, Corpus Christi, (2)Texas A&M University Corpus Christi*

Abstract: Microbial communities have a major impact on the world's biogeochemical cycles. Studying these communities could advance the knowledge necessary in understanding the energy producing and consuming cycles involved in an environment. High-throughput methods focus on rapidly getting data on isolates, but previously relied on dilution methodology that is not only time consuming but could still allow the bias of stronger competitors or cells found in a larger quantity over potentially novel microbe. We plan to sort cells in a way that minimizes the competition between them and explore the individual needs of single cells that originated from the same collection site. By using fluorescent activated cell sorting (FACS) we can differentiate live cells from dead ones and aliquot them in any desired quantity. Sediment samples from varying depths were collected on a research cruise in the oligotrophic Western Flank of the Mid-Atlantic Ridge. Previous data show that this area has a high affinity for nitrogen-based metabolisms with metagenomic data revealing nitrate reduction and nitrate oxidizing genes. The sediment samples ranged in depths of range from 0-2 cm, 2-4 cm, 4-6 cm, and 8-10 cm and were processed through flow cytometry using FACS into 96-well plates in quantities of 5 cells and the last two wells holding 20 cells. The depths are all tested in three different media types. When absorbances are found to be steadily increasing and approaching a stationary phase, we will sequence the isolates genome and begin to characterize the ecophysiology such as salinity, pH, and temperature.

Characterizing the Molecular Defects Associated with *Arabidopsis thaliana* LON2 Mutations

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Stefanie King[*]; DurreShahwar Muhammad and Bonnie Bartel, *Rice University*

Abstract: Peroxisomes house several crucial metabolic reactions, including fatty acid beta-oxidation, that produce reactive oxygen species that must be sequestered to prevent cellular damage. Dysfunction of peroxisomes in humans can lead to severe metabolic disorders, but current knowledge of fundamental peroxisomal processes is insufficient and calls for more research. LON2 is a peroxisomal chaperone and protease protein that, through a not yet fully elucidated mechanism, prevents excessive peroxisomal degradation via pexophagy. LON2 contains three domains: the N-terminus, the AAA ATPase domain, and the protease domain, whose functions in the model plant *Arabidopsis thaliana* remain largely uncharacterized. To determine the functional dynamics of the domains, I am comparing a series of *lon2* lines containing various missense mutations or a truncation in the N-terminus. I present progress toward characterizing these mutants using analysis of protein levels and molecular defects. Preliminary data show protein levels of LON2 and other key peroxisomal proteins, including green fluorescent protein localized to peroxisomes, are altered in the mutant lines. Together these data support the hypothesis that LON2 mediates pexophagy. Further analysis is needed to determine if this mediation is dependent on LON2 levels or the function of particular LON2 domains.

Co-Occurence of Pathogenic and Avirulent Agrobacteria within Individual Plants

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Veronica Mateo*; Priscila Guzman and Thomas Platt, *Kansas State University*

Abstract: Plants are complex systems that house diverse microbial communities. These communities are important, in part, because they affect plant health. We aim to identify how often sunflower, *Helianthus annuus*, microbiomes harbor the plant pathogen *Agrobacterium tumefaciens* as well as avirulent agrobacteria. We hypothesize that avirulent and pathogenic agrobacteria will often co-occur such that competition is a common feature of this organism's ecology. *A. tumefaciens* infection involves genetic transformation of plant cells via the transfer of a small fragment of DNA located in the bacteria's tumor inducing (Ti) plasmid into the host genome. The expression of the virulence factors required for this is regulated by the VirA-VirG two component system in response to phenolic cues produced by plants. Following transformation, the plant's physiology changes to benefit the bacterial pathogen. The plant cells will divide rapidly, leading to the formation of tumors associated with crown gall disease. Transformed plant cells also produce metabolites that pathogenic strain can catabolize. We sampled 20 sunflower root samples, including three with visible root galls, from different locations within the Konza Prairie. We preserved 360 isolates from these plants so that we can characterize the phenotypic and genetic attributes of the agrobacteria present. We are using a P_{virB}::*lacZ* reporter system introduced to a random sample of isolates to evaluate how many of them are able to induce expression of this promotor, consistent with the presence of a VirA-VirG two component system. I will also evaluate the ability of these isolates to induce tumor formation on potato tissues.

Morphology and Localization of Vacuoles in *Schizosaccharomyces Pombe* under Glucose Deficient Conditions

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Maura De Jesus* and Mark Chan, *San Francisco State University*

Abstract: *Schizosaccharomyces Pombe,* commonly known as fission yeast*,* is an important organism in studying the cellular responses to DNA damage and the process of DNA replication.Organelles are key compartments found in all eukaryotic cells and are essential for all cells. Vacuoles are organelles that degrade and store proteins in the cell. With many parallels found in mammalian lysosomes it is critical to know how vacuoles move with respect to its stage in the cell cycle. The study of size and localization of vacuoles as they proceed through medial fission in glucose deficient conditions will aid clarity to a better understanding of the cell cycle and cellular stress responses. Vacuole morphology can change depending on stimuli or stresses, such as fusion under hypotonic conditions and fission under hypertonic conditions.FM4-64 is a Lipophilic dye that enters vacuoles via the endocytotic pathway and fluoresces red. It is used as a marker in a wild type strain SP-175 for visualization of the vacuole. With the use of spinning disk confocal microscopy time series data sets are collected to further analyze using ImageJ. With further analysis I expect to find an enlargement of vacuole size and localization of vacuoles clustered at the cell tips as it undergoes cell division. My results may have implications in studies related to several lysosomal storage disorders such as Gaucher disease, Tay Sachs disease. Overall, through experimentation it is expected to find that glucose starvation of *Schizosaccharomyces Pombe* may lead to fusion and clustering of the vacuoles as a stress response.

Assessing the Sufficiency of the Hydrophobic Domain of Env9 for Lipid Droplet Localization in Saccharomyces Cerevisiae

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Sergio Platero* and Editte Gharakhanian, *California State University, Long Beach*

Abstract: Lipid droplets (LDs) are cellular organelles consisting of a hydrophobic core surrounded by a phospholipid monolayer where several proteins, including metabolic enzymes, are localized. LDs are involved in lipid storage and metabolism functions, and have been implicated in several physiological disorders including metabolic diseases such as diabetes. However, much remains unknown regarding targeting of resident proteins to LDs and whether it is mediated by a targeting sequence . Our laboratory uncovered the S. cerevisiae ENV9 gene as a homolog to human RDH12 and has mapped the localization of its product, Env9, to LD's; we have also established Env9 as an oxidoreductase involved in regulation of LD biogenesis. We hypothesize that the hydrophobic domain (HD) of Env9, which is necessary for its localization to LD's, is also sufficient for directing a heterologous protein to LD's, and hence, contains a targeting signal to LD. To test our hypothesis, we will microscopically assess the localization of endoplasmic reticulum (ER) protein, Env10, upon addition of Env9 HD. We are currently generating the plasmid construct that will be expressing Env10-HD-GFP fusion protein by utilization of homologous recombination directly in yeast. The construct will be confirmed via DNA sequencing. Using Nile Red as an LD marker stain, localization of the GFP-tagged Env10 protein will be assessed in live cells via confocal fluorescent microscopy and will be compared to localization of wild type Env10 as well as WT Env9.

Regulation of MLK3 Under Heat Stress Conditions in Ovarian Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

David Honda*; Luis Cedeno-Rosario and Deborah Chadee, *The University of Toledo*

Abstract: Cancer can result from the deregulation of key proteins involved in cell proliferation. An example of one of those proteins is the Mixed-lineage Kinase 3 (MLK3) protein, a mitogen-activated protein kinase kinase kinase (MAP3K) that is required for ovarian cancer cell proliferation. When ovarian cancer cells are subjected to heat stress for an extended period of time, MLK3 protein is degraded and cell proliferation is inhibited. However, the mechanism(s) that control MLK3 protein levels under heat stress conditions are not well defined. Cyclin dependent kinases (CDK) are critical regulators of cell cycle progression, and we hypothesized that CDKs may modulate MLK3 protein levels in heat stress conditions. To test this, ovarian cancer cells were exposed to heat stress at 42°C and treated with CDK1 and CDK2 inhibitors over the course of 8 h, and MLK3 protein levels were analyzed by western blotting. Our results showed that in ovarian cancer cells exposed to heat stress, MLK3 was rapidly degraded between 2-4 h, and cell cycle progression was inhibited. Treatment of cells with the CDK1 inhibitor, RO-3306, did not affect the heat stress-induced MLK3 degradation; however, treatment of cells with the CDK2 inhibitor, SNS-032, blocked heat stress-induced MLK3 degradation. Therefore, under conditions of heat stress, CDK2 promotes a decline in MLK3 protein levels which correlates with inhibition of ovarian cancer cell cycle progression. In conclusion, further characterization of this mechanism will give us insights into ovarian cancer cell proliferation and in the development of ovarian cancer treatments.

The Nuclear Zn Transporter ZIP11 Is Necessary for the Proliferation of HeLa Cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Julia Kan*, *Wesleyan University* and Teresita Padilla-Benavides, *Wesleyan Univeristy*

Abstract: Zinc (Zn) is an essential trace element as part of several biological processes, including transcriptional regulation, signaling, and catalysis. A subcellular network of Zn transporters ensures the adequate distribution of Zn to maintain homeostasis. Among these, the family of importers Zrt/Irt-like protein (ZIP) constitutes 14 members (ZIP1-ZIP14) that mobilize Zn into the cytosol. Expression of these transporters varies among tissues and during developmental stages. The presence of ZIP transporters at various cellular locations is essential for defining the net cellular transport of Zn. Normally, the ion is bound to proteins or sequestered in organelles and vesicles.

Research has focused on Zn internalization in mammalian cells. However, little is known regarding Zn mobilization within the cells and the organelles, including the nucleus. ZIP11 is the only ZIP transporter localized in the nucleus of mammalian cells. However, the cellular role and the mechanism and direction of transport of ZIP11 are not defined. We hypothesized that ZIP11 is a nuclear Zn transporter essential to maintaining nuclear Zn homeostasis in mammalian cells. To test this idea, we knocked down *Zip11* in normal fibroblasts and HeLa cancer cells. Preliminary data shows that partial deletion of *Zip11* reduced the proliferation of HeLa cells, and when HeLa cells reached confluency, they acquired an epithelial morphology. None of these phenotypes were detected in HEK293T cells, suggesting that ZIP11 might be relevant for the proliferation of cancer cells. Our work has the potential to discover a novel molecular mechanism where nuclear Zn homeostasis is essential for cancer progression.

Unraveling Potential Analgesics Metabolizing Bioprospects Using Functional Metagenomics

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Cristian Sanlatte*, *University of Puerto Rico Mayagüez* and Carlos Ríos-Velázquez, *University of Puerto Rico at Mayagüez*

Abstract: Over the counter drugs have become one of the most reliable and fastest solutions to relieve common muscle pain and inflammations. For example, drugs such as ibuprofen (IBU) and paracetamol (PA) are highly used within the pharmacological industry, hospitals, and the common household. However, its overuse has placed it as an environmental threat to aquatic environments. Furthermore, the presence of these compounds have an adverse effect on the aquatic biodiversity evidenced by cases of oxidative stress damage. Therefore, as a means of removing these contaminants, this research aims to search for bioprospects capable of metabolizing the active compound of IBU or PA using culture independent techniques. Centralia, Guajataca reservoir and Guánica's Dry Forest metagenomic libraries were screened by growing metagenomic clones in M9 medium with IBU or PA as its sole Carbon source. The plates were incubated at 37°C and candidate colonies were scored daily for 5 days. A total of twenty-eight potential analgesics metabolizing bioprospects (PAMB) were isolated. The growth of seven PAMB was reconfirmed using optical density in M9 liquid media supplemented with IBU or PA. From the PAMB screened, six candidates showed considerable growth under the conditions tested. These where evaluated through molecular analysis to confirm the presence of a fosmid. Current work is in progress to identify its metagenomic fragment and perform mutagenesis experiments that validate the candidate's ability to use the analgesic as its Carbon source. Considering that IBU and PA are currently emerging contaminants, these PAMB represent an alternative method towards bioremediating these contaminants.

Using the Bioid Approach to Identify Proteins Interacting with the P0 Protein from Turnip Yellows Virus

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kellen Henning*; Mansour Dughbaj; Jordan Shoemaker and Melanie Sacco, *California State University, Fullerton*

Abstract: RNA silencing is a conserved antiviral mechanism in plants. Dicer-like enzymes cleave viral double-stranded RNAs into virus-derived small interfering RNAs (vsiRNAs) that are incorporated into the RNA-induced silencing complex (RISC) with Argonaute (AGO) proteins. The vsiRNAs guide AGO1 endonuclease activity to cleave target viral RNAs. All plant RNA viruses have evolved viral suppressors of RNA silencing (VSR) that interfere with RNA silencing in their hosts. Turnip yellows virus (TuYV), an economically important *Polerovirus* infecting a wide range of crop plants, uses its VSR protein P0 to target AGO1 for autophagic degradation, preventing RISC formation. In *Nicotiana glutinosa*, the P0 protein triggers immunity against TuYV involving the hypersensitive response (HR). This project aims to identify potential protein-protein interactions involving P0 during infection or elicitation of HR using the BioID proximity-labeling technique to covalently tag P0-interacting proteins with biotin *in vivo*. Beta-glucuronidase (GUS), wild-type P0, and mutant P0 genes were each ligated into pBin61 to create fusion proteins with the promiscuous biotin ligase BirA* and a hemagglutinin (HA) epitope. The wild-type P0 fusion was functionally validated by agroinfiltration into *Nicotiana* plants for VSR and HR assays, showing that BirA* fusion does not impair P0 activities. Pull-down assays were used for validation of BioID construct expression by immunoblotting and streptavidin-HRP detection of biotin-tagged proteins. Tandem mass spectrometry will be done to identify potential P0 target proteins. This work will advance our understanding of TuYV infection in plants, which is important for developing virus-resistant crops.

Single Cell Analysis of Vacuolar Ph Using Confocal Microscopy

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Anyce Godoy*[1]; Roberto Carlos Segura[2]; Jean Luke Campos[3]; Jamie Calma[4] and Mark Chan[1], *(1)San Francisco State University, (2)University of Washington, (3)University of California, San Francisco, (4)Department of Plant and Microbial Biology, University of California, Berkeley*

Abstract: In order for ion storage, protein degradation and protein folding to occur properly, vacuolar pH must lie within a specific range. Due to the breadth of the vacuoles function, pH regulation has direct implications in cellular age. This impact could provide insight into human diseases such as lysosomal storage diseases and Alzheimer's disease. Despite this, there have been few studies to directly observe to what extent vacuolar pH impacts other vacuolar phenotypes. In our previous work, we have observed vacuolar pH via confocal microscopy to collect single-cell data using the pH-sensitive vacuolar dye, BCECF-AM. However, the use of this dye resulted in data with high levels of variance, which has led to inconclusive results. To rectify this, we have developed a fluorescent protein tag that utilizes an eGFP-mCherry double tag, which allows us to measure vacuolar pH without the use of dyes. This tag works similar to other pH-sensitive dyes, leading us to hypothesize that our protein tag will yield similar results to our previous findings. In this work, we compare the effectiveness of this protein tag to our previous findings with BCECF-AM. Our preliminary results show that this protein tag has a similar pH indicator range to other pH probes, and is more stable than other probes, highlighting its advantages as a pH indicator. Taken together, our findings show that our double-tag indicator has the potential to provide better quality data, which will allow us to further understand the impact of vacuolar pH on other cellular functions.

A Dominant Modifier Screen for Genetic Interactors of Jagunal in Drosophila

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Gerson Ascencio Martinez* and Blake Riggs, *San Francisco State University*

Abstract: The endoplasmic reticulum (ER) is a continuous network of membrane tubules and flattened cisternae. It is a multifunctional organelle involved in proteins and lipids synthesis, secretory proteins and post-translational modification of proteins. Recent studies have shown that the ER is partitioned asymmetrically in proneuronal cells during mitosis in early embryonic development of Drosophila just prior to gastrulation. Furthermore, this asymmetric ER partitioning relies on the highly conserved transmembrane protein Jagunal (Jagn), however, the molecular pathway that drives Jagn-dependent ER partitioning is currently unknown. Here, we hypothesize that Jagn interacts with cell fate determinants to drive the generation of neuronal cell diversity. In order to identify possible genes that interact with Jagn, we performed a dominant modifier screen in the Drosophila compound eye. Expression of JagnRNAi in the Drosophila compound eyes results in a rough eye phenotype in 80% of the eyes examined. Based on this, we crossed a collection of deficiency lines covering the entire 3rd chromosome and examined for either enhancement or suppression of the rough eye phenotype. We have identified six suppressors and six enhancers of Jagn-induced rough eye lines phenotype. These deficiency lines include genes involved in organelle assembly and regulation, kinetochore/microtubule attachment, and actin proteins associated with vesicle and organelle movements. Future directions will include imaging and characterizing the genes in the identified enhancers and suppressors. Identified targets will provide important insight into the molecular pathway involved in ER organization and partitioning. Interconnecting to jagunal homolog 1 that cause Severe congenital neutropenia for future studies.

Studying Metabolism in a Model Animal Using an ATP Sensor Protein

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jose Soto*; Madeline Rivera and Morris Maduro, *University of California, Riverside*

Abstract: The nematode *Caenorhabditis elegans* is a powerful model system to study fundamental biochemical processes such as those in metabolism. This project involves identifying determinants of metabolic rates by studying the function of the intestine in wild-type and mutant *C. elegans* animals. A key component of metabolism in all living cells is the availability of adenosine triphosphate, or ATP, the main source of chemical energy transfer. The Maduro lab has found that partially compromised specification of gut in the embryo leads to increased fat storage in surviving adults. They previously identified genes whose expression changes in the gut of these strains. Two of these genes are *fstr-1* and *fstr-2*. In wild-type animals *fstr-2* is expressed, and in specification- compromised animals (e.g. the strain MS404), it is *fstr-1* that is expressed. The two genes make related proteins that may be important for import of food into gut cells. We hypothesize that these strains differ in their metabolism, such that the concentration of ATP in the living animals would be different. Using an engineered protein that responds to endogenous ATP levels in living cells, through Förster resonance energy transfer, or FRET, we will measure steady-state levels of ATP in the living animals. Our results suggest that the ATP sensor protein produces detectable signal that shows signal differences, as expected, in control and genetic backgrounds that influence ATP levels. We are continuing to develop the use of this sensor in *C. elegans* and use it to measure metabolism in the various mutant backgrounds.

Resistance to Sonic Hedgehog Signaling Inhibition in Pancreatic Ductal Adenocarcinoma

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Halee Scott* and Joshua Morgan, *University of California Riverside*

Abstract: Of the solid malignancies, one of the deadliest is pancreatic ductal adenocarcinoma (PDAC), which is the most common form of pancreatic cancer. In regards to cancer mortality, pancreatic cancer is the 5th most common cancer death with a median survival of <2 years and a 5-year survival rate of 6%. The Sonic Hedgehog (Shh) signaling pathway was shown to play a role in PDAC proliferation and invasion. In both *in vitro* and *in vivo* models, Shh inhibition was shown to decrease tumor progression in PDAC but had an inverse effect clinically, exacerbating other aspects of the tumor development. One feature the previous *in vitro* and *in vivo* PDAC models did not account for is the surrounding stromal microenvironment. It has been shown that inhibition of the Shh pathway triggers senescence in the adjacent stromal cells, although the specific mechanism is unclear. Recent data has also shown suppression of the Hippo pathway in the stromal response to PDAC, and we hypothesize Shh inhibits Hippo in the PDAC stroma, leading to persistence. To test this, we grew fibroblasts (NIH3T3) and treated them with Shh inhibitors Vismodegib and Sonidegib for 24 hours. Following treatment, cells were fixed with paraformaldehyde and stained for Gli1 and YAP, markers of the Shh and Hippo pathway, respectively. By elucidating the role of the tumor microenvironment in PDAC we hope to provide a more robust model which could accelerate the identification of therapeutic targets that exhibit potency in both tumor and stromal aspects.

The Antenna's All the Difference: How Does Having a Ciliated Centriole Change Centriole Function?

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Anais Tsai*[1]; Emily Ho[1]; Garrison Buss[1] and Tim Stearns[2], *(1)Stanford University, (2)Stanford, Genetics*

Abstract: The primary cilium is the antenna of the cell; both in physical presentation as a thin 1-5μm projection from the cell surface and in its role in signal transduction, mechanosensing, and cell cycle regulation. At the base of the cilium is the centriole. Docking of the centriole to the cell membrane is necessary for cilium formation. However, centrioles also have additional overlapping roles in the cell as part of the Microtubule Organizing Center (MTOC) and the mitotic spindle poles. Centrioles must function as the MTOC even while anchoring a cilium. However, centrioles lack an associated cilium when the mitotic spindle forms. The current view is that the cilium must be disassembled for successful completion of mitosis, raising the question: **How does having a cilium-bearing centriole affect MTOC activity and spindle formation?** We used chemical and genetic cell biology tools to observe aberrant ciliation states in mammalian cells. First, we manipulated the number of cilia to show that ciliated centrioles are capable of forming functional MTOCs. Surprisingly, ciliated MTOCs nucleated microtubules at faster initial rates than nonciliated centrioles in both monociliated and multiciliated cells. Second, we altered the timing of cilia disassembly by forcing cells with stabilized cilia into mitosis. We show mitosis can occur while the cilium is present, but partial disassembly still occurs and may be necessary for successful mitosis. Our results suggest that centriole ciliation status enhances MTOC activity in interphase but restricts successful mitotic exit.

Impact of Artificial Sweeteners on Cellular Growth and Signaling Pathways

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Patricio Ruano*; Nitika Parmar and Crystal Vargas, *California State University, Channel Islands*

Abstract: Several varieties of artificial sweeteners (AS's) such as Aspartame, Stevia Extract, and more are used as a zero-calorie sugar substitutes - especially in Latinx diabetic communities. Previous research on artificial sweeteners have produced results indicating contradictory benefits and hazards, largely in cancer suppression or induction. In this two-part study, we examined effects of various concentrations of artificial sweeteners on *E. coli* and mammalian cell growth. The mTOR pathway is largely a regulator of cell proliferation and can be sensitive to nutrient uptake in mammalian cells. As such, we explored how normal mammalian cell lines (HEK298) and cancerous mammalian cell lines (TOV112D) differed in health and protein concentration of the proteins within this mTOR pathway when grown in cultures containing AS's as compared to positive control cultures containing full glucose media and negative controls containing glucose-free minimal media. Western blots, SDS-PAGE, Bradford's Assays, and ELISAs were used as analytical tools to determine protein concentrations present in growth cultures. Results indicated that normal mammalian cell lines largely responded negatively to presence of AS's as opposed to glucose, with general protein concentrations being lower in cells treated with AS's. This study explores implications of alternatives to sugars that are widely consumed in communities already vulnerable to health disparities. Uncovering previously unknown effects of these AS's will provide useful implications that can influence viability of these alternatives.

Inflammatory Macrophages Contribute to Gut Inflammation through Continuous Notch Signaling

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

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Abstract: Inflammatory Bowel Disease (IBD) is the general term used to characterize chronic inflammation of the gastrointestinal tract. In spite of the extensive research efforts, the precise pathogenic factors that cause IBD remain unclear. However, immune dysregulation and intestinal barrier defects are believed to be two major factors contributing to IBD pathogenesis. In attempt to understand the biological factors contributing to immune dysregulation and intestinal barrier defects, we utilized two animal models of IBD: i) the chronic DSS-induced colitis model and ii) the spontaneous enterocolitis development in IL-10-deficient mice. We found in these animal models of IBD, the inflamed colonic epithelium have increased Notch targeted gene hairy and enhancer of split-1 (Hes1) expression and a decrease in atonal homolog 1 (Atoh1) expression when compared to B6 mice. Additionally, ex vivo analysis revealed the inflamed colon harbored intestinal macrophages with increased Notch ligand expression. Furthermore, the conversion of macrophages into inflammatory macrophages resulted in the upregulation of Notch ligands. Lastly, we found inflammatory Notch ligand-positive macrophages reduced secretory cell differentiation and barrier integrity in a co-culture system with colonic organoids. Based on these findings, we conclude that chronic intestinal inflammation is maintained by inflammatory macrophages through continuous Notch signaling.

Innervation Dynamics Regulating Changes in Growth Rate during Axolotl Limb Regeneration

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kristina Kelley*; Kaylee Wells and Catherine McCusker, *University of Massachusetts, Boston*

Abstract: The axolotl (Ambystoma mexicanum) is used to study regeneration because of its ability to regenerate fully patterned limbs that are almost identical to intact, un-amputated limbs. There are two stages of regeneration. During the first stage, a blastema forms and the limb is initially patterned. During the second stage, the fully patterned "tiny limb" grows in size until it is proportional to the size of the animal. Following patterning and differentiation into the missing limb structure, the "tiny limb" initially undergoes rapid growth (early tiny limb). The growth rate decreases as regeneration progresses into the late tiny limb stage. We have discovered that during regeneration, size is regulated through non-autonomous signals. We have also found that one non-autonomous signal, nerve signaling, is required for the observed increased cell proliferation, survival, and size in the tiny limb. As regeneration proceeds through the late tiny limb stage, abundant and disorganized nerve bundles become more consolidated, as in unamputated limbs. This could be due to axon pruning in the regenerate; however, this has never been studied before. Although the mechanisms of nerve driven growth are unknown, we hypothesize that nerves supply factors that are necessary for growth in the tiny limb. One such factor is BMP, which has been shown to be required for the growth of the early regenerate. This project aims to analyze the neuronal BMP gene expression and innervation dynamics at the time of the growth rate change during limb regeneration.

Investigating Sequence Features of eIF3 and eIF4A Target mRNAs

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Cameron Baker*[1]; Angélica M. González-Sánchez[2] and Jamie H.D. Cate[2], *(1)Fullerton College, (2)University of California, Berkeley*

Abstract: Translation regulation is critical for maintaining cell homeostasis and its misregulation leads to diseases such as cancer. Translation initiation is highly regulated and requires several eukaryotic initiation factors (eIFs). One of the most pivotal initiation factors is eIF3, which has been found to serve as both a scaffold in preinitiation complexes and a regulator of translation for certain mRNAs. Another essential initiation factor is eIF4A, which unwinds mRNA in preparation for recruitment to initiation complexes. Both eIF3 and eIF4A have been found to bind to and regulate translation of the *JUN* mRNA. This suggests a new mechanism for translation regulation that can also act on other mRNAs in the cell. A compiled cross-reference analysis of eIF3 target mRNAs and eIF4A target mRNAs led us to find a subset of mRNAs that are targeted by both. Of the 17 mRNAs that were found to interact most significantly with eIF3 and eIF4A, we found that 7 have common functions of RNA binding and nuclear processes. Literature search, genomic sequence analysis and secondary structure prediction will be conducted on these specific mRNAs to find common sequence features. From this analysis, we will be able to propose potential regulatory mechanisms involving eIF3 and eIF4A and design reporter constructs to test these. As a whole, this study broadens the understanding of the mechanisms of translation regulation mediated by eIF3 and eIF4A, which serves as a blueprint for targeting disease.

Epigenetic Reprogramming in a Dish – an *in Vitro* Model of Transgenerational Epigenetic Inheritance

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jake Lehle; Amanda Gomez* and John R. McCarrey, *University of Texas at San Antonio*

Abstract: Epigenetics are the mechanism by which eukaryotes regulate the normal expression of genes within the genome over the lifespan of the organism. Epimutations, which are changes to normal DNA methylation or histone modification patterns, can disrupt normal gene expression and progress into disease states. Furthermore, disease states that result from endocrine disrupting chemicals (EDC) induced epimutations have been shown to be heritable. The process of transgenerational epigenetic inheritance allows epimutations to be passed on through several generations, even though these epimutations are expected to be. While previous work has shown EDC's can alter the epigenome, the mechanisms and key players by which these chemicals induce epigenetic changes, and what cell types are susceptible to epigenetic changes remain unknown. In order to predict differences in relative susceptibility to the induction of epimutations when exposed to EDCs, we will use immunofluorescence cytochemistry staining (ICC), western blots, and RT-PCR to determine the presence or absence of certain hormone receptors known to be disrupted by EDC exposure. Based on previous RNA-sequencing results, we hypothesize somatic cell types will express the hormone receptors androgen receptor (AR), estrogen receptor alpha (ERα), estrogen receptor beta (ERβ), peroxisome proliferator-activated receptor gamma (PPARγ), and retinoid X receptor (RXR), which increases the cell type's vulnerability to EDC exposure compared to pluripotent and germ cell types, which only express RXR. This project is designed to confirm the expression of these receptors as they have been shown to play a role in differential cell type-susceptibility to EDC-induced epimutations.

Structural Genomic Variations Underlying Colony Morphology Switches in Budding Yeast

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Hyatt Vincent* and Lydia Heasley, *Colorado State University*

Abstract: Despite its perceived simplicity as a single-celled fungus, the budding yeast *Saccharomyces cerevisiae* remains an invaluable resource for the study of genome structure and function. This is because its genome is very similar in structure and content to that of higher eukaryotes. Decades of laboratory research using *S. cerevisiae* have made it the best understood eukaryotic cell type. Yet, little is known about how the structure of the yeast genome helps cells to express traits which enable them to survive in natural environments. For example, many natural isolates undergo morphological shifts in response to changing nutrient sources. Our group has been studying a morphological shift displayed by the wild yeast strain YJM311. Cells of this strain form smooth colonies in sugar-rich conditions, but in sugar-limiting conditions, cells instead form complex colonies characterized by a lacy colony shape. In this study, we surveyed the existing literature surrounding such morphological switches in *S. cerevisiae* in order to assess what is currently known about how the structure of the genome contributes to the expression of such complex phenotypes. We find that colony morphology switches can be modulated by existing genomic heterozygosity as well as by loss-of-heterozygosity, gains or losses of whole chromosomes (i.e., aneuploidy), and gross chromosome rearrangements (GCRs). In this review, we present a general discussion of what is known of this subject, highlight outstanding questions, and present preliminary work from our own group, in which we are using YJM311 to define the genome structure-phenotype relationship underlying complex morphological traits.

Differential Epistasis Associated with Obesity in Mice

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Brianna Little*; Ruby Sharma and Mingzhou Song, *New Mexico State University*

Abstract: Epistasis is the statistical interaction between genetic variants such as single nucleotide polymorphisms (SNP) in genomic DNA. These interactions when associated with a disease or a trait become markers of the underlying biological processes. A prior study obtained 126 SNPs in 1,063 mice from the LG/J x SM/J advanced intercross line. These SNPs were reported to be significantly associated with 50 traits in mice collected over different days and experimental settings. In particular, 46 of the 126 SNPs were found to be associated with significant change in mice body weight. The study did not investigate epistatic interactions between two SNPs in association with the traits. Thus, we expanded upon the study to characterize average mice weight across all experiments with SNP-to-SNP epistatic interaction change between under- and over-weight mice. We used an optimal univariate clustering strategy to determine the two weight categories from average weight. Two-way SNP-to-SNP contingency tables were constructed using wild type, homozygous, heterozygous allele frequencies. The tables of the same SNP-pair were compared between the two weight categories. All such SNP-to-SNP interactions were evaluated for difference in interaction using a recent Sharma-Song statistical test of second-order differential patterns. We uncovered multiple SNP-to-SNP interactions with significant difference in their joint distribution across the two weight categories. We also found outstanding allele combinations that were clearly different between the weight categories suggesting their potential relevance to mouse obesity.

CRISPR Screens to Discover Host Factor Dependencies for Sars-Cov-2 Infection

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Eleanor Wang*[1]; Sylvia Sarnik[1]; Scott Biering[1]; Eva Harris[2] and Patrick Hsu[1], *(1)University of California, Berkeley, (2)Division of Infectious Diseases and Vaccinology, School of Public Health, University of California*

Abstract: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), the virus causing coronavirus disease 2019 (COVID-19), has swiftly spread across the globe. As of July 2020, there are over 12 million confirmed cases and half a million deaths. Given the lack of approved drugs or vaccines, a better understanding of the viral life cycle is desperately needed for the development of rational therapeutics. To address this, we are performing genome-wide CRISPR screens on lung epithelial cells infected by live SARS-CoV-2 virus under BSL3 conditions. By identifying host factors that mediate viral infection and cytopathic effect, we aim to provide insight into mechanisms of COVID-19 pathogenesis and inform development of novel therapies.

Revealing Cellular Pathways That Influence Neuronal Proteinopathies in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Shagufta Khatoon* and Cindy Voisine, *Northeastern Illinois University*

Abstract: Molecular chaperones, highly conserved molecular machines, cooperate to maintain the cellular folding environment. The proteostasis network preserves the quality of protein folding, reducing errors in the folding process preventing protein aggregation and proteotoxicity. Proteotoxicity results from the accumulation of misfolded proteins, damaging cellular processes, and chronically, can lead to neurodegenerative disease. One hallmark found in neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS) is the accumulation of misfolded proteins. A correlation between aging, neurodegenerative diseases and chaperone dynamics has been shown. For our research, we expressed human TDP-43, an RNA binding protein that is associated with ALS, in the nervous system of the nematode *C. elegans*. We performed in-depth assessment to reveal changes in the active translatome to identify cellular pathways that change when TDP-43 is expressed in neurons. Our analysis may reveal pathways that fail to protect neurons from proteins that trigger proteostasis imbalances leading to disease.

Analyzing the Impact of Tdp-43, an Amyotrophic Lateral Sclerosis (ALS) Associated Disease Protein, Expressed in *C. Elegans* neurons

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kimberly Nu-Tall*; Cindy Voisine; Rogelio Alvarado; Shagufta Khatoon; Helena Puccini de Castro and Yuriy Khlopas, *Northeastern Illinois University*

Abstract: Proteostasis, a protein quality control system, maintains the folding of the proteome, a collection of diverse and structured proteins which form protein-protein interactions facilitating communication within cells. Within the proteome, protein aggregation occurs when misfolded proteins clump together intra or extra cellularly, which may lead to disease. One essential branch of the proteostatsis network includes molecular chaperones, which help to protect the proteome from misfolding and aggregation, preventing proteotoxicity. We are interested in identifying the changes in proteostasis sub-networks in cells that encounter an aggregation prone disease protein.

We will be using the nematode *C. elegans* with a transparent cuticle, allowing *in vivo* imaging of aggregation prone disease proteins. We generated transgenic animals that express TDP43, a protein that aggregates in patients with amyotrophic lateral sclerosis. TDP-43 plays a major role in splicing regulation, RNA transport, and transcription. Using these transgenic animals, we generated a dataset of sequenced mRNA fragments to identify genes that were differentially expressed in TDP-43 expressing animals compared to wild type controls. From the profiling data, we expect to learn how expression of the TDP-43 protein will alter cellular pathways. Our goal is to understand the impact of TDP-43 on neuronal functionality, shedding light on our understanding of neurodegenerative diseases.

Analyzing Gene Expression in *C. Elegans* Expressing Tdp-43

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Rogelio Alvarado*; Yuriy Khlopas; Kimberly Nu-tall; Helena Puccini de Castro and Cindy Voisine, *Northeastern Illinois University*

Abstract: Proteostasis maintains protein levels, locations, interactions, and transitional change preventing protein misfolding, aggregation, and proteotoxicity. Protein aggregation, a trademark of many neurodegenerative disorders, causes irreparable neuronal damage in the brain. Decreases in the fidelity of the proteostasis network leads to protein aggregation and cellular damage. Comprehending the contribution from distinct branches of the proteostasis network can shed light on how cells maintain a functional proteome. Ribosomes are molecular machines that translate mRNAs into a sequence of amino acids, which fold into a particularly shaped protein. A segment of mRNA, approximately 30 nucleotides, is protected within the ribosome. Deep sequencing of these mRNA fragments can quantitatively measure gene expression rates, a reflection of protein synthesis. Our experiment will use this analysis to review how gene expression is affected in the nematode *C. elegans* that expresses human TDP-43 in its nervous system. *C. elegans* genome has been sequenced and is 40% homologous to the human genome. TDP-43 is an RNA binding protein that aggregates in neurodegenerative disorders, such as amyotrophic lateral sclerosis, a fatal progressive disease that affects motor neurons. We can identify changes in gene expression rates in *C. elegans* expressing TDP-43 compared to rates in wild type animals, revealing pathways that have been altered. It is likely that expression of proteostasis related genes that participate in the ubiquitin proteasome system, the branch responsible for protein clearance, will decrease. These changes in the proteostasis network impacts cellular health and contribute to disease progression.

Effects of Animal Space Use on Pathogen Transmission Potential in Brush Mice

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Allen Charleston* and Karen Mabry, *New Mexico State University*

Abstract: The potential for pathogen transmission between animals is influenced by animal space use and contacts between individuals. We are evaluating the risk of pathogen transmission between individual brush mice (*Peromyscus boylii*), a species that harbors Sin Nombre virus (SNV), which causes hantavirus pulmonary syndrome in humans. We are using relocations of mice obtained by tracking animals fitted with VHF radio-transmitters using automated radio-telemetry. We are using these data to investigate home range overlap and estimate likelihood of contact and pathogen transmission between *Peromyscus*. We predict that the home ranges of male mice will overlap the home ranges of more conspecifics and will have a higher proportion of their home range that overlaps others than will female mice. We predict that in a year with a higher population density (2017), home range overlap will increase as compared to a year of lower population density (2018). In conclusion, research on animal movement is important for studies of disease ecology because it can help identify factors that may lead to higher pathogen prevalence and potential spillover from animal vectors, leading to infections in humans.

Investigating the Effects of Advanced Diabetes and Aging on Pancreatic Alpha Cells

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Vincent Castillo* and Mark O. Huising, *University of California, Davis*

Abstract: Diabetes is a devastating disease for individuals of all ages, but in particular for elderly individuals where the mortality rate is significantly increased by diabetes. To better understand how to treat diabetes, much focus is put on the hormones that control blood glucose levels as well as the source of these hormones: the pancreatic islets. Type 2 diabetes is characterized by hyperglycemia stemming from insulin resistance, and, as it progresses, insulin insufficiency from islet beta cell failure. Another feature of the disease is that glucagon, a counterregulatory hormone from islet alpha cells, is found in excess in early type 2 diabetes, and is later hyposecreted in advanced diabetes. While much attention has been paid to the issues surrounding beta cells, aspects of alpha cell regulation remain unexplored. I hypothesize that both diabetes and the effects of aging induce a change in alpha cell responsiveness that underlies glucagon dysfunction seen clinically. To test this hypothesis I propose to use mouse models of diabetes and follow alpha cell behavior and identity over time. Using confocal microscopy, I will record alpha cell responses to specific physiological cues, such as epinephrine, arginine vasopressin, amino acids and glucose. I will look at how the responses to these stimuli change with age (young and old) and disease state (lean and diabetic). By doing so, I aim to contribute a better understanding of the fundamental differences that aging with and without diabetes confers upon alpha cells and how this could possibly inform improved treatments and outcomes.

Genomic Amplification Mutants Form in the Absence of Stressful Conditions in *Acinetobacter Baylyi*.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Cynthia Recendez*; Constancia Dominguez; Daniel Davis; Jennifer Herrmann; Kelly Faeth; Rola Ghobashy; Habeeba Awwad; Mario Lopez; Nancy Villanueva; Elizabeth Reis; Semarhy Quiñones, PhD and Andrew Reams, PhD, *California State University, Sacramento*

Abstract: Genomic amplifications are a type of DNA mutation where sections of a genome are present with multiple copies. They have been observed in all living organisms, including cancerous cells. Here, we use the bacterial system, *Acinetobacter baylyi,* to specifically study the formation of genomic amplifications. Previous studies suggest genomic amplifications form as a response to stressful conditions by a process called Adaptive Mutagenesis. Alternatively, we propose their formation is due to random events taking place during cell growth in the absence of stress. In testing these two hypotheses, *A. baylyi* grown in a non-selective environment was transferred onto three identical agar plates by replica plating, a technique where cells grown on a primary non-selective plate are inoculated onto secondary plates with selective growth media, while keeping track of colony positions relative to the primary plate. In our bacterial system, colonies growing on the secondary plates contain genomic amplifications to relieve the selection imposed. If the new colonies grow on different positions relative to each secondary plate, then the genomic amplifications formed in response to stress. But, if the new colonies grow on the same position across all secondary selective plates, then the cells that formed these colonies were already present in the non-selective primary plate. Our results show colonies growing on the same position when screened across all secondary plates, suggesting the genomic amplifications formed while growing on the primary non-selective plates. Thus, genomic amplifications were present in the population before the cells were transferred onto the secondary selective plates.

Vesicle Dynamics and Attached F-Actin Fiber Length Effects Investigated By Computer-Based Simulations.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jean Claude Zarate*, *Worcester Polytechnic Institute, Computer Science* and Luis Vidali, *Worcester Polytechnic Institute, Biology and Biotechnology*

Abstract: Vesicle transport is essential for eukaryotic cells, for example in plant cells, growth and cell division are controlled by the transport and fusion of vesicles containing cell wall materials. Hence, understanding vesicle dynamics is vital to advance our knowledge of how plant cells grow. The goal of this project is to test the hypothesis that attaching an actin filament will alter the diffusive properties of a vesicle, and that the diffusive behavior of the filament will become independent of the vesicle at a distance similar to the filament's persistence length. To test this, we decided on using the software Cytosim with a custom Python script that supervises multiple concurrent Cytosim simulations and exports them in CSV format for further analysis in R. We validated the correctness of the diffusion engine by using Mean Square Displacement analysis of vesicles of different sizes and compared against a range of theoretically derived diffusion coefficients. This validation showed the simulation engine is accurate. To validate filament behavior we calculated its persistence length from simulations and compared against that of published experimentally obtained values. We found the values to be in the expected range. We are currently simulating attaching filaments of different sizes to a single vesicle. This will provide information about how the diffusion coefficient of the vesicle is affected by filament length, allowing us to test our hypotheses. Future simulations will incorporate additional vesicles and filaments as well as the addition of molecular motors.

Investigating the DNA Substrate Cleaved in the Absence of REV1 in DNA Damage Tolerance in *Drosophila Melanogaster*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Sofia Lombana Rengifo*; Mai Tran and Mitch McVey, *Tufts University*

Abstract: DNA damage tolerance (DDT) mechanisms allow cells to mitigate replication damage that can cause replication fork collapse. The two major pathways of DDT are translesion synthesis and template switching, the latter further categorized into fork reversal and homology-directed repair. REV1 is a translesion synthesis polymerase that recruits other translesion polymerases via its C-terminus. Data collected by our lab show that in *Drosophila melanogaster*, REV1 has additional DDT functions that are not associated with its C-terminus, potentially in template switching. Flies lacking the entire REV1 gene are more sensitive to the alkylating agent methyl methanesulfonate (MMS) than flies missing the REV1 C-terminus. Interestingly, the loss of SLX4, which serves as a scaffold for structure-specific endonucleases (SSEs), partially rescues the MMS sensitivity of rev1 mutants. We hypothesize that in the absence of REV1, replication forks are left unprotected and vulnerable to potential cleavage by SSEs, leading to double-stranded DNA breaks. The goal of the present study is to identify the substrate being cleaved by SSEs. In humans, the SMARCAL1 protein mediates fork reversal. Drosophila have a SMARCAL1 homolog called MARCAL1, which may perform a similar function. We have generated a rev1-marcal1 double mutant and are currently testing its sensitivity to MMS. We predict that the loss of MARCAL1 in a rev1 mutant background might prevent the MMS-induced formation of reversed forks that can be cleaved by SSEs, thereby increasing survival. These results will better characterize REV1's functions outside of translesion synthesis.

The Correlation between the Genetic Sequence of *Demodex* skin Mites and the Ethnic Origin of Its Human Host

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

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Abstract: *Demodex* are microscopic mites that live in the sebaceous glands of mammals. Two species in particular, *Demodex folliculorum* and *D. brevis*, have an intimate commensal relationship with humans, and this relationship dates back since the emergence of humans as a species. As humans have migrated and undergone genetic makeup changes, *Demodex* species appear to have coevolved and diversified with their hosts. Researchers have identified four clades of *Demodex* based on a strong correlation between sequence similarity of *Demodex* and the ancestry of their host (Lam and Trautwein). However, the current sample size is somewhat limited in number and geographic origin. Our work aims to contribute to the existing work by utilizing the ethnic diversity in Hawaii that expands the data to include people of Asian, Pacific Islander and mixed descent. Samples were collected from 34 human hosts of 15 ethnicities. *Demodex* DNA was isolated and an approximately 960 base pair segment from the Cytochrome C Oxidase III to the NADH Dehydrogenase 3 gene was amplified and sequenced. The resulting sequences were then aligned with the curated Demodex sequences in GenBank. We found that Demodex isolated from people of Pacific Islander descent aligned closely to sequences from people of Latin American and Asian descent, and farthest from European descent. This is consistent with the hypothesized migrational history of Pacific Islanders. As more data become available, we hope the resolution of the relationships increases, allowing for a unique way to contribute to the evolutionary origins of the Pacific Islanders.

Mosquito Arbovirus Susceptibility and Insecticide Resistance Surveillance

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Alyssa Wheeler[*] and Caio Martinelle França, *Southern Nazarene University*

Abstract: Mosquito-borne diseases have affected millions of people each year causing severe illnesses and death in many cases. Knowledge and surveillance of arbovirus spread and increasing insecticide resistance among mosquitoes is essential in aiding control efforts and conserving public health. Our project was a collaboration with the NASA Globe Observer program, which allows citizen scientists to collect and record data to efficiently monitor for the presence of medically important vectors around the globe. We specifically focused on screening lab-reared larvae, collected during the 2019 NASA GO OK! project, from wild-caught *Aedes albopictus* mosquitoes from several counties around Oklahoma. *Aedes albopictus* mosquitoes are common vectors of flaviviruses such as West Nile virus, Zika, chikungunya, and yellow fever virus and pose an acute threat to global health. We first scanned the mosquitoes for insecticide resistance using an internal control primer, actin. To test for the allele-specific knockdown resistance (kdr) gene, we created a melting curve analysis that tested for an overall result of insecticide susceptibility or resistance. Additionally, we isolated the nucleic acids from each mosquito and used RT-qPCR and an allele-specific primer, G-block, to target the NS5 region of the DNA strand to genotype and detect any flaviviruses present in the *Aedes albopictus*. Our data suggest that the lab-reared *Aedes albopictus* are highly susceptible to insecticides and could become vectors of flaviviruses through contact with external factors. These results highlight the growing importance of arboviral surveillance and control efforts to conserve and improve public and global health.

Annotating Contig 53 of Drosophila Melanogaster

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Janette Garcia[*] and Siaumin Fung, *Vanguard University of Southern California*

Abstract: DNA densely packed with histones, heterochromatin, is associated with silencing or transcription of inactive genes. While, the loosely packed chromatin, euchromatin, is associated with actively transcribed genes. The F element, dot chromosome in *Drosophila melanogaster* is composed of mostly heterochromatin, yet has active transcribed genes. The goal of our research is to elucidate the regulatory motif within the dot chromosome by comparing the dot chromosome genes with gene located in the euchromatin, D element. In this study, Contig 53 in D element from Drosophila Takahashi is characterized with 7 features. Through the creation of a gene model or outline of where exons and introns begin and end, instances of where regulatory motifs occurs can be observed. The Genome Browser allows for visualization of the predicted genes and isoforms. B.L.A.S.T. allows for the alignment of genes between the two species. FlyBase contains genetic and molecular data for *Drosophila melanogaster*. By annotating and comparing different contigs or gene segments of the two species and the divergence between two different species *D. melanogaster* and *D. takahashii* can be visualized as well as any silencing of genes that has occurred through evolution. Our research shows that although many of the *jim* isoforms vary slightly, data can be correlated with RNA seq, Gene scan predications, and TopHat predictions. Of 11 total isoforms of *D. melanogaster,* seven share almost 90% similarity to the DNA of *D. takahashii*. This shows that through evolution these specific *D. takahashii* and *D. melanogaster* contig 53 have only diverged marginally.

Pro-Inflammatory Cytokines Induce Amyloid-Beta in Mouse Embryonic Stem Cell Derived Pyramidal Neurons

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Juan Martinez Mejia*; Steven Shao and Tzvia Abramson, *San Jose State University*

Abstract: Treatments for neurodegenerative diseases like Alzheimer's are challenging because diagnosis occurs too late in the stages of development. Amyloid-beta plaques and neurofibrillary tangles have been key signatures of Alzheimer's disease and are responsible for the degeneration of neurons. Thus, the use of mouse embryonic stem cells (mESCs) to create *in-vitro* models of neurodegenerative diseases is a critical component in discovering drug therapies and approaches in regenerative medicine. The goal of our project was to show that a cocktail of proinflammatory cytokines could significantly induce expression of amyloid-beta in mESC derived pyramidal neurons. In our experimental design, we chose to differentiate mESC's in a 21-day protocol and derive them into pyramidal excitatory neurons. Pyramidal neurons themselves are commonly found in the hippocampus, the region of the brain associated with memory and cognitive function. Once derived, we verified that our cell type was healthy and expressed pyramidal neuron specific markers with immunostaining for EMX-1, DAPI, and BACE-1. Based on new research, we hypothesized that using a combination of human recombinant pro-inflammatory cytokines Interferon-gamma (IFN-Y) and Tumor necrosis factor-alpha (TNF-α) could significantly induce amyloid-beta levels in mESC derived pyramidal neurons. After treatment with cocktail, we used qPCR assays to quantify expression levels of MAP-2, BACE-1 and EMX-1. Results showed elevated levels of expression of both MAP-2 and BACE-1. In conclusion, our results indicated that our derived neuronal culture expressed healthy neuronal cell markers (MAP-2) and elevated levels of amyloid-beta (BACE-1) and may serve as a viable model for Alzheimer's disease pathology.

Identifying Wolbachia Variants in Various Drosophila Species to Investigate Host-Endosymbiont Molecular Interactions

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

eliza Paneru*[1]; Yonah Radousky[2] and William Sullivan[2], *(1)University of California, Santa Cruz, (2)University of California Santa Cruz*

Abstract:

Wolbachia is one of the most successful bacterial endosymbionts on Earth, and is present in up to 60 percent of all insect species. It achieves this widespread distribution through a combination of vertical transmission through host oocytes, reproductive manipulations, and suppression of viral infections. Interestingly, *Wolbachia* strains exhibit considerable variation with respect to these properties. For example, while *Wolbachia* is routinely transmitted through the female germline, in some strains, it first undergoes transmission through the soma to arrive at the germline. Once there, different strains exhibit different subcellular localizations. Here, we examined a wide diversity of *Drosophila* (Fruit Fly) species to identify *Wolbachia* strains with different vertical transmission patterns, which can be used to identify symbiont genes underlying these processes. First, we collected divergent *Drosophila* species from across the world and identified their natural infection state by PCR amplification. Then, we investigated *Wolbachia* localization patterns in the oocytes of infected flies by confocal microscopy. From this work, we have identified several variant strains and host species that do not exhibit the standard anterior/posterior localization patterns seen in *D. melanogaster* infected with w.Mel wolbachia strain. These results will be immensely valuable to future bioinformatic and experimental work to disentangle the genes and mechanisms used by host and symbiont for successful germline transmission.

Using Yeast to Identify Wolbachia Effector Proteins

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Joseph Alas* and Grant Hartzog, *University of California, Santa Cruz*

Abstract: Wolbachia is a bacteria endosymbiont of eukaryotes. Wolbachia infects >65% of all insect species including filarial nematodes and certain nematodes that cause river-blindness and elephantiasis. Wolbachia may also impact human health. First, Wolbachia infected insects are resistant to infection with certain viruses, including Zika. Second, Wolbachia are essential for life in some microfilaria nematodes, allowing these organisms to be targeted by antibiotics. Wolbachia are transmitted vertically, through the eggs of infected females. Wolbachia involves strategies to favor its reproductive success in mixed populations of infected and uninfected host organisms to spread in a population. We are interested in understanding how Wolbachia interacts with host organisms to manipulate their reproductive success. To date, there is no system for growing Wolbachia outside of their eukaryotic hosts, limiting our ability to perform genetic or biochemical analyses of these organisms. To overcome this limitation, we express candidate Wolbachia effector proteins in *Saccharomyces cerevisiae*, and examine their ability to alter the growth or behavior of yeast cells. This approach is based upon the observation that Wolbachia infects a spectrum of species and the hypothesis that the cellular targets of Wolbachia are likely to be proteins that are highly conserved across evolution. To date, we have designed a yeast overexpression vector that allows for high throughput cloning of codon optimized, chemically synthesized Wolbachia genes. Pilot studies show that we can achieve efficient cloning efficiencies with this vector and have identified at least two Wolbachia proteins that interfere with normal yeast cell growth.

Determining the Expression Levels of Lincrna-Cox2 in Resident and Recruited Alveolar Macrophages

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Benny Mosqueira*[1]; Susan Carpenter[2] and Elektra Robinson[1], *(1)University of California, Santa Cruz, (2)University of California Santa Cruz*

Abstract: Advancements in RNA-sequencing have provided us with an unprecedented view of the human genome. One of the most fascinating findings is that less than 3% of the genome codes for protein-coding exons, yet more than 85% of the genome is transcribed. We are now faced with the challenge of understanding what these RNA genes do and whether they play key roles in biological processes. The largest group of RNA produced from the genome is Long noncoding RNA (lncRNA). LncRNAs are described as transcripts greater than 200 nucleotides in length that do not code for protein. Our lab pioneered the studies of lincRNA-Cox2, which has a dual regulatory role controlling its neighboring gene (*in cis)* as well as genes on other chromosomes (*in trans)*. We have preliminary data suggesting lincRNA-Cox2 is most highly expressed in the lung. Here we will use RNA-sequencing data of resident and recruited alveolar macrophages (AMs) harvested from an Acute Lung Injury (ALI) mouse model to determine the kinetics of lincRNA-Cox2 expression using mice treated with lipopolysaccharide (LPS) for 0, 3, 6 and 9 days. We will also determine whether alveolar or interstitial macrophages express lincRNA-Cox2 most highly. We hypothesize that recruited alveolar macrophages will have higher expression than residential because lincRNA-Cox2 is critical in regulating pro-inflammatory pathways in bone marrow-derived macrophages. These data will enable us to focus our future mechanistic studies on the cell type where lincRNA-Cox2 is most highly expressed.

The Role of Multiethnic P-Glycoprotein Drug Transporter Variants in Chemotherapy-Induced Peripheral Neurotoxicity (CIPN)

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Cristela Samaniego* and Sascha Nicklisch, *University of California, Davis*

Abstract: Chemotherapy-induced peripheral neurotoxicity (CIPN) is the most common side effect of cancer treatment, resulting in permanent pain and loss of sensation in hands and feet. Based on their mechanism of action, CIPN-causing chemotherapeutics are divided into several classes, including platinum-based compounds, taxanes, and protease inhibitors. Cumulative exposures and mixtures of these substances can further aggravate CIPN. In the central nervous system (CNS) and peripheral nervous system (PNS), the multidrug-resistance transporter P-glycoprotein (P-gp) is the major determinant of drug uptake and disposition. However, P-gp has lower expression levels in the blood-nerve-barrier of the PNS as compared to the CNS blood-brain-barrier. Genetic differences in this transporter gene, based on individual or ethnic background, have been shown to alter P-glycoprotein's protective efflux function and further complicate effective chemotherapy. The aim of this study is to determine the molecular interactions of human P-gp with chemotherapeutics known to cause CIPN. In addition, we seek to determine the effects of two so-called single-nucleotide polymorphisms (SNPs) that are associated with altered transport function, including S893A and S893T. We will test the hypothesis that single CIPN-causing chemotherapeutics or their binary combinations can block P-gp, and that this effect is different in SNP-carrying P-gp variants. We will clone, express, and purify three P-gp variants (WT, S893A, S893T) and determine the molecular interactions with 6 known CIPN-causing drugs using an optimized ATPase activity assay. The results of this project will identify CIPN drugs as substrates or inhibitors of human P-gp and inform co-administration protocols to alleviate CIPN across ethnic groups.

Environmental Sensing and Social Motility Are Regulated By Mechanosensation in Trypanosoma Brucei

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Melvin Williams*; Tiffine Pham; Monica Hernandez; Kristy Nguyen and Veronica Jimenez Ortiz, *California State University, Fullerton*

Abstract: Millions of people and animals in Sub-Saharan Africa are susceptible to a deadly infection known as African Sleeping Sickness caused by the protozoan parasite *Trypanosoma brucei.* From the colonization of an insect vector to the infection of a mammalian host, *T. brucei* possesses a very dynamic and complex life cycle that encompasses a variety of environments. A mechanism by which these parasites can sense stimuli and regulate their intracellular conditions in response to these external changes must exist. In bacteria, mechanosensation plays a role in pathogenesis by inducing the expression of virulence factors, regulating quorum sensing, and forming biofilms. While the role of mechanosensation is well characterized in bacteria, its function in protozoan parasites such as *T. brucei* remains unclear. We have identified a mechanosensitive ion channel (TbMscS) homologous to a small conductance mechanosensitive channel found in *E. coli*. The protein is expressed in both life stages of the parasite, with slightly higher levels in procyclic forms. Endogenous tagging of TbMscS confirmed its localization to the flagellar attachment zone. Reduction of TbMscS expression by RNAi induced defects in both cell volume regulation under hyper-osmotic conditions and social motility behavior, which is the ability for the parasites to form radial projections from the initial site of inoculation on semi-solid agar plates. Our results indicate a

connection between TbMscS and the parasites ability to adapt to environmental stimuli. The data presented suggests its possible role in flagellar functions such as motility, osmolyte trafficking, and detection of changes in the plasma membrane tension.

Evolutionary Blooming of RNAi

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Claudia Hernandez- Chavez* and Juris Grasis, *University of California, Merced*

Abstract: Every animal has an innate immune system, which is a primary defense against pathogens. By utilizing comparative genomic techniques and analyzing the genomes of animals at the base of animal evolution, we aim to identify the antiviral genes and evolutionary relationships in these animals. More specifically, our goal is to identify the innate antiviral genes that play a role as to how cells defend against parasites and viruses. RNAi is able to recognize RNA molecules and neutralize targeted viral RNA molecules, therefore inhibiting their expression. It is also responsible for the mediation of the RNA- induced silencing complex or RISC, a process that is essential to gene regulation and as our defense against viral infections. The components of RNAi that will be further examined include Dicer (responsible for the activation of RISC), Argonaute (controls binding of miRNA, siRNA, and piwi-RNA), and Aubergine (which is the scaffolding protein that holds the process together). Our hypothesis is that RNAi has existed since the beginning of animal evolution and has been present in basic organisms such as Choanoflagellates and Placozoas. Through this research, we will provide a better understanding of how innate immune systems work and how they function in vertebrate animals. Ultimately, this information can be applied to better understand the immune systems found in humans as well.

Lithium Chloride and Its Effect on Vacuole Physiology of Saccharomyces Cerevisiae

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ryan Acbay* and Mark Chan, *San Francisco State University*

Abstract: The vacuole of Saccharomyces cerevisiae, also known as Budding Yeast is essential for maintaining cellular homeostasis by balancing pH, degradation of proteins, and processing and holding of toxic metals. Budding Yeast Vacuoles are homologous to the lysosome organelle. Understanding its unique metabolic processes under LiCl metallic stress can aid in research of brain injuries, bipolar disorder, and neurodegenerative diseases. This study involves exogenously adding LiCl concentrations to GFP tagged BY4741 Budding yeast cells treated with sorbitol for osmolarity balance. The cells were exposed to various concentration for various times. The vacuole membrane and the cells were viewed in Brightfield. These tests were used to preform image analysis of vacuole phenotype in Image J and further processed in Matlab for 3-D readings of physiological features. Preliminary results for this method showed stressed vacuole physiology for all exposures. Greater exposures lead to smallest vacuoles with non-spherical morphologies. Lesser exposure time and lower LiCl concentration yielded smaller vacuoles compared to wild type. The vacuoles were also caught during inheritance and showed segregation structures in a majority of cells, inconsistent with their expected cell cycle stages. Future experiments will target the cells ability to restore homeostasis and to track the lasting effects inherited by the Bud.

Culture with Fibroblast Growth Factor 2 (Fgf2) and Gonadotropins Enhances Aspects of Late Folliculogenesis in Photoregressed Siberian Hamster Ovaries

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Simon A. Chau*; Kevin Trinh and Kelly A. Young, *California State University, Long Beach*

Abstract: Fibroblast growth factor 2 (FGF2) is an intraovarian growth factor essential to folliculogenesis, granulosa cell proliferation, and steroidogenesis. However, few studies have examined the effect of FGF2 on the seasonally-regressed ovary. Exposure of photoperiodic Siberian hamsters to photoperiod typical of the non-breeding season reduces gonadotropins resulting in ovarian regression. We hypothesized that culturing photoregressed ovaries with FGF2, with or without gonadotropins, would facilitate the return to ovarian function as measured by changes to folliculogenic factors. To address our hypothesis, hamsters were housed in inhibitory photoperiod for 16-weeks. Photoregressed ovaries were cultured for 15 days in one of four treatment groups: no treatment control (NT), gonadotropins (follicle-stimulating hormone and luteinizing hormone; GT), FGF2, and GT+FGF2. Tertiary follicles and corpora lutea numbers, as well as mRNA expression of cyclooxygenase-2 were significantly higher in the FGF+GT group as compared to the NT group. In contrast, no differences were noted in secondary follicle number, insulin-like growth factor-1 mRNA or luteinizing hormone receptor mRNA across groups. Both media estradiol concentrations and inhibin alpha mRNA expression peaked in the GT alone group as compared to all other groups. While synergy between FGF2 and gonadotropins may increase aspects of late stage folliculogenesis, FGF2 itself may impede estradiol production in regressed ovaries, mirroring what is observed in cycling rats. Importantly, FGF2 alone is not sufficient to promote a full return to ovarian function; a balance of FGF2, gonadotropins, and other factors are likely needed for complete resumption of both folliculogenesis as well as steroidogenesis in the photoregressed ovary.

Examining the Role of the E3 Ubiquitin Ligases Mindbomb and Neuralized in Tissue Regeneration

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Madison Balagtas*; Jack Allen and Ricardo Zayas, *San Diego State University*

Abstract: The Notch pathway is a cell-cell signaling pathway that regulates cell fate during development and tissue homeostasis. Notch is a cell-surface receptor that interacts with transmembrane ligands on neighboring cells. Notch signal activation is dependent upon the action of the E3 ubiquitin ligases Mindbomb (Mib) and Neuralized (Neur) that ubiquitylate Notch ligands in the signal-sending cell. Ubiquitylation of Notch ligands promotes their endocytosis, the action of which is necessary to release the Notch intracellular domain in the signal-receiving cell to activate downstream genes. We use the planarian *Schmidtea mediterranea* to investigate the role of Mib and Neur in tissue regeneration. These animals possess pluripotent stem cells that allow them to completely regenerate after injury. We identified five *mib* and five *neur* genes in planarians and cloned them for dsRNA synthesis. We perturbed the function of these genes using RNAi and initial experiments did not show any obvious defects during homeostasis. Whole-mount *in situ* hybridization (WISH) using neuronal markers *chat* and *synapsin* following RNAi likewise did not show changes in expression pattern. Functional redundancy between the multiple *mib* and *neur* genes in planarians is a possible explanation for the lack of phenotypic effects observed during RNAi experiments. To test this we will perform extended RNAi treatments, concurrent RNAi for multiple genes, and perform WISH after injury to examine regeneration-specific roles for Mib and Neur. [J.M.A was supported by the ARCS foundation and M.B. by NIH IMSD R25GM058906; this work was funded by NSF IOS-1350302 and NIH R01GM135657 to R.M.Z]

A Molecular Timeline for the Innate Immune System Development in Marine Medaka (*Oryzias melastigma*)

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Marissa Brown*[1]; Elizabeth DiBona[1] and Dr. Frauke Seemann[2], *(1)Texas A&M University - Corpus Christi, (2)Texas A&M University*

Abstract: The innate immune system is the first line of defense in vertebrate development against pathogens, abnormally developed cells, and environmental pollutants. Multiple pathways exist to target environmental pollutants, such as the complement cascade, inflammatory responses, cytokine and chemokine mediators, phagocytosis by macrophages, and the activation of the adaptive immune system. Research has shown during critical phases of innate immunity development, exposure to environmental toxicants may contribute to increased hypersensitivity and higher risk of autoimmune diseases in adult-life stages. This presentation uses the marine medaka embryos as a model to determine these critical phases of innate immunity development in fish by comparing immune genes involved in innate immunity, such as immune initiators (*C1q, MBL, TLR-3, TLR-5, CRP*), mediators (*C3, IL-1β, IL-10, TNF-α, TGF-β, IFNγ, MYD88, M-CSF*), and effectors (*C8a, NF-κB, LYZ, HEP, TCR-b, TCR-γ*) in naïve and bacterial (*Edwardsiella tarda*) challenged individuals. During the bacterial challenge, 1 day post fertilization (dpf), 3 dpf, 5 dpf, 7dpf, 9dpf, and 11dpf individuals were analyzed to determine gene expression and the critical phases seen during innate immunity development. By comparing gene expression between naïve and challenged individuals during innate immunity development, the activation of the innate immune pathways and the molecular changes presented can be used in further immunotoxicity research.

Genome Minimization of the Fast Growing Marine Bacterium Vibrio Natriegens

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

James Chang*, *University of Central Florida* and Tanya Tschirhart, *Naval Research Laboratories*

Abstract: The marine bacterium *Vibrio natriegens* is the fastest-growing, non-pathogenic organism known. V. *natriegens'* short generation time and resiliency in a wide range of environments offers many advantages over *Escherichia coli* as a model organism. However, V. *natriegens* requires extensive development before it can be a next generation synthetic biology chassis for molecular biology applications. Despite significant development of bioengineering tools, limited genomic and proteomic studies on *V. natriegens* suggests more research is needed to support chassis development. In this study we conducted a genome comparison between several V. *natriegens* strains using bioinformatics tools which can be used to identify essential genes, a set of genes proposed to be essential for the organism to survive and thrive in defined laboratory conditions. The broad characterization of the genome will allow researchers to identify large stretches of non-essential/non-growth supporting DNA and mark them for deletion and creation of genome-minimized strains. Recent research suggests that reduced genomes can provide unexpected benefits to the cell such as increased growth rates. In addition, we investigated the differential expression of proteins during different growth conditions to monitor cell response and identify the associated metabolic pathways. In combination, this dual approach will provide the foundation for downstream chassis development.

Distribution of SNP rs4430796 in Hispanic Population of Southern California As a Predisposition Method of Developing Type II Diabetes

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Alondra Maiz-Zapata*; Kevin Banco Hernandez; Sandra Camacho and Itzel Callejas-Macias, *Vanguard University of Southern California*

Abstract: One in ten people have diabetes in America, about 13% are Hispanic descent. From this 13% of Hispanic adults, 50% of that population will develop diabetes at some point in their life. As the Hispanic community keeps growing as the years go by the increase in diabetic patients goes up. Physically, mentally and financially, diabetes makes a big impact in people's lives as the disease progresses. Genetics can play a big role in identifying and preventing diseases, one way of that is by detecting single nucleotide polymorphisms (SNP). The rs4430796 in gene HNF1β which is a transcription factor expressed in the liver and pancreas associated with type II diabetes. The goal of this experiment is to identify the prevalence of rs4430796 SNP in Hispanic descent which has been associated with diabetes. We are analyzing 50 control and 50 diabetic samples from Hispanics living in Southern California. After buccal samples were collected and the DNA was extracted, a polymerase chain reaction (PCR) was running. To confirm the SNP we used an enzymatic digestion using *SfaN1* enzyme. This experiment will help contribute to the overall knowledge in the distribution of SNPs associated with type II diabetes in the Hispanic population of Southern California. If a person learns he or she possesses the SNP, this could help take preventive measures before the disease sets in by making better diet choices, increase the physical activity and keep a close monitoring of their blood sugar to catch the disease before it gets out of control.

Niche Partitioning in Congeneric Scorpions

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Dr. Lauren Esposito[1]; Aaron Goodman[2]; Thanh Tran[3] and Henry Brown*[3], *(1)The California Academy of Sciences, (2)California Academy of Sciences, (3)California academy of science*

Abstract: Species in the scorpion genus *Centruroides* (Scorpiones: Buthidae) are good candidates for the study of ecological niche partitioning because of their habitat plasticity, widespread geographic distribution, and presence of cryptic species. Currently, three species belonging to three subgroups of *Centruroides* are distributed along the Isthmus of Tehuantepec in southern Mexico, presenting a rare opportunity to study niche partitioning within a single genus. We examined the environmental, substrate, and habitat conditions of *Centruroides flavopictus* , *Centruroides gracilis* , and *Centruroides rileyi* within Estación de Biología Los Tuxtlas, west of the Isthmus of Tehuantepec. Our results demonstrate habitat partitioning occurs along humidity, temperature, and elevational gradients: individuals of *C. gracilis* were found in habitats of low humidity and high temperature, and were predominantly found on the substrate in human-mediated habitats; individuals of *C. flavopictus* were found in a larger range of humidity and temperature conditions within secondary and primary forest; and individuals of *C. rileyi* had the greatest habitat specificity, and were found in conditions of low temperature and high humidity on trees within primary forest. Furthermore, individuals of *C. rileyi* were found significantly higher in trees than those of *C. flavopictus* . This study represents the first example of niche partitioning within a genus of scorpion, and the first description of the ecological niche in an arboreal-specialist scorpion.

Environmental ESBL-Producing *Klebsiella Oxytoca* Carries a Multidrug Resistance Conjugative Plasmid Related to Clinical Isolates

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ruby Castillo*[1]; Amelie Garenaux[1] and Luis Mota-Bravo[2], *(1)University of California, Irvine, (2)University of California, Irvine MSP program*

Abstract: Antibacterial resistant pathogens cause the majority of hospital acquired infections, affecting about 2 million Americans every year. Of these infections 26,000 are caused by bacteria producing Extended Spectrum Beta-Lactamase (ESBLs), enzymes able to degrade a wide range of beta-lactam antibiotics. *Klebsiella oxytoca* is a bacterium that can cause serious infections in patients with a weakened immune system. Unrelated bacteria can share antibiotic resistance genes (ARGs) through conjugative plasmids, which are extrachromosomal DNA molecules that can be transferred between cells via cell-to-cell contact. Little is known about the presence of plasmids carrying ARGs in the environment. We hypothesize that environmental *K. oxytoca* are a source of conjugative plasmids containing ARGs. The resistance profile of an environmental *K. oxytoca* isolated in the US was established with a disk susceptibility test. Plasmids were extracted, sequenced using Illumina and Oxford Nanopore, assembled using Unicycler, and annotated using Geneious, Patric, CGE, and ISfinder. They were compared with sequences from the NCBI database using BLAST. A conjugation test was performed to identify conjugative plasmids. One plasmid, p1, was conjugative and carried a *blaCTX-M-15* gene coding for an ESBL. The p1 plasmid shared 100% coverage and 99.98% identity with two plasmids isolated from clinical strains in Canada. This study demonstrates the importance of studying antimicrobial resistance in the environment. Indeed, ARGs and plasmids found in the clinical setting, including plasmids carrying ESBL-encoding genes, can also be found in the environment in different parts of the world.

Cholera Toxin Disassembly By Thioredoxin-like Domains of Protein Disulfide Isomerase

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Antonio Torres*; Antonio Mele; David Caraballo Delgado and Ken Teter, *University of Central Florida*

Abstract: Cholera is a diarrheal disease prevalent in developing countries suffering from water poverty. This is due to the etiology of cholera, which is an infection due to ingestion of water containing *Vibrio cholerae* from fecal contamination. Cholera toxin (CT), a virulence factor released by *V. cholerae*, is comprised of two “A” subunits, CTA1 and CTA2, and a B pentamer. CT binds to GM1 on the surface of an infected individual’s cells and is internalized for delivery to the endoplasmic reticulum (ER) via vesicle carriers. In the ER, the disulfide bond linking CTA1 to CTA2 is reduced and protein disulfide isomerase (PDI) dislodges CTA1 from the rest of the toxin, allowing it to enter the cytosol. CTA1 then engages in a signal cascade that ultimately results in a diarrheal response.

PDI has four thioredoxin-like domains, but it is currently unknown which domains contribute to the disassembly of CT. The objective of this project was to understand the structural basis for CT disassembly by PDI. To achieve this goal, PDI deletion constructs containing various subsets of the domains were purified and run in an ELISA disassembly assay using plates coated with GM1 and CT. It was found that the two N-terminal thioredoxin-like domains were sufficient for CT disassembly.

These findings suggest that full-length PDI is not necessary for disassembling CT. Even an incomplete deletion construct can disassemble CT with comparable efficiency. This knowledge will lead to further experimentation that could, in the future, lead to the development of cholera treatments and preventatives.

Topological Domain Boundaries Regulate Local Gene Expression in Embryonic Cells of *Drosophila Melanogaster*

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Maria Jose Blanco-Salazar*; Rodrigo Arzate-Mejía; Sylvia Garza-Manero and Félix Recillas-Targa, *Instituto de Fisiologia Celular, National Autonomous University of Mexico*

Abstract: The mammalian genome is organized in Topologically Associating Domains (TADs) at the submegabase scale, where genomic regions inside a TAD interact frequently and are isolated by boundaries from regions located outside. Deletion of TAD boundaries allows ectopic enhancer-promoter interactions, which affects transcriptional programs and limb development. While TADs are observed in *Drosophila melanogaster*, there is contrasting evidence regarding the role of TAD boundaries in gene expression of the fly. To gain further insights into this issue, we selected a TAD of the *Drosophila* genome that encloses a single protein-coding gene called *tara*, by analyzing chromosome conformation capture data (Hi-C), and we asked whether these TAD boundaries regulate local transcription. We dissected the *tara* TAD boundaries using the CRISPR-Cas9 system in the S2R+ *Drosophila* embryonic cell line. We measured transcriptional levels of *tara* and neighboring genes by quantitative RT-PCR, finding a significant reduction of *tara* transcript levels in clones lacking both the 3´ and the 5´ boundaries, in comparison to controls. Interestingly, transcriptional activity of neighboring genes upstream and downstream the TAD of *tara* is also affected when boundaries were deleted, which may be explained by disrupted interactions with a previously reported superenhancer inside of the TAD.

Thus, we demonstrated that the TAD boundaries delimiting *tara* contribute to its transcriptional activity and that of neighboring genes, supporting a conserved role of TAD boundaries in the regulation of local gene expression. Nevertheless, future work is required to determine whether interactions within this TAD and with others are modified after removing its boundaries.

A Novel Region of Antibiotic Resistance Genes in Aquatic *Escherichia coli* Isolate Confers Resistance to Six Antibiotic Classes

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Camryn Zurita*[1]; Andrei Tatarenkov[2] and Luis Mota-Bravo[1], *(1)University of California, Irvine, (2)School of Biological Sciences, University of California, Irvine*

Abstract: Antibiotic resistance is a growing public health issue. Understanding the mechanisms behind the spread of plasmid borne resistance is crucial in the surveillance and treatment of bacterial infections. We hypothesize that aquatic environments are reservoirs of antibiotic resistance genes (ARGs) that contribute to the dissemination of these genes through horizontal gene transfer. The objective of this study was to identify the resistance profile and genetic content of an environmental *Escherichia coli* isolate. Isolate SW3232 was collected from Rock Creek pond in Kensington, Maryland and identified as *E. coli* by MALDI-TOF. The resistance phenotype was determined by disk diffusion tests. Plasmid annotation was completed using PATRIC, CGE, ISfinder and NCBI databases. Isolate SW3232 displayed resistance to six classes of antibiotics. The sequenced and assembled plasmid shows that the isolate contained one 127,496 bp plasmid. Analysis of the plasmid revealed a novel multidrug resistant region (MDR) containing eight ARGs flanked by several mobile genetic elements (MGEs). Bioinformatic analysis shows that sections of the MDR are found on plasmids of different incompatibility types belonging to several genera with 99% nucleotide similarity. Since the MDR described in this study has not been reported before, but contains regions similar to other isolates, this suggests that MGEs are responsible for the mobilization of ARGs. These findings provide evidence for transposition, as the genes are moving across genera and plasmid incompatibility types. More collection and genetic analysis of environmental isolates is needed to understand the mechanisms that contribute to the mobilization of ARGs in Gram-negative bacteria.

Identifying Rheumatoid Arthritis (RA)-Relevant Mirnas in Hispanic Patients

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kiara Esteves[*], *City University of New York John Jay College of Criminal Justice*; Lissette Delgado-Cruzata, *John Jay College of Criminal Justice*; Nickolas Almodovar, *John Jay College CUNY*; Milena Rodriguez-Alvarez, *SUNY Downstate Medical Center* and Maria Delgado, *Mount Holyoke College*

Abstract: Rheumatoid arthritis (RA) is an autoimmune disease that is characterized by joint inflammation, tenderness, and gradual disintegration of synovium that affects 1% of the worldwide population. Race/ethnicity disparities in RA clinical outcomes have been described and Hispanics with RA suffer from higher rates of disease activity and mortality than other populations. Epigenetic mechanisms have been suggested to play an important role in RA pathogenesis, and changes in microRNA (miRNAs) levels have been associated with RA. miRNAs are non-coding RNA responsible for the regulation of gene expression. We investigated levels of 800 miRNAs in 27 RA patients and 18 healthy controls, in a population 89% Hispanic. microRNAs were extracted from the serum circulating exosomes, measured blindly using Nanostring nCounter miRNA expression panels and analyzed using nSolver Analysis software. By applying stringent criteria, we identified 13 miRNAs that significantly differed ($p \leq 0.05$) between RA and non-RA individuals including 9 newly identified in this study. The top three miRNAs with the largest difference between cases and controls included *hsa-miR-223-3p* (cases=139.54±21.73 vs. control=401.32±18.48, p-value of 0.0212), *hsa-miR-451a* (cases=1123.78±284.36 vs. controls=1171.63±221.86, p-value of 0.0329), *hsa-miR-126-3p* (cases=82.62±11.67 vs. controls=48.04±5.98, p-value of 0.0137). Interestingly, all of these had been previously described as important in RA. We will conduct further analysis to determine whether the identified miRNA are associated with clinical RA characteristics. These findings have the potential to increase our knowledge of epigenetics of RA in Hispanics.

Do Xanthohumol Compounds Improve Metabolic Syndrome in Mice Via an Antibiotic Effect Against the Gut Microbiota?

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

June Winters[*1]; Yang Zhang[2] and Adrian Gombart[2], *(1)Fort Lewis College, (2)Oregon State University*

Abstract: Xanthohumol (XN), a prenylated flavonoid from hops (*Humulus lupus* L.), and its derivative tetrahydroxanthohumol (TXN) improve metabolic syndrome (MetS) and type 2 diabetes in diet-induced obesity animal models. XN and TXN reduce diversity of bacteria in the gut and this may occur via their well-characterized antimicrobial activities. These changes in microbiota composition affect immunity, inflammation, and gut barrier function. Antibiotic treatment in animals also improves MetS. We hypothesized that XN and TXN may improve MetS through an “antibiotic” effect on the composition of gut microbes and changes gene expression pathways similar to those pathways affected by antibiotic treatment. To test this hypothesis, we will compare ileum gene expression and biological pathways from XN and TXN-treated mice with those mice treated with antibiotics. Using bioinformatics analysis approaches, we compared ileum gene expression between mice fed a high fat diet (HFD) and mice who were fed a HFD with TXN and observed a decrease in immune response genes involved in inflammation and barrier function that are upregulated with obesity-induced barrier dysfunction. Our next step is to generate network pathways with GSEA using our gene list and network pathways from a publicly available gene list from mice treated with antibiotics. We will then compare the networks from the two conditions to determine if XN/TXN are affecting the same pathways as antibiotics. We expect that the pathways are similar and this finding would support our hypothesis that XN and TXN benefit the host through an “antibiotic” effect on the gut microbiota.

Toward Identifying a Novel Binding Site on the Human Serotonin Transporter through Computational Docking of VK03-51.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Payton Dupuis[*1]; L. Keith Henry[2]; Michael Tomlinson[2]; Krystal White[3]; Vivek Kumar[4]; Amy Newman[4] and Roxanne Vaughan[2], *(1)Montana State University, (2)University of North Dakota, (3)Palm Beach Atlantic University, (4)National Institute of Health*

Abstract: Selective serotonin reuptake inhibitors (SSRIs), such as S-citalopram (S-CIT), are antidepressants that block the reuptake of serotonin back into the presynaptic neuron. S-CIT can bind the serotonin transporter at a high-affinity (S1) and a low-affinity (S2) site. Characterization of a photoactivatable S-CIT analog, VK03-51, revealed a unique binding pattern consistent with it binding to S1 and a previously unknown site we term S3. To identify the S3 site, RosettaLigand was used to computationally dock VK03-51 into an inward-facing, ibogaine-bound, human serotonin transporter (SERT) derived from cryo-electronmicroscopy (PDBID 6DZZ). A total of 100,000 docked complexes were generated and scored, with the top 5% subjected to cluster analysis to identify probable binding sites. The structures were filtered by eliminating complexes where VK03-51 docking overlapped with S1 or S2 or in areas of the transporter inaccessible from the extracellular side. Additionally, the top VK03-51 complexes were compared to structures generated by parallel docking with the S-CIT analog VK03-83 which does not bind at S3 to perform a subtractive biding analysis. To facilitate subsequent biochemical discrimination of the binding sites, residues within 5Å of VK03-51 or the reactant azido N atom were determined for use in designing strategies for peptide mapping and substituted cysteine accessibility method analysis. Identification of the S3 site could have significant impact on serotonergic regulation based on its potential to allosterically alter transporter function without blocking substrate translocation offering a novel approach to modulate SERT function not currently available.

The Tsh Transcription Factor and the Transcriptional Co-Regulator Ctbp Interact in *Drosophila Melanogaster E*ye Development

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Kyle Helms* and Jennifer Curtiss, *New Mexico State University*

Abstract: Cell fate determination and proliferation need to be coordinated during development of multicellular organisms, and this requires tissue-specific gene transcription. Transcriptional co-regulators mediate between sequence-specific transcription factors and the transcriptional machinery to promote tissue-specific gene transcription. Current evidence suggests that the sequence-specific transcription factor, Teashirt (Tsh), and the transcriptional co-regulator, C-Terminal Binding Protein (CtBP), have roles in coordinating cell fate determination and proliferation during eye development in the fruit fly, *Drosophila melanogaster*. Whether these proteins interact physically during eye development has yet to be determined. We have used genetic and molecular tools to address this question. Over-expressing *tsh* in proliferating eye precursors results in loss of eye tissue, and loss-of-function mutations in *CtBP* suppress the effects of over-expressing *tsh*, suggesting that *tsh* and *CtBP* function in the same process during eye development. Furthermore, *in vitro* Glutathione-S-Transferase (GST)-pulldowns detect direct physical interactions between Tsh and CtBP, and co-immunoprecipitations from lysates of proliferating eye precursors confirm the interaction *in vivo*. These results suggest that Tsh and CtBP interact physically during eye development and that their interaction is important for proper eye development. We have used the genomic editing tool, Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR), to generate transgenic flies with an insertion of green fluorescent protein (GFP) into the *tsh* gene. Future experiments using this GFP-tagged *tsh* and mass spectrometry will help to identify any proteins complexed with Tsh/CtBP and provide further insight into to how this complex regulates proliferation during the development of the eye.

Immune Cell Alterations in the Deletion of Oxygen-Sensing Gene in Bone Cells

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Hanna Taglinao*; Betsabel Chicana Romero and Jennifer O. Manilay, *University of California, Merced*

Abstract: The purpose of this research project is to analyze the alterations in the immune cell development on mice with abnormal bone growth due to the gene deletion of the oxygen sensing gene, von Hippel-Lindau (*Vhl*). We hypothesize that bone growth can alter the immune cell compartments. Deletion of the *Vhl* gene in bone cells that express the gene *Dmp1* in osteocytes results in structural changes, such as high bone mass and a decreased bone marrow (BM) cavity. To delete this gene in *Dmp1* expressing cells, we utilized the Cre-Lox recombination system to conditionally knockout *Vhl* expressing cells in mice (VhlcKO). The structural changes in VhlcKO mice result in a reduction of conventional B cells, increased monocytes and granulocytes, and normal frequencies of T cells in the bone marrow. These results may indicate that *Vhl* may cause alterations in the bone marrow niche that affects B cells. Our next step is to test if these B cells are functional, and what are the alterations occurring in the bone marrow is leading to a B cell defect.

Using a Notch-Reporter Assay to Understand the Ability of Specific *NOTCH2NL* Alleles to Activate Notch Signaling

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Gifti Gemeda*[1]; Gary Mantalas[1]; Sofie Salama[2] and David Haussler[2], *(1)University of California, Santa Cruz - Genomics Institute, (2)UC Santa Cruz Genomics Institute and Howard Hughes Medical Institute*

Abstract: The main goal is to understand how the human specific gene NOTCH2NL affects neural development. Duplications and deletions in the region 1q21.1, which contains three NOTCH2NL genes, are associated with neurodevelopmental phenotypes such as microcephaly, macrocephaly, autism and schizophrenia. Notch signaling is essential for brain development, determining the timing and duration of neural progenitor proliferation and neural differentiation. The goal of this project is to understand the function of the various NOTCH2NL genes and alleles,

specifically their ability to activate the Notch pathway. Previous work has identified a surprising variety of alleles in healthy populations. Site directed mutagenesis and plasmid cloning is used to make the different alleles of NOTCH2NL. Previous work testing a small subset of these alleles has shown them to have varying potencies to enhance Notch signaling and interact with NOTCH receptors. We are using a CSL-Luciferase based Notch reporter assay to measure the ability of individual NOTCH2NL alleles to affect notch pathway activity. To determine the spectrum of NOTCH2NL alleles in the human population, Molecular Inversion Probes (MIPs) along with Illumina sequencing are used to assess the NOTCH2NL alleles present in a large number of individual genomes. By understanding the variation of NOTCH2NL in the general and affected population we will better understand the association of genotype and phenotype of NOTCH2NL and neurodevelopmental disorders.

Embryonic Exposure to Ibuprofen Causes Neural Crest Defects in Vertebrate Embryos

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Nikolas Morrison-Welch*, *California State University Northridge*; Sasha Machulsky, *California State University, Northridge* and Crystal Rogers, *Univeristy of California Davis*

Abstract: Over the counter (OTC) medications undergo a rigorous process proving that they are safe for adult consumption and use without the supervision of a medical practitioner. Such studies lack information regarding the safety of these medications on developing embryos. Our long-term goal is to determine how non-steroidal anti-inflammatories (NSAIDs) such as aspirin, ibuprofen, and naproxen affect embryonic viability by testing stage-dependent mortality rates, developmental delays, and phenotypic abnormalities after treatment. In this study, we have analyzed the effects of exposure to the cyclooxygenase (COX) inhibitor, ibuprofen, in two vertebrate species, chicken (*Gallus gallus*) and axolotl (*Ambystoma mexicanum*). We hypothesized that exposure to ibuprofen would create global embryonic defects. Using multiple concentrations, we tested the effects of ibuprofen on a vertebrate-specific stem-like cell type, neural crest cells. Neural crest cells create the craniofacial bone and cartilage, pigment cells, and the peripheral nervous system. Abnormal development of neural crest cells causes defects such as cleft palate, albinism, and deafness. Using immunohistochemistry we identified that ibuprofen exposure created morphological developmental anomalies in both species, increased expression of the neural crest progenitor marker, PAX7, and reduced the expression of the definitive neural crest marker, SOX9, suggesting that signaling through the COX pathway is necessary for the progression of neural crest cell development. Many such teratogenic defects are preventable. Using comparative anatomical, molecular, and biochemical analyses we hope to determine if the detrimental effects are specific to ibuprofen or are a global NSAID phenotype.

Embryonic Exposure to Ibuprofen Defects in Neural Crest Derivatives in Vertebrate Embryos

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Nikolas Morrison-Welch[1]; Sasha Machulsky*[1] and Crystal Rogers[2], *(1)California State University, Northridge, (2)Univeristy of California Davis*

Abstract: Exposure to everyday chemicals such as over the counter (OTC) medications can have detrimental effects on developing embryos, and 80% of pregnant women report using over the counter or prescription pain medication during gestation. Here, we are testing the effects of exposure to non-steroidal anti-inflammatories (NSAIDs) such as aspirin, ibuprofen, and naproxen, that all function to inhibit the cyclooxygenase (COX) pathway, on developing vertebrate embryos. Our project focuses on understanding the effects of NSAID exposure on the development of neural crest cells and their derivatives including the craniofacial bone and cartilage and the peripheral nervous system. Neural crest cells create multiple adult tissue derivatives and based on our preliminary data, we hypothesize that exposure to NSAIDs will create abnormalities including craniofacial clefts and peripheral nerve defects. Our long-term goal is to determine the phenotypic, survival, and molecular responses to NSAID exposure. Here, we tested the effects of ibuprofen and quantified morphological phenotypes in addition to using immunohistochemistry to identify molecular-level changes after ibuprofen exposure. We determined that exposure to ibuprofen caused microcephaly, neural tube closure defects, and high death rates in both organisms. In addition, in chick embryos, ibuprofen increased expression the neural crest progenitor marker, PAX7, and reduced the expression of the definitive neural crest marker, SOX9. Future studies will test if the COX pathway is necessary for progression of neural crest cell development and the formation of the peripheral nervous system.

Differential Expression of Novel Genes during Intestinal Regeneration in the Sea Cucumber Holothuria Glaberrima

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Joseph Salem-Hernández*; Arisnel Soto-Acaba; David Quispe-Parra; Joshua Medina-Feliciano and José E. García-Arrarás, *University of Puerto Rico - Rio Piedras Campus*

Abstract: Echinoderms have been widely used as animal model systems to study organogenesis. Whereas gene analyses and expression studies are scarce, the cellular mechanisms driving the sea cucumber's potential to regenerate their autotomized intestines have been widely described by us and others. In the present study, we further strengthen our previous analyses by characterizing transcriptional changes in intestinal tissue of the sea cucumber *H. glaberrima* via semiquantitative RT-PCR of various genes. Particularly we characterize *Orpin* genes, novel putative-calcium binding proteins associated to intestinal and nerve regeneration. Sea cucumbers 1- and 3-days post-evisceration mesenteric tissue was used for RNA extraction, purification, and cDNA synthesis. Furthermore, we optimized two sets of primers for Orpin genes (*Orpin* A and *Orpin* B), which appear to be 90% similar between themselves. Experimental validation by RT-PCR suggests that *Orpin* A and *Orpin* B present a differential expression during the 3-day post-regenerative stage when compared to non-regenerative tissue. We hypothesize that *Orpin's* expression might be regulated by alternative splicing since multiple bands can be observed in the RT-PCR product. Future directions include assessing the validity of our alternative RNA splicing hypothesis through further bioinformatic analyses and molecular experiments. In summary, assessing these gene profiles is crucial for further in-depth analyses of molecular markers, as well as elucidating new molecules associated to different processes of regeneration.

Effects of Pharmacological Inhibition of Nox-Derived ROS in Early Intestinal Regeneration in *Holothuria* G*laberrima*

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Christian Andino Del Valle*[1]; Valentina Grillo-Alvarado[2] and José E. García-Arrarás[2], *(1)Ana G. Méndez University - Cupey Campus, (2)University of Puerto Rico Río Piedras Campus*

Abstract: Sea cucumbers are known for their ability to completely regenerate lost body parts, such as their digestive tube, radial nerves, respiratory tree, among others; processes regulated by molecular signals. Among these, are the Reactive Oxygen Species (ROS), known to function as signals that initiate regenerative processes [1]. In our animal model, the sea cucumber *Holothuria glaberrima* (*H. glaberrima*), the process of regeneration begins after inducing the expulsion of its digestive system (evisceration). Afterwards, the wounded mesentery, previously attached the digestive tube, begins healing and a blastema-like structure gives rise to an intestinal rudiment, forming a newly functional intestine. This process depends on multiple cellular events, including cell proliferation, apoptosis, cell dedifferentiation, and remodeling of the extracellular matrix [2]. The aim of our study is to determine the possible role of ROS during early intestinal regeneration, by inhibiting NADPH oxidase (NOX), an important enzyme responsible for ROS production. Evisceration of sea cucumbers was induced by KCl injection; VAS2870 (the NOX inhibitor) was injected immediately after the evisceration. DMSO was used as control. At 4 days post evisceration (4 dpe), BrdU was injected in all animals. Then, they were dissected (at 5dpe), fixed in 4% paraformaldehyde (4% PFA), cryosectioned, and processed for indirect immunofluorescence, by using an anti-BrdU antibody. Cell proliferation and the rudiment area of the mesentery were reduced, for animals treated with VAS2870 ($p<0.01$). These results suggest a plausible role of ROS during early intestinal regeneration and may contribute to the establishment of the road map of these events.

Deep Sequence Analysis of *C. Elegans* Expressing Tdp-43, an Amyotrophic Lateral Sclerosis Associated Disease Protein

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Helena Puccini de Castro*; Cindy Voisine; Rogelio Alvarado; Shagufta Khatoon; Kimberly Nu-tall and Yuriy Khlopas, *Northeastern Illinois University*

Abstract: The functions of proteins vary among transport of substances, storage, digestion and other essential activities. Proteostasis maintains the synthesis, folding, and clearance of proteins within cells. When proteostasis capacity is overwhelmed/damaged by stress, various diseases emerge. Amyotrophic lateral sclerosis (ALS) is a progressive neurodegenerative disease, where misfolded proteins (e.g. protein TDP-43) accumulate in nerve cells in the brain and spinal cord. We want to determine how neuronal pathways change in response to the presence of the ALS disease protein TDP-43. To do this, we are using the nematode *C.elegans*, a transparent worm that reaches approximately 1mm during adulthood, has a short lifespan, and a rigid differentiation pattern. We expressed human TDP-43 in *C. elegans* neurons and observed a decline in neuronal function. Actively translated mRNAs in *C. elegans* that express neuronal TDP-43 will be compared to the actively translated mRNAs in wild type worms to identify differentially translated genes. We anticipate that our analysis will uncover the efforts cells undergo to rebalance proteostasis in the presence of aggregation-prone disease proteins. With this knowledge, recommendations can be provided to control or avoid diseases affected by imbalances in proteostasis.

Investigation of RNA Polymerase II Elongation Factor *Ell2* regulation By the Cataract-Linked RNA-Binding Protein Celf1 in Mouse Lens Development

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Francisco Hernández-Vargas*; Sandeep Aryal; Archana Siddam and Salil Lachke, *University of Delaware*

Abstract: The ocular lens, a transparent tissue, enables high-resolution vision by focusing light on the retina. Lens opacity is termed cataract and is the leading cause of blindness worldwide. To identify cataract-linked genes, we applied a novel bioinformatics approach called iSyTE (integrated Systems Tool for Eye gene discovery). iSyTE predicts that the gene *Celf1,* which encodes an RNA-binding protein, is highly enriched in the mouse lens at specific developmental time points, suggesting a critical function of Celf1 in mammalian lens development. In fact, *Celf1* lens-specific conditional knockout mice exhibit severe lens defects during embryonic development and onset of congenital cataract further supporting this hypothesis. To gain insight into Celf1-mediated cataract pathology, we performed high-throughput RNA-sequencing and identified a new factor, *Ell2* (Elongation factor for RNA Polymerase II 2), to be abnormally upregulated in *Celf1* deficient mouse lenses. Celf1-antibody based RNA-immunoprecipitation of wild type mouse lenses shows that Celf1 directly associates with *Ell2* mRNA indicating a potential regulation of *Ell2* gene expression by Celf1. To further investigate the function of Ell2 in the lens, I generated *Ell2* lens-specific conditional knock-out mice ($Ell2^{cKO/cKO}$) using Cre-lox recombination reaction. Interestingly, phenotypic analysis demonstrates that $Ell2^{cKO/cKO}$ mice present with abnormally smaller lenses compared to age-matched wild-type and heterozygous littermate controls. In summary, these results identify *Ell2* as a potential key regulator of mammalian lens development and suggest its involvement in Celf1-mediated cataract pathology. This study is significant because it provides a new pathological mechanism for cataract formation by a transcription elongation factor and an RNA-binding protein.

Human Kidney Organoids As in Vitro Model for the Study of Renin Regulation

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Pierina Barturen-Larrea*[1]; Ela Contreras-Panta[2]; Alejandra I. Romero-Morales[2]; Vivian Gama[2] and Jose A. Gomez[1], *(1)Department of Medicine/Clinical Pharmacology Division, Vanderbilt University Medical Center, (2)Department of Cell and Developmental Biology, Vanderbilt University*

Abstract: Renal renin expression plays a critical role in kidney development, hypertension progression, and kidney injury. In the United States about 44% of the population suffers hypertension and of those 50% does not respond to current available therapies. We modified a protocol to generate human kidney organoids from human induced pluripotent stem cells (hiPSCs). Kidney organoids were characterized by the expression of glomerular (WT1), tubules (CDH1 and LTL), and vessels (PECAM-1) cellular markers. We hypothesize that human kidney organoids will serve as a good in vitro model for the study of renin expression control. To stimulate the increase in renin expression, we treated kidney organoids with cyclic AMP, low sodium media, or exposed them to hypoxia conditions. We measured renin protein and mRNA expression. Renin mRNA expression increased after 7 days of cyclic AMP treatment as well as after 6 and 12 hours of exposure to hypoxia. We are currently evaluating renin protein expression and the functionality of Juxtaglomerular cells to release renin after changes in calcium concentration to assess the physiological relevance of these cells. An opposite result would suggest a poor glomeruli maturation. We are also developing protocols to improve organoid maturation and vascularization, through flow optimization or co-culture with mice tissue. Our results demonstrated that renin is expressed in the hiPSC-derived kidney organoids and open the possibility to use this model for renin regulation studies in development and disease, and for drug screening and regenerative therapy.

Uterine Position Effect in Fetal Growth Pattern of Rats after Environmental Exposure to Plastics

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Andrés Rivera-Ruiz*[1]; Chelsea Cary[2]; Sara Fournier[2] and Phoebe Stapleton[2], *(1)Universidad Ana G. Méndez, Recinto de Gurabo, (2)Rutgers University*

Abstract: Rat models are commonly utilized in developmental biology studies because of the similarities between rat and human development, both sharing hemochorial placentation. However, the experimental assessment of fetuses derived from multi-pup rat litters in comparison to singlet human pregnancy provides scientific difficulty. Little research has been done to find out the potential effects of the uterine position in the fetal growth of rats and if these effects vary after environmental exposure. The purpose of this study was to assess rat fetal growth overall and based on anatomical uterine positioning (ovarian, middle, and vaginal thirds) within the uterine horn after maternal pulmonary exposure to nanopolysterene particles (NP) late in gestation. We hypothesize that maternal exposure to NP would inhibit fetal growth and fetus implanted in the middle third of the uterine horn(s) would be larger than those on the ends. Pregnant rats (n=9-12) were exposed to NP through intratracheal instillation at gestational day (GD) 19 and sacrificed on GD 20, along with a sterile saline control group. The anatomical uterine positioning of the fetuses was identified, and their weights were measured and recorded. Preliminary data indicates pups from exposed dams were significantly smaller than control (2.59±0.02g vs. 2.68±0.02g, respectively). However, this outcome was inconsistent throughout the uterine horn and is based on significant anatomical positioning differences at the vaginal end of the right horn and middle of the left horn. These results indicate uterine positioning must be taken into account to achieve accurate conclusions from reproductive toxicological studies utilizing rodent models.

Wnt1 Transcriptional Regulation and Vertebrate Nervous System Development

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Kamilah Walker-Charles* and Arne Lekven, *University of Houston*

Abstract: The Wnt pathway is a signaling pathway that regulates cell fate and patterning; mutations in the Wnt pathway are known to cause several human diseases, including cancer. Wnt1 is active in the midbrain-hindbrain boundary and even though it is crucial to the normal development of the brain in vertebrates, how the Wnt1 pathway regulates cell fate, how the Wnt1 gene is itself transcriptionally regulated, and how other pathways regulate Wnt1 is unknown. The Lekven Lab has identified two enhancers, sequences that regulate other genes, that could be responsible for regulating Wnt1 in zebrafish: Conserved Non-coding Element (CNE)20 and CNE27, both of which are completely sequenced. Using zebrafish, transgenic reporter fish with different deletions of the CNE20 enhancer have been developed. Thus, it can be determined whether these parts of the enhancer may be vital to Wnt1 regulation by seeing if their absence causes the reporter gene expression from the transgenes to behave irregularly. From this data, we will infer specific activities that can be attributed to specific parts of the enhancer. The other part of this project seeks to conclude if there are specific transcription factor binding sites (TFBSs) within the enhancers CNE20 and CNE27 that are unique to each respective sequence. Using regulatory sequence analysis tools (RSAT), several possible TFBSs were identified, and going forward we will be testing the aptness of these TFBSs by altering their expression to conclude if they regulate the CNE20 and CNE27 enhancers.

Spontaneous Fractures of the Humerus Bone in the Absence of Stat3

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Noah Lopez*; Diana Rigueur and Karen Lyons, *University of California, Los Angeles*

Abstract: Signal Transducer and Activator of Transcription 3 (STAT3) is a transcription factor that is involved in cell proliferation, migration, and apoptosis. STAT family members are activated by cytokines and growth factors such as Interleukin-6. The Interleukin-6/STAT3 (IL-6/STAT3) signaling pathway is essential for proper immune response to invading pathogens and viral infections. Recent literature has found that the IL-6/STAT3 signaling pathway also plays an imperative role in the development of cartilage and bone. STAT3 thus has high implications as a therapeutic target for rheumatoid and osteoarthritis. However, the direct role and downstream effectors of STAT3 signaling in cartilage have not yet been clearly delineated. Through histology, skeletal preparations, and microCT scanning, our data show that conditional loss of Stat3 in mouse cartilage, via the Col2-Cre driver, is essential for proper growth plate formation in the limbs of the skeleton. Furthermore, loss of STAT3 results in spontaneous bone fractures of the humerus. Interestingly, these severe fractures are rapidly repaired, indicating an untapped mechanism for regeneration in bone. These studies will elucidate the imperative role the Stat3-mediated pathway plays in cartilage and in modulating the humerus during endogenous development and repair.

A Novel Zebrafish Mutant Reveals New Insight into the Regulation of Cilia Motility and Body Axis Formation

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Samuel Craig*; Zoe Irons; Elizabeth Bearce and Daniel Grimes, *University of Oregon*

Abstract: Motile cilia are responsible for several critical functions in development, including left-right patterning and cerebrospinal fluid flow. Their motility depends on the assembly of outer dynein arms: ATPases which power ciliary beating. Defects in dynein arm function occur in Primary Ciliary Dyskinesia, a disorder affecting 1:15,000–30,000 human births. Daw1 is a cytoplasmic protein thought to be required for cilia beating by controlling the import of dynein arms into cilia. Here, we use zebrafish as a model to understand Daw1 function during development and growth. We characterize $daw1^{b1403}$ mutants, a new *daw1* mutant line harboring a 2-amino acid deletion in a conserved region of the protein generated by CRISPR mutagenesis. We observe defects associated with motile cilia dysfunction in $daw1^{b1403}$ mutants, including otolith abnormalities, left-right patterning defects, and abnormal body axis curvature. Surprisingly, however, $daw1^{b1403}$ mutants exhibit recovery of body curve defects later in development; something we find to coincide with late-onset beating of cilia in the central canal of the neural tube. Consequently, we hypothesize that Daw1 is not essential for cilia motility per se, but only for timely onset of beating over developmental timescales. Later, we find that a small proportion of $daw1^{b1403}$ mutants develop abnormal three-dimensional spinal curvatures, something highly similar to the human condition of idiopathic scoliosis. This suggests that body axis straightening during early development is essential for preventing adult spinal curves in zebrafish. Ultimately, characterization of the $daw1^{b1403}$ leads to a greater understanding of abnormalities resulting from defective cilia motility and mechanisms of Daw1 function.

Impact of Natural Disasters on the *Ostrea Lurida* in the Southern California Estuary

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Brandon Quintana*; Hunter Lenihan and Erin Winslow, *University of California, Santa Barbara*

Abstract: The Olympia Oyster, *Ostrea lurida*, is the only oyster species native to the West coast of North America. *O. lurida* is a foundational species providing a myriad of ecosystem services. Populations ranged across the west coast, but declined due to development and pollution. The Carpinteria Salt Marsh, was home to one of the largest natural populations of *O. lurida* in Southern California. Oysters were found in 2017 but the Montecito Mudslides of 2018 covered the marsh with debris, killing oysters. This study explores impacts of the 2018 debris flow on *O. lurida* populations in Carpinteria, and restoration bottlenecks limiting their recovery. In order to investigate this, surveys and recruitment experiments were done on the oyster population.

Our annual surveys indicated a 90% decrease of *O. lurida* populations post debris flow. An ArcGIS map was made from survey data, and represents how *O. lurida* populations have changed through time. From recruitment experiments, involving natural substrate and artificial substrate, oyster larvae preferred artifical substrate. These findings inform mangement and increase oyster populations before they become locally extinct in Carpinteria. Using the survey map and locations of artificial substrate restoration work can begin where both exist and expand the area *O. lurida* occupies over time. The decline of *O. lurida* has been a pressing issue within the field of restoration ecology. Still, researchers have not investigated the effects natural disasters have on this decline. The impact of natural disasters on ecosystems becomes increasingly important as disasters become more frequent due to climate change.

Does Analyzing Bulk Bone for Organic Carbon and Nitrogen Isotopes Return Similar Results to Analyses of Isolated Collagen?

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Pedro Valencia Landa*; Robin Trayler and Sora Kim, *University of California, Merced*

Abstract: Stable Isotopes of carbon and nitrogen from bone collagen are commonly used as indicators of diet and ecology for a variety of modern and fossil mammals. While nitrogen is present only in bone collagen, carbon is present both in the organic (collagen) and inorganic (mineral) phases of bone. Currently, demineralization of bone is both time consuming and may lead to undesirable damage of the extracted collagen, potentially altering isotope compositions. We compared isotope compositions from demineralized and unaltered bone to quantify the effect and necessity of demineralization. We selected samples of bone and dentine from modern gray wolves (*Canis lupus*) and a modern domestic goat (*Capra hircus*). An aliquot of each sample was demineralized using 0.1 M HCl. We analyzed the nitrogen and carbon isotope composition of the extracted collagen and the bulk material (bone, dentine) using a Costech Elemental Analyzer. Preliminary results show that demineralization shifted δ^{13}C values significantly lower and did not significantly shift δ^{15}N values. Therefore, we recommend demineralizing bone collagen before analysis of nitrogen and carbon isotopes is made.

Characterizing Potential Tetrodotoxin Resistance in Pacific Chorus Frogs, *Pseudacris regilla*

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Katherine Montana*; Rebecca Tarvin and Valeria Ramírez-Castañeda, *University of California, Berkeley*

Abstract: Animals that frequently encounter toxins often evolve toxin resistance. While toxic prey select for resistant predators, physical contact between an organism and a toxin in its environment may also drive this phenomenon. We hypothesized that resistance to tetrodotoxin (TTX) may have evolved in Pacific chorus frogs (*Pseudacris regilla*) when they live in close contact with *Taricha* spp. that use TTX for chemical defense. We tested this prediction by sequencing the muscle voltage-gated sodium channel gene $\mathrm{Na_v}$1.4 (SCN4A) in *P. regilla* specimens that are sympatric with *Taricha spp.* to look for amino acid (AA) substitutions that may confer TTX resistance. Results show a substitution in the p-loop of $\mathrm{Na_v}$1.4 in the *P. regilla* samples sequenced, also present in the snake *Rhabdophis tigrinus* and connected to TTX resistance. Variation in several other AA substitutions may further support weak resistance, but we found no AA substitutions known to provide high levels of resistance. To assess potential for TTX exposure, we surveyed *Taricha* and *Pseudacris* abundance in Bay Area ponds. Preliminary data suggest that the abundance of *Taricha* spp. peaked in early February. Observations of *P. regilla* were rare. iNaturalist data predict that the mating season of *Taricha* spp. peaks in March while the mating season of *P. regilla* peaks in April. Thus, breeding activities of *P. regilla* and *Taricha* spp. do not heavily overlap, suggesting *P. regilla* may not often interact with newts during the height of their breeding season and may not experience high levels of TTX in the environment.

The Chemical Sensing of Disease Vector Mosquitoes

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Kim Ha*; Jeffrey Riffell and Eleanor Lutz, *University of Washington, Seattle*

Abstract: Several species of mosquitoes are carriers for life-threatening diseases such as malaria, Zika and Dengue. The ability of adult mosquitoes to search for human hosts and transmit disease is affected by their size and fertility, which correlates to larval foraging behavior. Targeting larvae may be more effective in improving public health since the larvae are concentrated and immobile in this stage. To improve current methods of disease vector management, we are

interested in studying how different species of disease vector larvae navigate to chemical cues, and determining if behavioral differences exist among these disease vectors. We are also interested in identifying how the habitat and environment have influenced the search behavior of these mosquitoes. We used video tracking to investigate larval behavior when foraging or avoiding a repellent substance for four different species of mosquitoes: *Aedes aegypti, Aedes albopictus, Anopheles arabiensis,* and *Anopheles coluzzii.* We expect different foraging behavior between genera and similar behavior between sub-genera because the sub-genera share similar evolutionary histories and thus, similar habitats. We found significant differences between species in behavioral metrics such as time spent moving, foraging behavior, and repellent avoidance. These results suggest there is more variance in mosquito larval behavior than previously known. This suggests that altering control strategies for each species may make larval mosquito control more effective. The implications of investigating these disease vector species may lead to improved applications of larvicides by identifying the ideal location and quantity of larvicide to add to water sources to match larval foraging behavior.

"Evidence of Horizontal Gene Transfer in the Pea Aphid Acyrthosiphon Pisum"

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Denver Nicole Cooper* and Jennifer Kovacs, *Spelman College*

Abstract: The purpose of this study is to understand the role of horizontal gene transfer (HGT) in eukaryotic evolution. HGT is known to be widespread in prokaryotes and allows for the rapid acquisition of traits for mutation and gene duplication. HGT can explain how genes are independently transferred to multiple unrelated species. More recently, it has been found that HGT has allowed for the independent acquisition of traits in multiple distantly unrelated species in a variety of multicellular eukaryotes. In this study, HGTs will be studied to see if a gene is transferred among niche-sharing eukaryotic species. An ecological niche is a role a species has in its environment regarding how it survives, how it gains nutrition, and how it reproduces. A species' niche includes all of its interactions with biotic and abiotic factors in its environment. The study aims to discover if HGTs are shared by related niche-sharing species and absent from more closely related, but non-niche sharing species or if HGTs provide ecologically relevant traits to their host species. In this study, we used a newly designed bioinformatic pipeline to identify shared HGTs in the genome of the pea aphid *Acyrthosiphon pisum* and other phloem-feeding arthropods. This will test the prediction that shared HGTs are more likely to be found in distantly related, niche sharing species than in closely related, non-niche sharing species. This research will aid in discovering the unique relationship between niche-sharing species and their genetic makeup

"Host Responses to Low-Dose Pathogen Priming in House Finches"

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Guadalupe Ceja* and Dana Hawley, *Virginia Polytechnic Institute and State University*

Abstract: Many species in wild populations are exposed to variations in frequency and dose of pathogens that can spread infectious diseases amongst populations. *Mycoplasma Gallisepticum* (MG) is a novel pathogen house finches and causes severe cases of conjunctivitis, impacting the birds' ability to see and evade predators. Finches are known to be exposed to frequent low doses of MG while feeding and socializing around bird feeders, which serve as hotspots for MG. The MG-finch model for researching recurrent pathogen exposures and disease dynamics can serve as a model for various host-pathogen interactions, like in the case of humans with the mycoplasmic infection "walking pneumonia."

The goal of the project was to see how low-dose exposures at a young age modulate the response to a low-dose, secondary exposure later in life. In this experiment, birds that were primed with varying doses of MG were re-inoculated with a secondary dose 34 days later in order to see what priming level would best prepare them with immune protection against a secondary infection and reduce clinical signs (visible conjunctivitis). This was quantified using ELISA antibody testing from eye swab samples, DNA extractions from blood, clinical eye scoring, and qPCR.

Birds that were given high primary doses demonstrated significant levels of protection against a broad range of dose levels in a secondary infection. However, as shown in qPCR and ELISA results, birds that received a low primary dose still maintained immune protection and had lower clinical signs when infected with a secondary low dose of MG.

Phenotypic Plasticity in Root Architecture Under Differing Nitrogen and Water Availabilities in *Baccharis Salicifolia*

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Miguel Ochoa*; Summer Marsh; Gregory Vose and Travis Huxman, *University of California, Irvine*

Abstract: As droughts in California become more severe, understanding how native populations will respond, adapt and perform is crucial to conservation success. When compounded with elevated concentrations of soil-borne nitrogen from anthropogenic-based deposition, water availability in plants may drive plasticity in their root morphologies. In this study, a genome-wide (multi-population) representation of the riparian coastal sage scrub species *Baccharis salicifolia* (colloquially known as mulefat) was used to model trends in the plasticity of belowground structural architecture in response to

resource availabilities. Individuals from throughout the plant's natural distribution were sampled and propagated in favorable conditions until ready for transplant. After, individuals were randomly separated into one of four treatments consisting of a combination of low and high water and nitrogen, respectively. Propagation facilitated cloning and WinRHIZO software was used to scan root structures. Individuals were also subjected to a simulated drought, where a zero-water time-to-death scenario was used to determine plant performance under severe drought conditions. Though preliminary, current collected data suggests that *B. salicifolia* exhibits a plastic behavior in regard to root morphology, root-shoot biomass allocation patterns, and chemical composition (carbon-to-nitrogen ratios). Differences in plastic responses arising from a plant's location of origin, sex, and ontogeny is also expected. Final data to be collected and analyzed for publication in fall 2020.

Whydah You Have to Have Such a Big Vocabulary? Using a Syllable Library to Compare Song Dialects of Southern California and Africa Pin-Tailed Whydahs (*Vidua macroura*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Sydnee R. Dunn* and William J. Hoese, *California State University, Fullerton*

Abstract: The pin-tailed whydah (*Vidua macroura*) is a passerine songbird, native to Africa that has recently established a breeding population in southern California. The pin-tailed whydah is an obligate brood parasite and lays its eggs in the nests of other species. Songbirds typically learn their song from conspecific males, though other brood parasites in the family Viduidae mimic their hosts. Song is culturally transmitted and varies over time and space. Thus, a newly established population of pin-tailed whydahs may differ from its source population. We hypothesized that pin-tailed whydahs in southern California would sing different songs compared with individuals in their native African range. We recorded songs from males in southern California, collected recordings from males in Africa, and are building a syllable library to compare vocalizations in order to document how they differ. Preliminary results based on the characterization of one southern California male (50 songs) and one Africa male (10 songs) indicate that these birds share some syllables, while other syllables are distinct to each region. Therefore, California birds may have diverged via cultural evolution from their native dialect and may be influenced by their host species during song learning. Investigating song in newly established populations of pin-tailed whydahs may provide insight into how this species persists in its new habitat.

Collared Peccary Wallows and Their Effect on an Amphibian Community in a Lowland Tropical Forest in Costa Rica

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alondra Medina*[1]; T. Mitchell Aide[1] and Kelsey Reider[2], *(1)University of Puerto Rico, Rio Piedras, (2)Murray State University*

Abstract: Environmental change and anthropogenic activities have caused widescale biodiversity loss in the tropics. Medium-to-large mammals, including peccaries (Tayassuidae), are threatened with extirpation, habitat loss and extinction. Peccaries act as ecosystem engineers for amphibians by creating and maintaining aquatic microhabitats called wallows, but further research is needed to fully understand this relationship. In this study, we assessed the herpetological community composition in wallows created by the collared peccary (*Pecari tajacu*) in a lowland wet forest of northeastern Costa Rica. We compared species richness between peccary wallows and the adjacent leaf litter matrix using multiple detection methods. We complemented standardized visual encounter surveys with passive acoustic monitoring to compare community composition and richness in wallows and paired control plots. We found a total of 15 amphibian and reptile species occupying wallows and 12 species in leaf litter plots for a combined total of 20 species. NMDS results show no significant difference of composition at the community level. However, using occupancy analyses, we found individuals who significantly showed preference for wallows (*Cruziohyla sylviae*, *Kinosternon leucostomum*, *Norops oxylophus*, *Smilisca baudinii* and *Smilisca phaeota*) or understory plots (*Dendrobates auratus* and *Sphenomorphus cherriei*). Species accumulation curves showed greater detection efficiency using acoustic monitoring (13 spp.), than leaf litter surveys (7 spp.) and visual encounter surveys (6 spp.). Our study shows that collared peccaries serve as ecosystem engineers for the herpetological communities in northeastern Costa Rica and suggests that if their populations continue to decline, it could negatively impact amphibians and reptiles in lowland tropics.

Diet Analysis of Native and Non-Native Ranid Species in Sierra County, New Mexico

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Mariangel Varela* and Wiebke Boeing, *New Mexico State University*

Abstract: A decrease in the amphibian population has been recognized since the 1970's and continues to be observed across the nation with causes varying from environmental changes to direct human involvement, including the introduction of invasive species. The invasive bullfrog (Lithobates catesbeianus) has been observed at the Ladder Ranch in Southern New Mexico where the federally endangered Chiricahua Leopard frog (Lithobates chiricahuensis) and its cousin the Plains Leopard frog (Lithobates chiricahuensis), currently reside. A study was done in the area to explore the potential impact the bullfrogs have on the native frogs. We conducted a diet analysis to determine diet overlap between the three species. Using a capture and release method in conjunction with a technique known as gastric lavage, we found that the diets consisted of mostly flying insects with bullfrogs also preying on birds, fish, and small amphibians. Overlap in diet preference was observed between the native and invasive frogs. These results support the possibility of predation and competition between the native and invasive frog species. Major efforts have been made to understand the declining amphibian numbers throughout the world. Our study allows for a further understanding of what might be causing the decline of the frogs within the area and what could be done to prevent their disappearance.

Novel DNA Capture Method Enables Sequencing of Mitochondrial Genomes and Sex Markers of the Southern River Otter (*Lontra provocax*) Using Scat and Other Degraded DNA

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Aurora G. Trejo*[1]; Lillian D. Parker[1]; Susette Castañeda Rico[1]; Jessica Quinta[1]; Margad-Erdene Ochirbat[1]; Nancy R. McInerney[1]; Maximiliano A. Sepúlveda[2] and Jesús E. Maldonado[1], *(1)Center for Conservation Genomics, Smithsonian Institution, (2)Departamento de Conservación de la Diversidad Biológica, Corporación Nacional Forestal*

Abstract: Recent advances in genomic research have allowed scientists to develop tools to assess the status of imperiled wildlife populations. Traditionally, this research requires high quality DNA collected from live animals, including blood, hair, or skin samples. Unfortunately, many endangered species are rare, elusive and difficult to capture, and developing tools that can help monitor their populations is imperative for conservation efforts. The southern river otter (*Lontra provocax*) is an endangered South American mammal with declining population sizes due to river system alterations and the introduction of the invasive mink into their habitat. Otter population sizes are poorly known and we aimed to address this knowledge gap by developing non-invasive methods that use DNA samples extracted from otter scat for genomic sequencing. We hypothesized that we would be able to sequence whole mitogenomes and a sex chromosome gene to study their genetic diversity, population structure and sex ratios. We designed probes to enrich these markers in 4 otter species (*L. provocax*, *L. canadensis*, *L. longicaudis*, and *L. felina*) and in the invasive American mink (*Neovison vison*). Preliminary analysis of our Illumina MiSeq® sequencing run reveals a high number of mitogenome sequence reads across all samples, indicating that the capture protocol was successful. Our next goal is to test the utility of these probes on otter scat samples as well as on museum specimens. Our method increases the potential of sequencing degraded material from otters, which ultimately will enhance our knowledge of southern river otter population health and empower conservation leaders.

Scolytine Species Distribution at Varying Elevations in a Costa Rican Montane Cloud Forest

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

David Hoekman and Natalie James*, *Southern Nazarene University*

Abstract: Due to its inverse relationship with temperature, elevation is a driver of biodiversity (Röder et al, 2016). Following a preliminary study by Dr. Derek Rosenberger et. al, the researchers in the current study measured abundance and diversity of Scolytinae (bark beetles) across a 1000m elevation gradient in a primary montane cloud forest in Costa Rica. It is hypothesized that beetle number and species variation will lessen as elevation increases. 20 traps were placed along two trails, every 50 meters in elevation from ~3050 meters to ~2120 meters, between January and March 2020. Insects were collected for approximately a week at a time, twice, to ensure ample collection for analysis. Beetles from both sampling rounds were photographed and examined to identify each species present. 776 beetles were collected from both rounds of collection, 260 from the first round, and 516 from the second. In general, fewer beetles were found at higher elevations. Species richness within samples also decreased with increasing elevation. However, this may be a confounding result of fewer beetles found at higher elevations. While this research effort greatly increased the sample size of bark beetle populations in the region, in comparison to Rosenberger’s project, more work is needed to make definitive conclusions as to the range, abundance, and diversity of bark beetle species in Costa Rican montane cloud forest environments.

Comparative Analysis of Factor H Protein Sequences Associated with Differential Survival of *Borrelia* Pathogens in Vertebrate Hosts

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Desiree Pante* and Weigang Qiu, *Hunter College at the City University of New York*

Abstract: Lyme disease, the most prevalent vector-borne disease in the United States, is caused by spirochete *Borrelia burgdorferi*, a bacterial pathogen carried by *Ixodes* ticks that parasitizes a variety of vertebrate hosts including humans, lizards, and birds. Previous studies have reported that lizards such as the Western Fence lizard (*Sceloporus occidentalis)* have borreliacidal factors in sera. We hypothesize that sequence variations in the Factor H (FH) protein, a regulator of the vertebrate innate immune system, is responsible for variations of host defense against *Borrelia* infection. A series of evolutionary and structural analyses were performed to test our hypothesis. Comparison of FH nucleotide and protein

sequences of vertebrate species allowed for phylogenetic reconstruction which revealed lizards diverged earlier in evolutionary history than the rest. FH protein structures were analyzed to identify important binding sites for complement binding. We have identified conserved gene structures between lizard, mouse, and human for primer design using a web-based browser we developed as a guide. Our findings will now enable the use of PCR amplification technology to further the understand FH sequence variability. We plan to use chromosome walking procedures to amplify and sequence exon regions in lizard genome interspersed by long intron sequences. Results from this study will serve to test association between FH protein variability with differential host immune responses to Lyme pathogens in nature from an evolutionary perspective.

An Evolution and Bioinformatics Exploration of Vitamin B12 Absorption

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Isaac Paredes*, *CUNY John Jay College of Criminal Justice* and Nathan Lents, *John Jay College of Criminal Justice*

Abstract: Animals require specific micro-nutrients from their diet to sustain life. The inability to synthesize some micro-nutrients places dietary restrictions for organisms. Vitamin B12 (cobalamin), a molecule important for DNA synthesis and neurological and hematopoietic functions, cannot be synthesized *by* any animal, but rather by the cyanobacteria within the gut. Cyanobacteria in humans are endemic to the large intestine however, absorption of cobalamin is restricted to the terminal ileal region of the small intestine, rendering most, if not all, of the cyanobacteria-synthesized cobalamin unusable. For absorption, free cobalamin must bind to a transport protein called the Cobalamin Intrinsic Factor (CBLIF) to form a complex that will then be endocytosed into cells. CBLIF is expressed in the stomach and terminal ileum. We hypothesize that mutations in the CBLIF gene promoter led to eventual expression in these locations. We have extracted the CBLIF promoter sequences of herbivores and carnivores whose genomes have been fully sequenced. We then scanned these promoters for sequence motifs that consistently correlate with either herbivory or carnivory and analyzed the overrepresented motifs for known transcription factor binding sites and other sequence elements. We then compared these promoter motifs across species to determine where the human CBLIF gene fits among the two groups of organisms. The goal of this study is to find when and how, phylogenetically, humans lost the ability to absorb the cyanobacteria-synthesized cobalamin in the colon. This information will shed light on the evolutionary history of the human diet and what our bodies have evolved to consume.

Comparative Transcriptomics of Anchialine Cave Shrimp

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Nancy Ortega* and Elizabeth Borda, *Texas A&M-San Antonio*

Abstract: Anchialine caves are subterranean cave ecosystems that are submerged with a stratified water layers (freshwater to marine) and lack a direct connection to the surrounding ocean. Cave systems are only accessible via land-locked entrance pools. Anchialine caves are dominated by invertebrate fauna, among which crustaceans are the most abundant and taxonomically diverse, with strict adaptations to a life in complete darkness, low oxygen, and limited food resources. The goal of this study is to gain insight into the genes associated with adaptation in anchialine cave environments, by evaluating two species of shrimp, *Halocaridinarubra* from volcanic lava tubes located in Hawaii and *Typhlatya* sp. from *cenotes of* the Yucatan Peninsula (Mexico). Publically available transcriptome data will be assembled *de Novo and* annotated to establish gene expression profiles for each species, and followed by comparative functional gene enrichment analysis to identify under- and over-expressed genes by biological function, molecular function, and cellular component.

Mobile Consumers Track Invertebrate Subsidies from Floating Algal Mats

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alexandra Cisneros Carey*; Philip Georgakakos and Mary Power, *University of California, Berkeley*

Abstract: During summer, floating algal mats in many rivers host large numbers of larval invertebrates that emerge as flying adults. In late summer, these mats detach and float downstream, subsidizing the cobble bars they strand on. We investigated whether adult odonates and Lycosid spiders, two groups of mobile consumers, track these patchy subsidies. In the South Fork Eel River (39˚44′ N, 123˚37′ W; 39˚44′ N, 123˚38′ W), Mendocino County, California, we moved 2.5x1 m^2 floating mats of the filamentous alga, *Cladophora glomerata,* along the river shoreline to create 7 experimental blocks, each with 1 algae and 1 no-algae plot. We measured invertebrate emergence from mats and consumer densities within 1m of the plot edge. Both consumers tracked emergence, which was on average 7% higher from algal plots. Odonates were on average 30% more abundant in plots with algal mats and lycosids on average 11% more abundant. Their ability to track spatially and temporally patchy algal mats, allowed these riparian consumers to exploit a trophic subsidy from aquatic production in the sunlit mainstem river. Mapping the origins, fluxes and fates of organic production that link freshwater, terrestrial, and marine food webs can reveal vital connections of ecosystems threatened by change.

Effects of Ammonia Concentrations on Growth Rates of Thermophilic Ammonia-Oxidizing Archaea

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Saul Cortez-Alvarado*; Louis Contreras; Talia N. Jewell and José R. de la Torre, *San Francisco State University*

Abstract: Nitrogen is an essential nutrient required for life, and microbial processes, including nitrogen fixation to ammonia, are critical for driving the global nitrogen cycle. In most ecosystems, ammonia oxidation, a metabolic process by which microorganisms oxidize ammonia to nitrite in order to generate energy, is the rate-limiting step of this cycle. Recent studies have shown that ammonia-oxidizing archaea (AOA) drive ammonia oxidation rates in most aquatic and terrestrial environments, and have suggested that the ecology of AOA is driven by their high affinity for ammonia and their adaptation to low substrate availability. To understand the ecology and role of AOA in the global N cycling, we examined how ammonia concentration affects the growth rates of three distinct lineages of thermophilic AOA. Triplicate cultures were inoculated into medium with initial ammonia concentrations varying from 250 μM to 100 mM. Specific growth rates were measured using nitrite production as a proxy for cell growth. As previously observed in mesophilic AOA, fastest growth occurred at the lowest initial ammonia concentrations. However, all three thermophilic strains grew faster and tolerated much higher ammonia concentrations that their mesophilic relatives. In particular, *Nitrososphaera nevadensis*GerE, a moderate thermophile cultivated from a hot spring in the Nevada Great Basin, grew four times faster than mesophilic strains and could tolerate ammonia concentrations of up to 100 mM, concentrations known to inhibit the growth of mesophilic AOA. These differences demonstrate that AOA are physiologically diverse and may be well adapted for a wide range of environmental substrate concentrations.

Comparison of Bite Force and Skull Dimensions between Urban and Rural Coyotes (*Canis latrans*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Lizbeth Jardon* and Theodore Stankowich, *California State University - Long Beach*

Abstract: Humans are capable of drastically altering their environment within a relatively short time frame, turning vast natural landscapes into bustling cities. Few organisms can adapt quickly enough to survive these changes; those who do often subsidize their diet with anthropogenic food since an animal's natural food source may not be readily available. A species with populations living in both urban and rural environments may, therefore, experience musculoskeletal changes in response to different selective pressures stemming from food diversity, availability, and acquisition difficulty. Here, we compare skull dimensions and bite force of coyotes (*Canis latrans*) from an urban population (Greater Los Angeles) with those from a rural population (Fresno County). Upper jaw length and width, mastication muscle masses, lower jaw lever length, and skull length measurements were recorded for each specimen; and upper jaw length/width ratio and bite force at the carnassial molar and lower canine were calculated. Current findings indicate urban coyotes have greater variation in upper jaw shape, with statistically nonsignificant trends towards wider snouts, longer skulls and a stronger molar bite force in urban coyotes. While more data is needed, trends suggest urban environments favor the development or evolution of powerful bites to allow for feeding on domestic pets.

Investigating the Transmission Dynamics of *Borrelia Burgdorferi* (*Bb*) in Northern California

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Serena Barasi*, *University of Guam* and Marie Lilly, *San Fransisco State University*

Abstract: Lyme disease is a prevalent tickborne disease in the West Coast, with a distinct host community from its Eastern counterparts. The western fence lizard plays a unique role in the ecology of lyme disease in the West Coast, due to its role as an incompetent reservoir for the lyme disease etiological agent, *Borrelia burgdorferi* (*Bb*). As an incompetent reservoir, it was hypothesiszed that the presence of the western fence lizard would likely lower the presence of *Bb* in the tick population, thus decreasing the transmission of *Bb*. However, a previous experiment (Swei et. al, 2011) showed that the removal of lizards actually resulted in a decrease in ticks since they did not move to more competent hosts and thus an overall decrease in *Bb*. We hypothesize that the western fence lizard maintains tick populations in the West Coast. In order to further investigate the transmission dynamics of *Bb* involving the blacklegged tick and western fence lizard, we looked at four years of field data (2016-2019) collected by the Swei lab and used the poisson regression to test the correlation between western fence lizard abundance and tick burden with density of questing nymphs (DON), density of infected nymphs (DIN), and nymphal infection prevalence (NIP). Preliminary results show that DON, DIN, and NIP are all significant (*p*=<2e-16; 0.02771; <2e-16). Understanding the transmission dynamics between *Bb*, the blacklegged tick, and the western fence lizard has the ability to improve the prediction and management of lyme disease risk.

Assessing the Impact of Micro-Environment on the Color of Painted Turtles (*Chrysemys Picta*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Georgina Jaimes* and Beth Reinke, *Northeastern Illinois University*

Abstract: An animal's environment plays a critical role in shaping the evolution of its phenotype. Phenotypes can be different between environments due to varying selective pressures. Painted turtles inhabit a variety of environments in North America. These habitats can range from being eutrophic to oligotrophic, standing water to still water, roadside ditches to pristine lakes. Both biotic and abiotic selective pressures can affect turtle coloration. The orange coloration that gives painted turtles their name is caused by a carotenoid, which can only be obtained from an organism's diet in vertebrates, and the availability likely varies between environments. In painted turtles, the pigment may serve as an antioxidant that can improve recovery from overwintering in this species, meaning that turtles with fewer carotenoids in their diet may have reduced chances of survival. Winters have become severe with global climate change so it is increasingly crucial to understand the influence of the environment on painted turtle survival. This project measures the effect of environment on turtle coloration by assessing multiple populations of painted turtles within Wisconsin. The color of the turtle's carapace, neck, and plastron was measured using a reflectance spectrometer. Additionally, color-standardized photographs of the turtle's carapace and plastron were taken and analyzed in Image J. We predict that turtles will have brighter colors and more intra-population variation in environments that are high in aquatic plant density. There will be less color brightness and variation in small bodies of water, such as brooks, since they contain fewer vegetation.

Perfect Mimicry between *Heliconius* butterflies Is Constrained By Genetics and Development

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Paola Alicea*; Riccardo Papa and Steven Van Belleghem, *University of Puerto Rico-Rio Piedras*

Abstract: Müllerian mimicry is a phenomenon in which species share an honest warning signal to the benefit of protection towards a mutual predator. Mimicry can be an example of how powerful natural selection is. However, the exact measure of such adaptive phenotypic convergence and possible causes of its imperfection often remain unidentified. Here, using R package *patternize* we first quantify wing color pattern differences in the forewing region of co-mimetic races of the butterfly species *Heliconius erato* and *Heliconius melpomene* and measure the extent to which mimicking races are not perfectly identical. Next, using recent CRISPR/Cas9 KO experiments of the gene *WntA*, which has been mapped to color pattern diversity in these butterflies, we explore the exact areas of the wings in which *WntA* affects color pattern formation differently in *H. erato* and *H. melpomene*. We find that, while the relative size of the forewing pattern is generally nearly identical between co-mimics, the CRISPR/Cas9 KO results highlight divergent boundaries in the wing that prevent the co-mimics from achieving perfect mimicry. We suggest that this mismatch may be explained by divergence in the gene regulatory network that defines wing color patterning in both species, thus constraining morphological evolution even between closely related species.

Bumble Bee Habitat Associations of the Flathead Reservation, Montana, USA

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Caleb Sandoval*, *Humboldt State University* and Janene Lichtenberg, *Salish Kootenai College*

Abstract: Bumble bees, genus *Bombus*, are declining worldwide, and the Confederated Salish and Kootenai tribes have interest in understanding the changes in bumble bee ecology on the Flathead Reservation in Western Montana. Bumble bees were found to be the main pollinator of the huckleberry, *vaccinium globulare*, a culturally important subsistent food source for the tribes. This report focuses on data collected June 2018 to August 2019. Bumble bees were captured with nets and various data were recorded, including elevation of the site, size and length of the bee, and the host plant where the bee was found when captured. The diversity of species was variable across the sites, with no distinct association with elevation, suggesting that a variety of species may be found at any elevation between 800 and 2000 meters. Furthermore, there was an association found between the diversity of flowering plants and the diversity of bumble bee species. Open meadow sites with numerous flowering plant species yielded greater bumble bee diversity than closed, densely forested sites, even those with thriving huckleberry. The growing body of knowledge of bumble bee ecology in this area of Western Montana will lead to informed decisions of land and resource management by the tribes and others to protect the populations of bumble bees and other pollinators, which will in turn support culturally important species such as the huckleberry. This is especially important as climate change continues to be a factor in the balance of ecosystems around the world.

Effects of Heat Stress on *Leptastrea purpurea* Reproduction and Larvae Settlement

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Nikko Galanto* and Sarah Lemer, *University of Guam*

Abstract: The impacts of climate change, such as rising seawater temperatures, are causing a serious threat to many marine organisms, including corals. Increased temperatures heavily disrupt the symbiotic relationship between corals and zooxanthellae, which ultimately lead to coral bleaching which affects coral survival and potentially their reproduction. We investigated the effects of heat stress in the heat tolerant scleractinian coral species, *Leptastrea purpurea*. *Leptastrea purpurea* colonies were kept in tanks and stressed by increasing water temperatures 2-3ºC above ambient. Larvae were collected once a week and placed in settlement trials. Several parameters were observed and compared between heat-stressed and control assays, including the number of larvae released, larva size, settlement time, survival and settlement preference. We found that heat stressed parental colonies released significantly higher amounts of larvae than control colonies. The heat-stressed larvae were found to be significantly smaller in size, but they survived and settled at the same rate as larvae from the control colonies. Lastly, larvae from both the heated and the control assays preferred to settle on crustose coralline algae as opposed to the plastic walls of their containment wells. Increased larvae production from heat-stressed colonies could be a physiological response to heat stress that could help this species cope with climate change. Further studies on heat-stressed *L. purpurea* larval fitness and long-term survival are however needed.

Signal Partitioning Allows Butterfly Wing Surfaces to Evolve Under Opposing Selective Pressure

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Kelsey Littrell* and Beth Reinke, *Northeastern Illinois University*

Abstract: Animal coloration is typically the evolutionary compromise of two, often opposing, processes, natural and sexual selection, that is inherently dependent on the environment in which the color is viewed. Sexual dichromatism is a widespread phenomenon typically driven by sexual selection. This dorsal surface of the wing of most butterflies (Order: Lepidoptera) is only visible during flying, courtship displays, or basking, while the ventral surface is visible while resting. Given this physical separation of colors, referred to as signal partitioning, dorsal and ventral wing surfaces can potentially evolve under completely separate selective pressures; this may be evident by comparing the evolution of sexual dichromatism of dorsal and ventral surfaces. We propose that there will be more sexual dichromatism on the dorsal surface of Lepidopteran wings than on the ventral side, and that since these signals are dependent on the light under which they are perceived, we predict that environments with a high percentage of vegetative cover and areas with a low percentage vegetative cover would produce the most profound sexual dichromatism, while intermediate areas would have little to no sexual dichromatism. To test these predictions, we use photographs of adults of the group Biblidinae, which consists of approximately 340 identified species. We will then use phylogenetically controlled methods (PCM) to assess whether the evolution of the sexual dichromatism on the dorsal and ventral surfaces occurs independently and varies by environment as hypothesized. This work is important for understanding signal partitioning and the evolution of sexual dichromatism.

The Blob, Elevated Eastern Pacific Ocean Temperatures, Affected Commercial Fishery Catch

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alisa Hernandez*; Trina Miller; Jada Smith; Nicholas Torres; Joann Lam; Madison Panzino; William J. Hoese and Kristy Forsgren, *California State University, Fullerton*

Abstract: For environmentally sensitive marine species, changing ocean temperatures can affect distribution and abundance. The Blob, an abnormally long and intense marine heatwave, affected eastern Pacific oceanic temperatures up to 140 m deep from 2013-2016. Other climatic patterns (PDO, ENSO) that occurred during the Blob may have exaggerated the elevation of ocean temperatures. To determine the impact of the Blob, we examined a 10-year-period (2009-2019) of ocean temperature and commercial fishery data. We hypothesized that species with warm water preferences would experience an increase in commercial catch, while catch would decrease in species that prefer cooler waters. We compared average ocean temperatures between depths of 5-300 m in southern California to commercial fishery catch data (a proxy for population abundance). There was a positive correlation between ocean temperature and catch data for Northern anchovy (*Engraulis mordax*), copper rockfish (*Sebastes caurinus*), lingcod (*Ophiodon elongatus*), and yellowtail amberjack (*Seriola lalandi*). A negative correlation between ocean temperature and catch data was observed for Pacific sardine (*Sardinops sagax)* and market squid (*Doryteuthis opalescens*). Chub mackerel (*Scomber japonicus*) catch was not related to ocean temperature. Increased ocean temperatures associated with the Blob likely impacted marine life by shifting the distribution of species and influencing fisheries. As ocean warming events become increasingly common, impacts seen in marine species can be indicative of future ecological and anthropogenic consequences as species distribution and abundance change.

The Impact of Environment on Painted Turtle Shell Shape

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Erik Maki* and Beth Reinke, *Northeastern Illinois University*

Abstract: Every animal must adapt to the environment they live in to survive. In aquatic habitats, an animal's ability to find mates, to forage for food, and to avoid predators is constrained by how effectively it moves through water. Painted turtles are a widespread species that have stable populations in a variety of aquatic habitats. They are ideal animals to study shape, because of the rigidness of their shells which impacts their movement. Populations living in bodies of water with high plant density and high turbidity should be rounder and wider to facilitate lumbering movement away from predators and to provide shelter from predators. In open, clear environments turtles should be flatter and narrower to increase hydrodynamic efficiency and speed to escape predators. Six populations of painted turtles in various habitat types in Sawyer County, Wisconsin, were sampled to assess whether shape differs according to this hypothesis. We photographed turtles dorsally, ventrally, and laterally and then used geometric morphometric methods (GMM) to analyze shape. Aquatic plant density, water clarity, and shoreline type was measured for each population. We used principal components derived from GMM and generalized linear models to determine if environment influences shape in this species as we hypothesized. It is important to understand the impact of environment on phenotype, especially as climate change results in changes in plant growth, water clarity, and shorelines composition.

A Search for the Genes That Allow Nudibranchs to Steal Anemone Stinging Organelles

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Abegail Bigasin*; Jessica Goodheart and Deirdre Lyons, *University of California, San Diego*

Abstract: Nematocysts are specialized stinging organelles made only by cnidarians to fend off predators or catch prey. However, multiple metazoan phyla that prey upon cnidarians have evolved the ability to sequester nematocysts for their own defense. The nudibranch gastropod *Berghia stephanieae* is an emerging research organism that possesses the ability to sequester nematocysts from the anemone *Exaiptasia pallida*. Nudibranch sequestration is not well-studied; we do not fully understand the cellular and molecular mechanisms involved, nor how this ability evolved. Nematocysts are endocytosed from digested food by specialized cnidophage cells that are housed in an organ called the cnidosac, which resides at the tips of cerata (dorsal appendages that contain branches of the digestive system). The proximal section of each ceras (singular cerata) contains digestive tissue, whereas the distal section contains the cnidosac and cnidophages. To find cnidosac genes that could be involved in *Berghia* sequestration, differential expression (DE) analysis was conducted on distal vs. proximal cerata. Four different DE tools were used, which identified a consensus of 70 genes, 58 of which were upregulated in the distal cerata. Ten of these genes are implicated in cytoplasmic processes in animals, suggesting that they could be involved in nematocyst sequestration. We plan to test where, and how, these genes function by using in-situ hybridization and CRISPR/Cas9 knockouts, respectively. We can then begin to frame hypotheses about the evolutionary origins of sequestration--for example the notion that sequestration might be related to nudibranchs' ability to deliberately shed cerata, and replace them through regeneration.

Macromorphological Variation of the Coral *Helioseris Cucullata*: Patterns in Populations from Curaçao

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Juliana Limon*[1]; Alejandra Hernandez-Agreda[2] and Pim Bongaerts[2], *(1)University of California, Santa Cruz, (2)California Academy of Sciences*

Abstract: The endemic coral *Helioseris cucullata* (Sunray Lettuce coral) was once one of the Caribbean's most abundant species; however, it is currently a rare coral due to a severe population decline. Like other plating corals, this species occupies distinct reef environments exhibiting a substantial morphological variation. Traditional taxonomic assessments are based on the description of microscopic traits measured on skeletal fragments. Nonetheless, the current low abundance of *H. cucullata* represents a challenge for such assessments. As part of the evaluation of the current status of this species in the Southern Caribbean, we assess the morphological diversity of *H. cucullata* using a non-invasive, photograph-based approach. Macromorphological features (morphology, area, number of skeleton whorls, corallite arrangements, and fluorescence) were quantified in pictures of colonies observed from shallow (8 m, 26 ft) to upper mesophotic depths (42 m, 138 ft) of three reef locations along the leeward coast of Curaçao. By collectively analyzing morphological features and correlating them with the characteristics of *H. cucullata* habitats, we identified morphological patterns along the depth gradient. Our results contribute to the description of the breadth of morphological variation of *H. cucullata* and identification of morphological traits requiring in-depth and fine-scale assessments.

Comparison of Grasping and Biting Forces Among Rodent Species in the Suisun Marsh, California

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jose calderon*, *california state university san marcos* and Diego Sustaita, *California State University San Marcos*

Abstract: Studying functional performance in rodents can help us understand how they use their habitat. For example, studying bite force might help us understand their feeding ecology. Similarly, studying grasping force might help us understand their climbing abilities. However, not much is understood regarding how biting and grasping forces vary among species that occupy the same habitat. We measured grasping and biting forces of four different species found in the Suisun Marsh, including the endangered salt marsh harvest mouse (Reithrodontomys raviventris), western harvest mouse (Reithrodontomys megalotis), California vole (Microtus californicus), and house mouse (Mus musculus) using a force transducer. In addition, we measured the relative sizes of the forefeet and rostrum of each individual to explore anatomical correlates of these forces. According to our preliminary results, peak grasping and biting forces (scaled to body size) were greatest in the California vole, followed by the western harvest mouse, salt marsh harvest mouse, and house mouse. This pattern could reflect differences in foraging and/or locomotion, such as the voles' tendency to burrow and the house

mouse's generalized behavior. Further analyses are currently underway to examine if and how forefoot size and rostrum length explain these bite and grasp force differences among species.

Quantification of Male and Female Feather Temperature in Relation to Color in American Robins (*Turdus migratorius)*

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Yessica Rodriguez* and Lauryn Benedict, *University of Northern Colorado*

Abstract: Studies of sexual dimorphism in animals have focused primarily on visible features such as those of size or appearance. American Robins (*Turdus migratorius*) exemplify physical differences between males and females, where males present darker plumage colorations. American Robins also use thermoregulation to control body temperature, using feathers to serve as a buffer between their body and the environment. This study was designed to test for a relationship between feather temperature and feather coloration in American Robins. I predicted that darker colored feathers would exhibit more absorption of heat compared to lighter colored feathers. I also predicted that because males exhibit darker feathers, they would exhibit more absorption of heat. Temperature readings of feathers collected during the summer 2019 field season were recorded and compared against color specifications from HEX codes in Adobe Photoshop. Feathers were placed on a self-made apparatus and exposed to three different wattages of light (80W, 125W, & 160W). The warmest areas on the feathers were located with a thermal imager, and then temperature was measured with a thermometer for accurate measurements of temperature. Measurements of temperature before exposure acted as the control group, and the three wattages of light gave the experimental groups. I tested for a correlation between color and temperature using statistical regression, and I also tested for a sex-based difference using t-tests. This research aimed to expand on the current understanding of sexual dimorphism in American Robins; findings may additionally account for other evolutionary observations that generally apply to avian species.

Spatial and Temporal Patterns in River Phytoplankton and Cyanobacteria Communities

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Lamia Benyamine*[1]; James Pack[2]; Kathi Jo Jankowski[3]; Douglas Baumann[4]; Barbara Bennie[4] and Molly Van Appledorn[3], *(1)University of Central Florida, (2)Centre College, (3)United States Geological Survey, (4)University of Wisconsin La Crosse*

Abstract: Phytoplankton serve as the basis of aquatic food webs, providing a food source for larger organisms and aiding in nutrient processing. These communities can sometimes contain species that produce toxins. Toxic blooms, although typically rare, have recently occurred in large rivers in the US Midwest. Few studies currently exist on phytoplankton communities on one of these large rivers, the Upper Mississippi River System (UMRS), especially on the factors influencing harmful cyanobacteria growth. Therefore, our main objective was to characterize the community of phytoplankton across 1,300 miles of the UMRS and understand their response to environmental factors. In doing so, we were able to assess the contributing factors leading to harmful cyanobacteria blooms. We were provided 181 samples collected by the United States Geological Survey from 1996 to 2012 to evaluate the environmental factors contributing to the variation of phytoplankton communities. Some differences observed consisted of northern stations being more diverse and distinct from those in the southern reaches. Cyanobacteria concentrated 15% of communities in the northern reaches but were nearly absent from other pools. Calculating the Analysis of Similarities, we found that field stations are significantly different in community composition. Using Canonical Correlation Analysis, we found that these differences were best explained by dissolved oxygen levels and the nitrogen to phosphorus ratio. These relationships increase our understanding of riverine phytoplankton communities, including environmental factors that promote cyanobacteria presence, which helps inform the management of the UMRS to reduce the risk of harmful species.

Modeling Pfas Biomagnification in the Chesapeake Bay

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Aliya Adams* and Thomas Ihde, *Morgan State University*

Abstract: Per- and polyfluoroalkyl substances (PFAS) are hazardous, man-made organic chemicals. These chemicals are found in firefighting foams, non-stick cookware, and numerous other products since the 1940s. PFAS are designed to resist heat and degradation, so they persist in the environment and accumulate at high concentrations in water, biomagnify in aquatic life, and humans by binding to proteins. PFAS increase human risk of decreased birth rates, increased neonatal mortality, skeletal deformity, increased cholesterol levels, decreased immune response, increased risk of pre-eclampsia, cancer, and more. Short-chain PFAS demonstrate less accumulation in tissues than long-chain, however, they have a lower adsorption potential and are harder to remove. Reports of environmental concentrations of PFAS are few and haphazard. This makes it challenging for environmental and human health agencies to develop fish consumption advisories. This pilot study aims to apply the spatially-explicit Chesapeake Atlantis ecosystem model to estimate PFAS concentrations magnified through the Chesapeake Bay food web and map these concentrations for a range of organisms. Ultimately, the project aims to validate model predictions by testing PFAS concentrations in Blue Crab (*Callinectes sapidus*) tissues from predicted low and high concentration areas. Blue crabs are the most valuable seafood species in the Chesapeake Bay, and thus critical to understanding human risks for consumption. This study will map PFAS concentrations in an area that has yet to be studied.

Multidrug Resistance Island on Environmentally Isolated *Escherichia coli* ST117

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Katie Ann Huy*[1]; Andrei Tatarenkov[2] and Luis Mota-Bravo[1], *(1)University of California, Irvine, (2)School of Biological Sciences, University of California, Irvine*

Abstract: Antibiotic resistant bacterial infections account over 700,000 yearly deaths worldwide. Mobile genetic elements and horizontal gene transfer (HGT) can mobilize antibiotic resistance genes (ARGs) into various species of bacteria, including *Escherichia coli*. The objective of this study was to describe and analyze the antibiotic resistance genes and mobile genetic elements in a plasmid from an environmentally isolated bacterium. SW3654 was isolated from San Juan Creek, CA and identified as *Escherichia coli* using MALDI-TOF. A resistance profile was determined with Disk Diffusion Tests (DDT). The plasmids were sequenced, assembled, and annotated. Plasmid characterization was performed using PATRIC, CGE, and NCBI databases. Gel electrophoresis revealed a conjugative 164 kb plasmid (P1), identified as IncFIB type. DDT showed resistance to 6 classes of antibiotics. A 22,896 bp multi-drug resistance (MDR) region in P1 harbored the resistance genes *aac(3)-IId, aadA5, aph(3'')-Ib, aph(6)-Id, blaTEM-1B, mph(A), sul1, sul2, tet(A),* and *dfrA17* associated with the resistance phenotype. Mobile elements IS15DIV and IS1 surround the region, as well as an integron integrase. Comparative analysis found plasmids with a 99% similar MDR region, however this is the first report of a plasmid harboring this unique region isolated from the environment. Similar phenotypic resistance is found in clinical *E. coli*, suggesting the environment may serve as a reservoir for ARGs. Our findings also show MDR can be mobilized between clinical and environmental bacteria, a phenomenon that should be studied in response to the growing threat of antibacterial resistance.

Influence of Climate Change Velocity on Future Species Distributions of Buzz Pollinators

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Amy Tian*[1]; Luis Carrasco[2]; Gregory Wiggins[2] and Mona Papeş[2], *(1)University of Chicago, (2)National Institute for Mathematical and Biological Synthesis*

Abstract: Climate change is driving range shifts in bees by causing ecological mismatches between flowering plants and their pollinators. Declining bee populations have fueled global conservation concerns given their importance to pollinating crops. While previous studies have modeled range shifts over time, it is not well known whether the velocity of climate change may outpace the dispersal ability of bee species. In this study, we model how the limited dispersal abilities of bees will affect future ranges by 2050. Our work builds on previously developed ecological niche models, which project baseline (1960-1990) and future (2050-2060) ranges of 15 North American buzz pollinator bee species under RCP 4.5 and 8.5 greenhouse gas emissions scenarios. We projected the velocities at which these species must disperse by calculating the distance between pixels of matching climates from the baseline to future distribution over time. Future species maps were created by identifying the areas where the travel velocities required were within a dispersal ability threshold of 5 kilometers per year determined from a literature review. We found, comparing across species, that the proportion of median lost area was up to 14% change with a limited dispersal ability. Our findings point to conservation areas of maximal benefit to be in Ohio, Indiana, Illinois, and the Northeastern US. We found an overall decrease in habitable area which suggests dispersal ability has important implications for future distributions and that modeling with climatic conditions alone are insufficient to predict realistic climate change outcomes.

The Genes of Bioluminescence in the Genome of a Species of Comb Jelly (*Beroe ovata*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

T. Danielle Hayes*; Joseph Ryan; Daniel Groso; Melissa DeBiasse and Mark Martindale, *Whitney Laboratory of Marine Bioscience, University of Florida*

Abstract: Bioluminescence is widespread in the ocean and has evolved more than 30 times within the animal tree, nevertheless we lack a detailed understanding of how it is gained and lost. Comb jellies (ctenophores) consist of about 200 species, most of which are bioluminescent. To date, only one bioluminescent ctenophore genome (*Mnemiopsis leidyi*) has been published. In order to have a basis of comparison, we sequenced and assembled the genome of the bioluminescent ctenophore *Beroe ovata* using both short- and long-read sequencing technology. Identifying the genes responsible for bioluminescence, called photoproteins, is challenging using standard gene prediction methods because these genes are short, highly similar, and in tight clusters. I manually annotated 20 photoproteins on 4 distinct scaffolds. I identified photoprotein loci by BLASTing *M. leidyi* photoproteins against the *B. ovata* genome. Next, I aligned transcripts to these loci and identified start and stop codons as well intron-exon junctions (when present). I identified several photoproteins that contained introns, which has never been observed in *M. leidyi*. Also, I found that roughly half of the photoproteins had multiple stop codons suggesting that these are pseudogenes. Given the predominance of bioluminescence in the deep sea and the relative rarity of it in surface-dwelling animals, the presence of a large number of pseudogenes suggests that *B. ovata* had likely transitioned to shallow waters a long time ago. This work identifies several historical genomic events that shaped the bioluminescent properties of a modern day comb jelly and provides insight into its historical ecology.

Evolution of the TGF-β Signaling Pathway within Ctenophora

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Daniel Groso*; Joseph Ryan; Melissa DeBiasse and Mark Martindale, *Whitney Laboratory of Marine Bioscience, University of Florida*

Abstract: As the sister group to the rest of animals, ctenophores (comb jellies) provide key information about the last common ancestor of Metazoa. Nevertheless, there has been limited comparisons of genomic evolution within Ctenophora despite the publication of two ctenophore genomes more than six years ago. We recently sequenced the genome of the ctenophore, *Beroe ovata*. As part of this project I have characterized components of the TGF-β signaling pathway in *Beroe ovata*. This pathway plays a key role in developmental signaling in all animals. I have identified ten TGF-β ligands and four TGF-β receptors in *Beroe*. I used a hidden Markov model approach to identify *Beroe ovata* TGF-β ligands and receptors. I aligned these *Beroe* sequences to the TGF-β ligands and receptors of *Mnemiopsis* and several other non-ctenophore animals. I then conducted phylogenetic analyses using IQ-TREE and RAxML to predict the best maximum likelihood phylogenetic tree. Using this tree, I determined that *Beroe* has retained all of the TGF-β ligands and receptors that are present in *Mnemiopsis*, and discovered that at least one of the ligands and receptors present in the last common ancestor of *Mnemiopsis* and *Beroe* was lost in *Mnemiopsis*. As TGF-β ligands play a critical role in early development, we will follow up this work by identifying where and when this gene is expressed during development in *Beroe*. This work represents one of the first genomic comparisons made between ctenophores and provides insight into evolutionary events that shaped the diversity of developmental programs in these creatures.

How Does Temperature Affect Eczema?

Discipline: Life Sciences
Subdiscipline: Environmental Science

Kathy Le* and Katharine Kelsey, *University of Colorado Denver*

Abstract: Inflammation of the skin can result in red, dry, scaly patches. Depending on the environment, there can be everyday triggers that can result in these types of inflammation. This is a disease known as Eczema. For this disease, there is research showing different temperature thresholds and lengths of exposure to the natural heat. There is no true definition on how this is caused on skin, however researchers have shown that temperature can be a potential environmental factor. Sunlight plays a major role in the potential environmental factor. To add on, seasonal factors correlate to climate change as well. Summer is naturally hot. Studies have shown, the higher the temperature, the more likely eczema shows up.Through this literature review it has been known that eczema is seasonal. However, diving deeper into the research, it shows that eczema is tied into certain thresholds or lengths or exposure outdoors. Once people are exposed to direct sunlight there are frequencies and intensities that can be measured. This meta analysis research provides a starting point to further explore how temperature affects eczema in different aspects of climate change. Eczema is a condition of dry skin that is related to warm temperatures and we know it is increasing with climate changing but we don't know the symptoms, therefore use a literature review to analyze this.

Arthropod Diversity during Red Mangrove (*Rhizophora mangle*) Leaf Decomposition in Wet Months

Discipline: Life Sciences
Subdiscipline: Environmental Science

angely torres*, *Universidad Ana G. Mendez* and Maria Barberena, *universidad Ana G. Mendez*

Abstract: Red mangrove forests are highly productive ecosystems where decomposition recharges soil nutrients, decomposition by-products dissolve in water and become a source of nutrients for aquatic organisms in adjacent water bodies. Decomposition is performed by fungi and bacteria, and associated arthropods that have been shown to accelerate decomposition. Although red mangrove forests are an important nutrient source for adjacent water bodies there are no studies of red mangrove leaf decomposition and the variation of associated arthropod diversity during wet and dry periods in Laguna Grande Fajardo, Puerto Rico. This study reports on a decomposition experiment to determine mass loss and the diversity of arthropods during wet and dry periods. To accomplish this, three landward transects located in the red mangrove forest at the natural reserve of Las Cabezas de San Juan in Fajardo, Puerto Rico. Along each transect, three locations were selected and in each location decomposition bags filled with 10g of red mangrove leaves, bags were collected at specific intervals. This represents 3 transects x 3 locations x 4 collection dates for a total of 36 samples. Collected samples were placed in Berlese funnels for one week for arthropod extraction, then oven dried for one week to determine dry mass. These data were used to determine dry mass loss and arthropod. Preliminary data showed the presence of Collembolla, Malacostraca, Acari, Orthoptera and Decapoda.

Natural Versus Non-Natural Bolus Matter in Black-Footed Albatross, *Phoebastria Nigripes,* and Laysan Albatross, *Phoebastria Immutabilis,* from Midway Atoll National Wildlife Refuge (NWR), Northwestern Hawaiian Islands (NWHI)

Discipline: Life Sciences
Subdiscipline: Environmental Science

Allyson Ijima* and Pavica Srsen, *Windward Community College*

Abstract: Mōlī or Laysan albatross (*Phoebastria immutabilis)*, and Kaʻupu or Black-footed albatross (*Phoebastria nigripes),* both indigenous to Hawaiʻi, are considered near-threatened by the International Union for Conservation of Nature (IUCN). Specifically, Midway Atoll NWR, managed by the United States Fish and Wildlife Service (USFWS), hosts the largest populations of these species. Both Mōlī and Kaʻupu are found on NWHI where 70% and 95% of breeding pairs, respectively. While the human disturbance at NWHI might be minimal, the area receives a significant amount of floating marine debris due to Pacific Ocean currents, which are affecting these open-ocean seabirds' foraging habits. The diet of these two species was examined using the albatross boli (indigestible material thrown up by an albatross chick) collected at Midway Atoll NWR in 2019. We found that non-prey items (e.g. fishing line and plastic fragments) were present in all bolus samples, contributing up to 24% of the bolus' weight. Furthermore, there were significant differences in the size of the ingested non-prey items between the two species. The mōlī boli contained significantly higher weight of plastic items larger than 2 cm, as opposed to the Kaʻupu (13% versus 2%, respectively, of total bolus weight). Additionally, Mōlī boli contained a significantly higher amount (69% of bolus weight) of non-prey items (both natural, e.g. coral fragments and man-made, e.g. as plastics) than the Kaʻupu (52% of bolus weight). These findings suggest that Mōlī or Laysan albatross might be more vulnerable to the effect of floating marine debris.

Predicting the Spread of Invasive New Zealand Mud Snails in the Carmel River

Discipline: Life Sciences
Subdiscipline: Environmental Science

Natalie Vaughn*, *California State University, Monterey Bay* and John Olson, *California State University Monterey Bay*

Abstract: The New Zealand Mud Snail (NZMS) is an invasive species threatening the health of stream ecosystems. In 2000, NZMS was documented in California at Owens River and have since spread across the state, including the Carmel River in 2016, where they threaten steelhead trout. With their fast reproduction rate and ability to outcompete native invertebrates, NZMS could potentially prevent the recovery of steelhead in the Carmel River. We examine where NZMS are currently found in the Carmel River watershed and predict where they could possibly spread to based on their physiology. The spread of NZMS was monitored from 2017-2019 and water chemistry and velocity data were collected across the watershed. Using this data, a map was created to predict areas within the watershed that the snails could potentially spread to. In addition, a species distribution model(with an area under the curve of 0.989 and a correct classification rate of 0.95) was created based on data from all over California and applied to the watershed to predict areas susceptible to invasion. From 2017-2018, NZMS spread upstream over 3 kilometers, but expansion did not continue in 2019. According to the two maps created, the spread of the snails stopped well below where they were expected to expand to. There is no obvious reason as to why this expansion stopped, since water chemistry remained consistent and precipitation has been moderate the past two years. It is possible that competition may be a factor or dispersal by vectors could have decreased.

Determining the Viability of Using Native Oyster Species for Bioremediation in Compromised O'ahu Waterways

Discipline: Life Sciences
Subdiscipline: Environmental Science

Andrea Grant*[1]; Anne Brasher[2] and Pavica Srsen[1], *(1)Windward Community College, (2)University of Hawaii*

Abstract: Clean water supports subsistence activities, recreation, and the perpetuation of cultural practices. However, water-quality degradation is being increasingly observed around the Hawai'ian islands. We have initiated a restoration project for native oysters (*Dendostrea sandvichensis*) that will filter contaminants in the nearshore areas, improving water quality for the marine organisms living there, and people that fish and swim in the waters. We placed juvenile native oysters, obtained from the UH Hilo Pacific Aquaculture and Coastal Resources Center (PACRC) in cages at Marine Corps Base Hawai'i at Kāne'ohe Bay, and the Hawai'i Yacht Club and the Waikiki Yacht Club in the Ala Wai Harbor. One cage was placed in each of two sites at the Ala Wai Canal, and two cages at each of three sites in Kāne'ohe Bay. Each cage initially contained 150 oysters, with 50 individuals given numbered tags, allowing us to track individual growth rates. Tagged oysters were measured monthly and water quality parameters were monitored at each site. Average growth and survival rates were higher at Kāne'ohe Bay than at the Ala Wai Canal. After 5 months, percent survival was 37 and 60 at the two Ala Wai sites, and 83, 91, and 92 at the three Kāne'ohe sites. Oysters grew a mean of 2.35+/- 1.77mm after 3 months at the Ala Wai sites and a mean of 6.1 +/- 4.73mm at the Kāne'ohe sites. This project both re-establishes a native oyster, once common and now relatively rare, and improves habitat and water-quality conditions in nearshore areas.

Characterization and Isolation of Anoxygenic Photosynthetic Bacteria from Shrimp Ponds in Thailand

Discipline: Life Sciences
Subdiscipline: Environmental Science

Xelimar Ramirez*, *Interamerican University of Puerto Rico- Aguadilla Campus* and Elizabeth Padilla, *Interamerican University of Puerto Rico*

Abstract: Purple sulfur bacteria (PSB) and purple non-sulfur bacteria (PNSB) are characterized by their ability to perform anoxygenic photosynthesis. These groups are broadly found in coastal waters, enclosed lagoons, stagnant water, mangrove soils, estuaries, among others. In the present study, we studied the diversity of PSB community in enrichments derived from various environmental tropical samples (e.g., Thailand, Puerto Rico) associated with shrimp ponds, coastal mangroves, freshwater ponds, and Nymphaeaceae (water lilies) plant tissue. Since the 16S rRNA gene falls short in describing the diversity of phototrophic bacteria, other biomarkers (e.g., pufLM) were used construct phylogenies and examine biogeographic structure. Our data indicate that the majority of the sequences associated with freshwater ponds were related to marine, halophilic or salt-tolerant purple sulfur bacteria (e.g., Marichromatium, Allochromatium, Thiococcus, and Thiohalocapsa). In addition, phylotypes not closely associated with known species of PSB and PNSB were also found. Purple non-sulfur bacteria such as Rhodopseudomonas and Rhodoplanes related gene sequences were mostly found in samples from freshwater and from Nymphaeaceae (water lilies) plant tissue, suggesting a difference in the ecology and distribution of these bacterial groups potentially due to differences in habitat such as physical and chemical parameters (e.g. salinity). Our preliminary analysis showed a rich diversity of anoxygenic phototrophic bacteria. Since few environmental studies have described the diversity of purple in tropical environments with almost full pufLM gene sequences, more comprehensive efforts using NGS will provide greater resolution into the environmental diversity of phototrophic bacteria in these samples.

Effects of Freeway Pollution on Nitrogen Deposition on Desert Soil

Discipline: Life Sciences
Subdiscipline: Environmental Science

Soledad Guerrero Linares*; Stephanie Piper and Darrel Jenerette, *University of California, Riverside*

Abstract: Automobiles are major contributors to the release of nitrogen oxides into the air. These nitrogen oxides lead to smog production, and can cause respiratory illness in humans. They can also negatively affect the environment by increasing the amount of nitrogen deposited on the soil. The deposited nitrogen can undergo transformations, including changes in chemical form, exchanges with plant and microbial communities, and potential losses to the atmosphere or deeper soil. Increased nitrogen deposition is associated with increased soil acidity, which can alter plant and microbial communities, and further influence nitrogen transformations. These ranging effects make us question, how does freeway pollution affect soil nitrogen deposition and its consequences for soil and plant nitrogen availability? We hypothesize that nitrogen oxides emitted by cars increase soil nitrogen deposition. If our hypothesis is supported, we expect higher levels of nitrate, NO_3^-, and ammonium, NH_4^+ , nitrogen leaf content, and lower pH, in samples near the freeway. However, preliminary data suggested the opposite pattern with lower soil nitrogen availability closest to the freeway indicating that other processes could be affecting nitrogen deposition or its consequences for soil nitrogen availability. Therefore, the experiment will be repeated, with the recollection of soil nitrate, NO_3^-, and ammonium, NH_4^+, content with the addition of nitrogen leaf content, soil pH and branch washing across a gradient extending 1 km from the freeway. These results suggest large uncertainties in our current understanding of the effects of soil nitrogen deposition and its consequences on desert ecosystems.

The Role of Copy Number Variation in Insecticide Resistance of a Non-Target Crustacean, *Hyalella Azteca*

Discipline: Life Sciences
Subdiscipline: Environmental Science

Victoria Deery*[1]; Helen Poynton[2]; Kaley Major[2] and Donald Weston[3], *(1)University of Massachusetts, Boston, (2)University of Massachusetts Boston, (3)University of California Berkeley*

Abstract: Conserved genes are generally maintained in the same number of copies as the ploidy of an organism. However, if gene duplication provides a selective advantage, it may become common in a population. Acetylcholinesterase in insects are targeted by organophosphate pesticides (OPs), causing death through neurotoxicity. However, populations of *Hyalella azteca*, a crustacean used for sediment toxicity testing, have evolved resistance to OPs, due to point mutations in the acetylcholinesterase gene (*ace-1*). Our hypothesis is that populations duplicated their *ace-1* gene, developed a mutation in

one copy, but also preserved a wild-type copy. The mutated *ace-1* genes could provide resistance to OPs present in their environment and the wild-type gene preserves full functionality in the absence of OPs. To test for gene duplication, we examined copy number variation in multiple populations of *H. azteca* from California with and without resistance to OP insecticides. Two conserved reference genes, Ran Binding Domain and Uracil Phosphoribosyltransferase, were identified as single copy according to a Benchmarking Universal Single-Copy Ortholog (BUSCO) list. Using quantitative PCR, different populations of *H. azteca* were tested to confirm single copies of both reference genes. Within the same individuals, we expect to proportionally relate the amount from the assay of acetylcholinesterase activity with the organism's copy number variation of the *ace-1* gene determined by quantitative PCR. Confirming *ace-1* gene duplication in *H. azteca* will give insight into the role of evolutionary biology for risk assessments and sediment toxicity.

Inflammatory Gene Expression and Oxidative Stress in Human Lung Epithelial Cells Exposed to Combustion-Produced PM$_{2.5}$

Discipline: Life Sciences
Subdiscipline: Environmental Science

Heba Al Housseiny* and Patricia Silveyra, *The University of North Carolina at Chapel Hill, School of Nursing*

Abstract: Air pollution has become one of the greatest environmental health hazards to millions around the world. Exposure to air pollutants has been associated with respiratory and cardiovascular diseases, skin diseases, and long-term chronic diseases such as cancer and asthma. One of the major air pollutants is fine particulate matter ranging from 2.5 µm to 10 µm in aerodynamic diameter (PM$_{2.5}$ to PM$_{10}$). Growing evidence suggests that many of the adverse health effects of PM are associated with oxidative stress and inflammatory response. While cytokine expressions and protein carbonylation may serve as important biomarkers for numerous lung diseases, their role in PM$_{2.5}$-induced lung inflammation has not been extensively investigated, particularly in humans.

This work focuses on the identification of oxidative and pro-inflammatory factors induced as a response to exposure of human lung epithelial cells to combustion-produced soot (carbon black) in various surface chemistry forms. We exposed a human epithelial cell line (BEAS-2B) to lab-generated R-250 carbon black (nascent, nitric acid-treated, and ozone-treated carbon) and measured cell viability and gene expression of inflammatory cytokines (IL-1β, IL-6) and genes related to the inflammatory response and oxidative stress (SOD2, NFE2L2, HO-1, CCL2). Our data indicate that the surface chemistry and concentration of PM$_{2.5}$ play a critical role in the inflammatory and immune response and are associated with a decrease in cell viability and an increase in protein carbonylation and expression of several inflammatory cytokines.

Predicting the Occurrence of Plastic Ingestion in Seabirds: A Synthesis of Current Global Trends

Discipline: Life Sciences
Subdiscipline: Environmental Science

Julianna Ramirez*[1]; Myra Finkelstein[2]; Sami Michishita[2] and Liesbeth Van Hassel[2], *(1)Boise State University, (2)University of California, Santa Cruz*

Abstract: Plastic pollution is increasing in marine environments globally. For decades, researchers have quantified the prevalence of plastic ingestion in multiple marine species, but seabirds are arguably the most studied taxa with respect to plastic ingestion. Although many ecological drivers of plastic ingestion by seabirds have been identified such as taxonomy, foraging strategy, and diet, to our knowledge no assessment of the predictive factors for occurrence of plastic ingestion across seabird species has been published. We conducted a systematic literature review of the occurrence of plastic ingestion by seabirds worldwide and used a generalized linear model with a binomial distribution to determine the best predictors for the prevalence of plastic ingestion between seabird species. We focused on published literature that reported the presence of plastic ingestion in seabird species via stomach dissections or regurgitated samples from live animals. We expect, similar to prior studies, that foraging strategy and diet will continue to be strong predictors for the occurrence of plastic ingestion across seabirds. Our research will help inform the current state of plastic ingestion by seabirds across the globe by providing modeled predictors for occurrence that can help guide future risk assessment and mitigation strategies.

Modeling Fruit Orchards on a College Campus: The Carbon Sequestration Potential and the Economic Costs & Benefits

Discipline: Life Sciences
Subdiscipline: Environmental Science

Evelyn Jauregui*; Christine S. O'Connell; Shannon Hahn and Christie Manning, *Macalester College*

Abstract: Carbon sinks are able to sequester and store large amounts of CO2 from the atmosphere. By doing so, they help offset sources of carbon emissions. Although typically done on a larger scale, urban landscapes are capable of acting as carbon sinks. In 2004, the EPA measured that urban trees were able to sequester 88 megatonnes of CO2. What would the impact be if carbon sinks were developed on a smaller scale? This project looks at Macalester College, St. Paul, MN, in order to determine the implications of planting fruit trees on campus-wide carbon balance. We first consider the carbon sequestration capabilities of 6 semi-dwarf fruit trees on this campus and, second, we assess the economic costs and benefits of planting and growing the trees. Using iTree modeling, we predict that the carbon sequestered by fruit trees will offset, if not surpass, any carbon released from the planting stage and will push Macalester closer to their “Carbon Neutral by 2025” goal. Additionally, the costs associated with tree maintenance are likely to be lower than traditional lawn care in those replaced areas. Our initial results suggest that the mix of fruit trees leads to distinct changes to the carbon cycle and, further, that locally-made landscape management decisions drive differences in cost between treed and non-treed parcels. Based on these results, we can do the following: 1. Suggest changes to Macalester College land management that will benefit institutional carbon goals and 2. Develop recommendations for other institutions to encourage lower carbon footprints.

Oceanic Plankton - Not Throwing Away Their Shot

Discipline: Life Sciences
Subdiscipline: Environmental Science

Verenis Lucas[*], *Mount Saint Mary's University* and Richard Norris, *Scripps Institution of Oceanography*

Abstract: Like Hamilton’s arrival in New York, foraminifera occasionally lands in just the right place at the right time to make their “shot”. How does the stability of the oceanic ecosystems affect the ability of foraminifera to bloom? To test this idea, both the timing and abundance changes of fossil plankton were studied as they moved throughout the global ocean between 2-3 million years ago. We used a global network of deep-sea sediment cores to track the abundance and biogeographic movements of the planktonic foraminifera, *Globorotalia truncatulinoides*. Core chronology was established by comparing benthic δ18O for each site with the global chronology of Lisiecki and Raymo (2004). *Globorotalia truncatulinoides* evolved in the SW Pacific between 2.942-2.865 Ma, and subsequently dispersed into the tropical Atlantic by 2.528 Ma and then the tropical Pacific by 2.481 Ma. The species was always most abundant in the SW Pacific, whereas in the tropical oceans, foraminifer populations appeared for 20-100 kyr before dropping to such low numbers as to be undetectable. For example, in both the Caribbean and tropical western Atlantic, the species was only present for about 20 kyr, and then vanished for nearly 500,000 years. Even in the SW Pacific, there are strong fluctuations in population size that reflect changes in ocean circulation governed by the glacial-interglacial climate cycle. Oceanic plankton, like wind-dispersed dandelions, continuously disperse throughout the oceans, but only grow and bloom at rare times in what are otherwise unfavorable habitats.

Multi-Drug Resistance Plasmid Shared between Environmental and Community-Associated *Escherichia coli* Isolates

Discipline: Life Sciences
Subdiscipline: Environmental Science

Gisselle Jimenez[*]; Amelie Garenaux and Luis Mota-Bravo, *University of California, Irvine*

Abstract: The spread of antibiotic resistance is a worldwide epidemic that poses a threat to public health. Finding antibiotic resistance genes in *Escherichia coli* is especially worrisome since *E. coli* is the most common organism infecting outpatients. More specifically, strains carrying Extended-Spectrum Beta-Lactamases (ESBLs) are particularly difficult to treat. Conjugative plasmids are extrachromosomal DNA molecules that can be transferred between unrelated bacteria. We hypothesized that the environment is a source of conjugative resistance plasmids. The objective was to characterize the plasmids of an environmental resistant *E. coli* isolate from Baton Rouge, LA. The resistance profile was determined by disk diffusion test. A conjugation experiment was conducted using *E. coli* DH10B as the recipient. Plasmids were purified, sequenced with Illumina and Oxford Nanopore and assembled using Unicycler. NCBI BLAST and ISFinder were used to annotate and analyze the plasmid. It contained five plasmids. The largest (148.7 kb) was conjugative and carried the *blaCTX-M-27* (coding for an ESBL), *sul1*, *mph(A)*, *aadA5*, and *dfrA17* genes conferring resistance to Beta-lactams, sulfonamides, macrolides, aminoglycosides, and trimethoprim respectively. It shared a similar backbone and multi-resistance regions with 20 other plasmids found in different continents such as Europe and Asia. It is 99.86% identical to another *E. coli* plasmid from the USA associated with community-acquired urinary tract infections and carries similar resistance regions including genes coding for ESBLs. This study shows how the environmental bacterial gene pool constitutes a reservoir of antibiotic resistance genes carried on mobile genetic elements.

Characterization of a Genetic Suppressor of a Histone H3 Mutations That Perturbs Transcription Elongation in Budding Yeast

Discipline: Life Sciences
Subdiscipline: Genetics

Linh Nguyen[*]; Michael Doody and Grant Hartzog, *University of California, Santa Cruz*

Abstract: The basic unit of chromatin, the nucleosome is a protein/DNA complex consisting of 146 base pairs of DNA wrapped around a histone octamer. Nucleosomes are targets of regulation for many biological processes that function on DNA, such as gene transcription. We are interested in how histone H3, one of the four core histone proteins, regulates the structure and function of chromatin during transcription elongation. Our lab has previously identified histone H3 mutations which we hypothesize to disrupt chromatin structure, making chromatin more permissive to transcription elongation. We

isolated genetic suppressor mutations of one of these H3 mutations, *hht2-15R*. We hypothesize that this suppressor mutation restores normal chromatin structure in our H3 mutant. Whole-genome sequencing of a yeast strain carrying one of these suppressors revealed mutations in two genes; *IPP1*, which encodes an inorganic phosphatase, and *PEP12*, which encodes a t-snare protein involved in vacuole functions. However, genetic analysis shows that the suppressor falls in a single gene. We performed genetic linkage analysis to determine if either *PEP12* or *IPP1* is linked to the H3 suppressor mutation. Surprisingly, our data revealed that pep12-knockout and *hht2-15R* have synthetic lethal interaction. We hypothesize that vacuole functions are essential for cells' viability when chromatin structure are altered, and point-mutations in *PEP12* might give rise to *PEP12* nuclear function. The vacuole's functions have not been previously implicated in being essential for cell's viability. Thus, we are working to test our hypothesis and understand how the vacuole functions are essential when chromatin structure is altered.

Testing for and Comparing Curly Top Virus Strains in Leafhoppers and Chile Plants

Discipline: Life Sciences
Subdiscipline: Genetics

Athena Kvamme* and Rebecca Creamer, *New Mexico State University*

Abstract: Curly top virus affects a variety of crops in the Western United States, including sugar beets, tomatoes, and chile. It is transmitted by vector mainly through *Circulifer tenellus,* commonly known as the beet leafhopper, and can be devastating to fields. 2019 was a record year for these leafhoppers, and thus the virus was also highly prevalent. In an effort to track the viruses present in Southern New Mexico, chile samples were collected from the Leyendecker Plant Science Research Center and a nearby field. Leafhoppers were collected by sweep net weekly around Leyendecker from April 26 to October 10. These samples were tested with PCR for virus presence using the coat protein, and the strain of the virus was determined by targeting the Rep protein. We have found 5 strains of the virus: Worland, Pepper curly top virus, Colorado, Pepper Yellow Dwarf, and Leafhopper71. This is the first time the Colorado and Leafhopper71 strains have been recorded in New Mexico. So far, 50% of the chile samples collected in Leyendecker had the Pepper curly top virus strain. In contrast, the Worland strain has been identified in 48% of samples collected by a nearby field.

Modeling Copa Syndrome in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Genetics

Isabella Zafra Martinez*, *York College of Pennsylvania* and Andy Golden, PhD, *National Institutes of Health*

Abstract: There are approximately 7,000 known rare diseases in humans, 80% of which are monogenic. Treatments have been developed for less than 5% of these rare diseases. Therefore, there is a need for researchers to employ model organisms as tools for studying molecular mechanisms underlying these diseases. Whole-genome sequencing has allowed identification of disease-associated alleles for many of these rare diseases. The nematode *Caenorhabditis elegans* has 20,000 protein-coding genes, ~40% of these estimated to have human orthologs. Its physiological simplicity and short life cycle makes *C. elegans* a great model for studying genes associated with human disease. Using CRISPR-Cas9, we gcreate mutations in the worm that mimic mutations in these patients and can study the resulting phenotypes observed in the worm.

COPA syndrome is an autosomal dominant ultra-rare disease caused by missense mutations in the *COPA* gene which codes for a protein subunit involved in Golgi to ER transport. We generated a gene knockout and several disease-implicated human missense alleles in the worm ortholog *copa-1.* The deletion and a deletion of the 14 amino acid region that contains all 6 known patient alleles results in embryonic lethality. Using a fluorescent marker for an ER Stress marker (BiP) worm ortholog, *hsp-4*, we observed worm strains with patient alleles display heightened basal level of ER stress compared to wild-type worms, which increased with chemical ER stressors like Tunicamycin. Our goal is to uncover suppressing mutations in order to tease apart genetic interactors that contribute to this disease and identify possible future drug targets.

Optimizing Genotyping Protocol of the Purple Faced Langur

Discipline: Life Sciences
Subdiscipline: Genetics

Kimberly Louisor*[1]; Sandra Almanza[1]; Amy Lu[2] and Andrea Lee Baden[1], *(1)Hunter College, City University of New York, (2)Stony Brook University*

Abstract: Studying the endangered purple faced langur (*Semnopithecus vetulus*), a primate native to Sri Lanka, can give insight to the status of Sri Lanka's forests. With a quickly declining population of unknown size, we aim to study their genetic diversity to better understand the population demography and health of this Critically Endangered langur species in Sri Lanka, and by extension, its forests. Using total gDNA from fecal samples non invasively collected between 2018-2019, we are working to design an array of primers that will be used to genotype individuals from this population. Unfortunately, without a reference genome, we are limited to using primers designed for closely related primate species. We hypothesized that small dinucleotides with "CA" repeat motifs would give viable results. We tested n=13 primers that were previously designed for their closest relative, the Grey Langur (*Semnopithecus),* using PCR and gel electrophoresis. Thus far 62% (8 of

13) of the primers have been used to successfully amplify small microsatellite sequences. With these primer pairs, we are currently running multiplex PCR amplifications to genotype individuals for downstream population genetic analyses.

Phenotypic and Molecular Characterization of *C.Elegans* suppressor Strains

Discipline: Life Sciences
Subdiscipline: Genetics

Sandra Delgado* and Peter Okkema, *University of Illinois at Chicago*

Abstract: T-box transcriptional factors are important developmental regulators in all multicellular organisms. Defects in these factors are associated with a variety of human congenital diseases and cancers. However, the mechanisms of their functions are not yet understood. The T-box factor TBX-2 functions with the Groucho family transcriptional co-repressor UNC-37 to promote normal pharyngeal development in *C. elegans*. Double mutants for the hypomorphic mutations *tbx-2(bx59)* and *unc-37(e262)* express partial loss of pharyngeal function and a completely penetrant temperature sensitive lethal phenotype (Huber et al., 2016).

To identify novel genes that function with TBX-2 and UNC-37, previous students have isolated 7 new mutants that suppress *tbx-2(bx59); unc-37(e262)* lethality at the non permissive temperature.

My work focuses on the suppressor gene identified as Sup 19.1. Preliminary mapping hints that the Sup 19.1 mutation is linked to UNC-37 and is located either on the far right or far left end of LGI.

Our lab performed whole genome sequencing of all 7 suppressed strains. In the genome sequencing for Sup 19.1, we've identified 2 candidate mutations located at the left arm of LG1 that may be the Sup 19.1 suppressor mutation. The first candidate mutation is a missense mutation in a gene called C48G1C.5, which encodes a protein tyrosine phosphatase. The second is a nonsense mutation in the gene Y48G8AL.1 (or herc-1) that encodes an E3 Ubiquitin ligase.

*Drosophila Melanogaster G*ene *Mary Shelley* (*CG6191*), Co-Localizes with Notch Signaling Components in the Developing Wing

Discipline: Life Sciences
Subdiscipline: Genetics

Razan El Yaman*; Jacob Kagey; Ali Zamat and Amber Elinsky, *University of Detroit Mercy*

Abstract: *Drosophila melanogaster* is a well-established genetic model organism allowing for spatial and temporal gene disruption to understand gene regulation during development. Additionally, *Drosophila* share a number of well conserved developmental pathways with humans, and many of these are disrupted in human tumorigenesis. We are working to understand the developmental expression patterns of the *Drosophila* gene *CG6191*, *Mary Shelley (MS)*, knowing its human homolog, *Cables-1*, that's downgraded in human cancer, such as ovarian cancer. Here, we use the wing to identify the expression pattern of MS observed during wing development at various stages and use co-localization to identify what developmental pathway(s) MS is involved with. For expression studies, we utilized the MiMIC system to visualize expression patterns. We find that MS expresses along a distinct band of expression in dorsal/ventral boundary compartment of the wing disc, in a similar expression pattern to the Notch cell signaling pathway. To determine co-localization with other development pathways we co-stained MS expressing cells with known developmental pathway members. MS was found to co-localize with Delta expression patterns along D/V boundary. This co-localization was distinct from Notch and Wingless. To understand the developmental role of MS in the wing, we utilized RNAi knockdown, which resulted in reduced adult wing size due to apoptosis in larval stage. Data provides that MS may be involved with developmental Notch signaling and cell survival. Importantly, understanding the role of *MS* in the Notch signaling pathway may help us understand the mechanisms of mutations in *Cables1* lead to tumorigenesis in humans.

Loss of *Mary Shelly* (CG6191) in *Drosophila* Causes Compensatory Apoptosis in Imaginal Wing Discs

Discipline: Life Sciences
Subdiscipline: Genetics

Ali Zamat*; Razan El Yaman and Jacob Kagey, *University of Detroit Mercy*

Abstract: *Drosophila melanogaster* is an ideal model organism to study the genetics of gene regulation during development. Our research focuses on the gene CG6191, or *Mary Shelley* (*MS*), which is a previously uncharacterized gene. The human homolog, *Cables-1*, has been shown to be down regulated in a number of different human cancers including ovarian and endometrial. Using the imaginal wing discs as a model, we can utilize the UAS-Gal4 system to express RNAi targeted at MS to understand the phenotypic consequences. When MS is reduced in the posterior side of the wing disc, we observe a strong increase in cell death, which is shown through staining of the *Drosophila* caspase DCP-1. Also, non-autonomous apoptosis results on the anterior compartment of the wing, despite no disruption of MS gene expression. The apoptosis observed in the larval stage alters the size and shape of the adult wing dramatically when MS is reduced. From this data we hypothesize that the JNK signaling pathway may be activated within the apoptotic cells of the posterior where MS is knocked down. This activation of JNK would then create a long-distance cell death signal, resulting in non-autonomous and compensatory apoptosis. To test this we plan to utilize the JNK reporter Puckered>LacZ, to see if the cells are capable of regenerating back into its original form. A more thorough understanding of the mechanisms that drive apoptosis after a

reduction in MS could help to better understand the molecular consequences resulting from a loss of Cables-1 in human tumor development.

Genetic Variability of the Fcγ Receptor in the Population and Its Role in Disease Dynamics and Pathogenesis

Discipline: Life Sciences
Subdiscipline: Genetics

Leah Darwin* and Susan Holechek, *Arizona State University*

Abstract: Dengue is a vector borne disease estimated to affect 390 million people worldwide, and is transmitted mainly by *Aedes aegypti*. DENV has four known serotypes, DENV-1, DENV-2, DENV-3, DENV-4, all circulating in Mexico. Patients infected can develop Dengue Fever (DF), Dengue Hemorrhagic Fever (DHF) or Dengue Shock Syndrome (DSS). DHF and DSS are associated to reinfection with a secondary serotype due to antibody dependent enhancement (ADE). The FcγIIA receptor protein has shown to be responsible for the potential reinfection of DENV due to ADE. The antibody-virus complex binds to FcγIIA receptor protein, infecting the host cell and facilitating viral replication. Data collected from a local population in Arizona was sampled in order to determine the genotype distribution for the Fc receptor. In this work a system of ordinary differential equations is constructed and used to describe how the distribution of FcγIIA polymorphisms in a susceptible population affect the potential of a Dengue outbreak. Through the use of this model it was shown that increased rates of reinfection due to genetic variation allow the virus to persist in a population resulting in an epidemic. This result can guide preventative measures to aid highly susceptible populations at a genetic disadvantage.

The Role of the Female Nervous System in Sexual Conflict and Sexual Selection: An Exploration into *Drosophila Melanogaster M*ating Plug Ejection

Discipline: Life Sciences
Subdiscipline: Genetics

Mikaela Matera-Vatnick*; Dawn Chen and Mariana Wolfner, *Cornell University*

Abstract: In many insects and mammal species, a mating plug forms in the female reproductive tract soon after she starts to mate with a male. The plug prevents female remating and enables sperm storage until the plug is ejected. In multiply mated *Drosophila melanogaster* (fruit fly) females, the timing of the mating plug ejection influences the paternity share of her mates, thereby playing an important role in sexual conflict and selection. Nonetheless very little is known about the neuronal mechanisms by which females control mating plug ejection. The goal of this project is to leverage natural genetic variation in the mating plug ejection time across a panel of genetically diverse *D. melanogaster* lines to reveal key genetic variants associated with mating plug ejection through a genome-wide association study (GWAS), and to ultimately investigate the mechanistic basis of mating plug ejection. We hypothesized significant variation across the lines since they were isolated from a natural population. Results show significant variation in mating plug ejection time across 16 lines I have assayed. Pairwise comparisons show that 45 out of the 120 pairwise tests have significantly different ejection times. Future directions include assaying 14 additional lines, performing the GWAS and functionally testing revealed candidate genes. Our results support our hypothesis and will likely reveal significant genetic variants that are associated with ejection timing. These insights will allow us to better understand the role of the female nervous system in controlling mating plug ejection and the female contribution in mating outcomes and sexual selection.

Healthy Longevity on the Hispanic Population Living in the Rio Grande Valley

Discipline: Life Sciences
Subdiscipline: Genetics

Chun Xu; Kimberly Moreno* and Victoria Padilla, *University of Texas Rio Grande Valley*

Abstract: Through the past decades, life expectancy has increased drastically in all ethnic groups. One of the ethnic groups with the highest mortality rates in the United States is the Hispanic population. However, the Hispanic population also have high rates of low education, low economic status and of chronic diseases (e.g., Alzheimer's disease, cardiovascular diseases, obesity, and others). Unfortunately, there are limited studies being conducted in the Hispanic populations to find a correlation between healthy longevity and specific genes in addition to lifestyles factors. The purpose of this investigation is to find specific genes and lifestyle factors that may contribute to healthy aging. 100 and still counting Hispanic individuals, older than 85 that reside in the RGV were recruited. Saliva samples, as well, four different questionnaires; medical history, demographics, familism, and lifestyle were collected from participants. Saliva samples and questionnaires were also collected from descendants (siblings and offspring) since this study will be design as a family/case control design. The second section included laboratory work to obtain DNA from saliva sample by purifying and checking DNA concentrations to analyze specific genes and quantify the data using t-test, c2 test in the SPSS v25 and other statistical tests. This research is still ongoing, we expect that genes and their SNPs, that have been previously associated with longevity in other ethnic groups, will be linked with longevity on the Hispanic population. Also, it is expected that there is a correlation between healthy ageing and lifestyle factors that may clarify the Hispanic Paradox.

Using Protein Binding Microarrays to Analyze DNA Binding Differences of Human Transcription Factor Isoforms

Discipline: Life Sciences
Subdiscipline: Genetics

Violet Kimble*[1]; Kaia Mattioli[2]; Sabrina K. Phanor[2]; Patrick K. Kimes[3]; Sachi Inukai[2]; Tong Hao[3]; Gloria M. Sheynkman[3]; Juan I. Fuxman Bass[4]; Marc Vidal[3] and Martha L. Bulyk[2], *(1)Drew University, (2)Brigham & Women's Hospital/Harvard Medical School, (3)Dana-Farber/Harvard Cancer Center, (4)Boston University*

Abstract: There are approximately 20,000 protein-coding genes in the human genome, but it is estimated that this set of genes encodes ten times as many unique mRNA isoforms. However, the role that distinct isoforms play in biological processes is underexplored. I aim to understand how isoforms of one particular class of proteins--transcription factors (TFs)--may have different biological effects. TFs regulate gene expression by binding to specific DNA sequences and recruiting transcriptional machinery. If TF isoforms of the same gene bind to different DNA sequences, they are likely to have different effects on gene expression. TF-DNA binding can be assayed in high throughput using a technique called in vitro protein binding microarrays (PBMs), which flows fluorescently-tagged TFs over a DNA microarray. TF binding to a given DNA sequence can then be read out by fluorescence, mapped back to specific DNA 8-mers. I have performed an analysis of PBM data to characterize the DNA binding differences between human TF isoforms. Specifically, I have analyzed the DNA binding patterns of the reference and alternative isoforms of eight disease-associated TFs: ELF2, HMBOX1, IKZF2, NFATC1, OTX2, PKNOX1, TBX5, and TEAD2, and see evidence that TF isoforms of the same gene have different DNA binding patterns. My analysis expands on existing knowledge of human TF binding diversity and points to the importance of understanding TF isoforms, as the vast majority of TFs have multiple different isoforms whose DNA binding patterns are unknown. Unpacking TF isoform-level complexity is pivotal to further our understanding of human gene regulation.

NFATc1 As a Novel Atrial Fibrillation Susceptibility Gene

Discipline: Life Sciences
Subdiscipline: Genetics

Alexandra Acuna*; Yueqin Yang, PhD; Dr. Natalia Torres, PhD and Martin Tristani-Firouzi, MD, *Nora Eccles Harrison Cardiovascular Research and Training Institute (CVRTI), University of Utah*

Abstract: Atrial Fibrillation (AF) is the most common type of cardiac arrhythmia. It is a progressive disease that increases the risk of stroke, heart failure, and sudden death. Familial AF (several family members affected with a young-onset presentation at <40yo) has a strong genetic component. Using whole-exome sequencing, we identified a novel autosomal-dominantly segregating mutation (M527L) in the Nuclear Factor of Activated T-Cells 1 gene (*NFATc1*) within a family with young-onset AF. *NFATc1*, not previously linked to arrhythmia, codes for a transcription factor important in heart development, and pathological hypertrophy. In order to understand the direct effect of NFATc1 in ion channel genes expressed in the heart, we transfected the mouse immortalized atrial HL-1 cells with small interfering RNA (siRNA), predicted to induce gene silencing through targeting complementary mRNA for degradation and consequently reducing protein levels. We hypothesize that silencing NFATc1 will impact relevant cardiac gene expression leading to increased cardiac excitability and substrate for developing AF. To test this hypothesis, we will use qPCR to quantify changes in ion channel gene expression in the transfected HL-1 cells. We expect to find altered ion channel gene expression, particularly in genes related to Ca^{2+} homeostasis. If qPCR shows no change directly in gene expression, we will investigate how other forms of channel activity regulations (e.g., phosphorylation) may be altered in the transfected cells. This information will provide insight into the mechanism by which NFATc1 contributes to AF in the general population and may allow for more accurate treatment for Familial AF patients.

Discovering New Sleep Genes in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Genetics

Clarissa Nassar* and Cheryl Van Buskirk, *California State University, Northridge*

Abstract: Although sleep is a behavior that all animals appear to engage in, its cellular function is unknown. Because sleep has been conserved throughout evolution, it can be studied in simpler organisms such as the roundworm *Caenorhabditis elegans* (*C. elegans*). Intriguingly, this worm sleeps when it experiences cellular damage from environmental stressors such as UV, heat, and bacterial toxins. This form of sleep is known as stress-induced sleep (SIS), and failure to engage in SIS following noxious exposure is associated with decreased survival. These observations suggest that cellular damage drives sleep need and that a key function of sleep is to repair cellular damage. In support of this notion, zebrafish show increased sleep after UV-induced DNA damage, and this sleep is associated with increased cellular repair. Thus, the identification of novel sleep genes in nematodes may help us to better understand the fundamental role of sleep in vertebrates. To identify additional sleep genes in *C. elegans*, our lab has undertaken a genetic screen for SIS-defective mutants. The goal of this project is to characterize one of these sleepless mutants and to identify the associated sleep gene, with the ultimate goal of uncovering a deeply conserved element of sleep regulation.

Identification of Genes Involved in the Formation of Genomic Amplification Mutations in the Soil Bacterium *Acinetobacter Baylyi*

Discipline: Life Sciences
Subdiscipline: Genetics

Jennifer Serrano*, *California State University, Sacramento* and Semarhy Quinones-Soto, *California State University,Sacramento*

Abstract: Genomic amplifications are mutations that result in repeated sections of a genome. Existing in almost all living organisms, most of what we know about their formation is unknown. It is important to understand the mechanisms of genomic amplifications as they are key factors in antibiotic and herbicide resistance, cancer cell growth, and anticancer drug resistance. This study focuses on the identification of genes involved in the formation of genomic amplifications using the soil bacterium, *Acinetobacter baylyi*. Student researchers from a course-based research experience (CURE) performed reversion assays where *A. baylyi* mutants unable to utilize benzoate (*ben*-) as food source were grown on benzoate-only minimal medium. After a long incubation period, newly formed Ben+ colonies accumulated on the benzoate-only plates. The *A. baylyi ben-* tester strain used in the CURE was genetically altered to lack the transcription activators needed to grow on benzoate. Past analyses of Ben+ revertants showed increase in gene products due to amplification of benzoate degrading genes, even in the absence of their transcription activators. The goal of my project is to analyze the reversion data collected by the CURE students using *A. baylyi* knock-out mutant strains of genes suspected to be involved in the formation of genomic amplifications. Preliminary findings show a decrease in the accumulation of new Ben+ colonies suggesting some of the gene knockout strains were unable to form genomic amplifications. Successful identification of these role player genes may serve as future targets for gene amplification manipulation and the advancement of anticancer drug development.

Gene Regulation: How Nucleosome Occupancy at the Promoter Can Regulate Transcription

Discipline: Life Sciences
Subdiscipline: Genetics

Znala Williams* and Hinrich Boeger, *University of California, Santa Cruz*

Abstract: Transcription requires gene activation. One aspect of activation requires the removal of nucleosomes from the promoter by activators. Once removal has occurred, how do cells prevent the other nucleosomes from invading the promoter region? Do the cells set up boundaries to preserve regions of low nucleosome occupancy? We analyzed nucleosome occupancy, by topology, at the active promoter of the PHO5 locus in saccharomyces cerevisiae(baker's yeast) to answer this question. There are several hypotheses on how this barrier is achieved. The position of the +1 Nucleosome is unique because its biochemical properties allow it to attract certain chromatin remodelers and receive special markings from them. In particular, the protein SET1 only tri-methylates the histone H3K4 of the +1 Nucleosome, which may be essential to how the barrier is maintained. It may also be a result of the TATA-binding protein TBP being so large that the nucleosome is sterically hindered from moving further. After performing a series of mutations, we found that when SET1 was disabled nucleosomes gained the ability to breach the promoter. Our experiments prove that SET1 must be fundamental to maintaining this barrier, which supports the claim from our first hypothesis. We concluded that H3K4 methylation by SET1 at that position is required to establish a nucleosome block, preventing intrusion of nucleosomes into the promoter.

Genetic Associations between Common Variants in the Genetic Architecture of Individuals with Obesity and Type 2 Diabetes and Sars-Cov-2 Outcomes

Discipline: Life Sciences
Subdiscipline: Genetics

Andrew DePass*[1]; Timothy Majarian[2]; Magdalena Sevilla[2]; Kenneth Westerman[2] and Alisa Manning[2], *(1)Quinnipiac University, (2)Broad Institute of MIT and Harvard*

Abstract: Diabetes is a disease that affects 1 in 11 adults in the global population, and type 2 diabetes (T2D) accounts for the overwhelming majority of diabetes in adults. Obesity is a risk factor for both T2D and insulin resistance, the primary driving factor of T2D in adults. T2D and obesity have been implicated as comorbidities leading to worse outcomes in individuals with COVID-19 after Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) infection. The genetic basis for COVID-19 susceptibility and disease severity are largely unknown. COVID-19 genetic susceptibility has been largely focused on genes that contribute to the presence of Angiotensin Converting Enzyme 2 (ACE2), the key receptor that allows for SARS-CoV-2 interaction with human cells. Here, we investigate if obesity and T2D are modifying factors in the associations of common genetic variants with COVID-19 outcomes. We performed a gene-environment interaction analysis using the UK Biobank data resource and considered T2D status and obesity status as environment factors and SARS-CoV-2 hospitalization, laboratory confirmed SARS-CoV-2 infection, and SARS-CoV-2 death as outcomes. Our results will implicate regions of the genome where the mechanisms leading to T2D and/or obesity also contribute to COVID-19 outcomes. We will prioritize genes within these regions using bioinformatic tools that integrate gene pathways and gene functions. This study could identify possible targets for COVID-19 treatment and prevention.

Acute Endurance Exercise Induces Transcriptional Changes in Gastrocnemius Tissue

Discipline: Life Sciences
Subdiscipline: Genetics

Talha Lone*[1]; Nicole Gay[2] and Stephen Montgomery[2], *(1)Duquesne University, (2)Stanford University*

Abstract: Exercise is considered an important intervention for the prevention and treatment of diseases such as obesity. Yet, how exercise serves to improve these conditions on a molecular level is poorly understood. To evaluate exercise molecular underpinnings, we levied data generated by the Molecular Transducers of Physical Activity Consortium (MoTrPAC) to address the gap in knowledge by generating a vast resource of multi-tissue, longitudinal, multiomics data sets related to exercise response. We specifically considered transcriptome data from samples at 7 time points immediately following a single bout of acute endurance exercise exclusively in male rats. Specifically, we investigated patterns of alternative splicing that were different between exercised rats and unexercised controls at each post-exercise time point. We focused on gene expression in gastrocnemius tissue, a lower leg skeletal muscle.

We observe the greatest number of significantly different splicing events 48 hours after exercise (adjusted P value < 0.05). However, we see differential splicing events due to exercise at all 6 preceding time points as well. Pathway enrichment analysis was performed with the set of differentially spliced genes to link these exercise-induced changes to known biological processes, where we found evidence of several genes being differentially spliced at multiple time points, such as Ppargc1a and Nr4a3– genes that have been previously implicated in exercise response. In the future, this analysis can be extended across both sexes and multiple tissues to identify coordinated changes in splicing across organs.

First Report of Plasmid-Borne *dfrA14* Trimethoprim Resistance Gene in Environmental *Klebsiella Oxytoc*a

Discipline: Life Sciences
Subdiscipline: Genetics

Iris Molina*; Andrei Tatarenkov and Luis Mota-Bravo, *School of Biological Sciences, University of California, Irvine*

Abstract: Antibiotic resistance is a global health concern as bacteria harbor and share large conjugative plasmids (>40kb) encoding resistance. Small plasmids that carry multidrug resistance genes are rare, thus the importance of their study. We hypothesize that natural environment serves as a reservoir of resistant bacteria. The objective of this study is to characterize the plasmids of environmental *Klebsiella oxytoca* isolate SW3205 from Rock Creek Kensington, Maryland, describe antibiotic resistance genes, and identify possible dispersal mechanisms. Isolate SW3205 underwent susceptibility tests, identification, DNA extraction, sequencing and bioinformatic analyses. The isolate SW3205 carried three plasmids measuring 197 kb, 6.8 kb, and 3.2 kb. The 6.8 kb plasmid was identified as Col and contained a cluster of four antibiotic resistance genes: *sul2-DstrA-dfrA14-DstrA-strB,* encoding resistance to Sulfisoxazole and Trimethoprim. Comparative analysis with BLAST showed that this plasmid exists as part of larger plasmids, known as cointegrates, as well as on its own in *Salmonella, Escherichia*, *Citrobacter, Shigella, Yersinia* and *Klebsiella* bacteria. The isolation sources include human, animal, environmental, and food samples from America, Asia, Europe, and Africa. Since this Col plasmid was found among different species and environments across the globe, it has spread through horizontal gene transfer. SW3205 is the first reported environmental *Klebsiella oxytoca* isolate carrying a Col plasmid and *sul2-DstrA-dfrA14-DstrA-strB* antibiotic resistance cluster, demonstrating that the environment is an important reservoir of resistant bacteria. Further studies shall explore its distinctive recombination and its role in the spread of antibiotic resistance genes in bacteria.

Analysis of NOTCH2NL Gene Variants and CNVs in Autism Cohorts

Discipline: Life Sciences
Subdiscipline: Genetics

Shamari Waller* and Colleen Bosworth, *University of California, Santa Cruz*

Abstract: Characterizing the variations in human lineage-specific genes responsible for brain development and expansion has posed a challenge in the field of genomics. Advancements in sequencing technology has allowed us to identify specific regions in the genome that can provide insight into neurodevelopmental disorders. Our research investigates NOTCH2NL gene and its role in brain expansion and human cortical development in human evolution. NOTCH2NL, found in the Q21 region on chromosome 1, is in a location in the human genome that undergoes distal duplication syndrome. This syndrome has increased the amount of varied copies of NOTCH2NL humans have, affecting the signaling of NOTCH receptors responsible for brain/intellect development. Within the NOTCH2NL region we explore that there may be an inherited variant activating the Autism Spectrum Disorder (ASD) phenotype. Using clinical data from Simons Research Initiative, we align patient sequence data to the hg38 human reference genome and a NOTCH2NL consensus genome. The alignments will reproduce the sequence data in a variant call format (VCF) outputting a list of any gene variants that arises. The VCF will help produce singly unique nucleotide (SUN) identifier maps that graph the frequency of a variant at each base position within the NOTCH2NL gene. We can then filter the cohort for variants in >1% of the population (dbsnp) and not known to be benign (clinvar), leaving us with locations of unique variants. After we have characterized unique variants and their locations, we can further investigate how the activated ASD phenotype can be inherited in NOTCH2NL gene variants.

Simulating Genealogical Searching to Analyze Distant Relative Misidentification in Forensic Investigations

Discipline: Life Sciences
Subdiscipline: Genetics

Emily Samperio[*], *California State University : San Francisco* and Rori Rohlfs, *San Francisco State University*

Abstract: Genealogical searching, also known as long range familial searching, is a forensic technique used to identify a suspect through their long distant relatives using a genetic genealogy database. A genetic relationship is established from a relative to a suspect through shared inheritance of autosomal DNA segments which are Identical-By-Descent (IBD). More distant genetic relationships have shorter and fewer shared IBD segments due to the number of meiosis events that have occurred since the last common ancestor. Over 60% of individuals of European descent can be identified using long range familial searching, however the risk of unwarranted investigation in our diverse population is unknown and may be impacted by IBD variability. Long distance relatives, particularly those from some population genetic backgrounds, may share a large amount of IBD segments due to chance, prompting investigators to inaccurately infer a closer relationship. For example, a 5th cousin may share a large enough IBD tract to resemble a 3rd cousin. If IBD variability is disregarded, then investigators could search family trees that don't contain the offender. In this study, we investigate rates of misidentification by using simulations to estimate IBD variability on a large empirical pedigree (FamiLinx) containing 86 million individuals. We've organized and represented FamiLinx using Networkx, a Python package used for large network data manipulation. We then simulated genetic variants for individuals in these pedigrees using SLiM, a forward population genetic simulation software. Results from this work could provide preliminary estimates of distant relative misidentification in genealogical searching.

Using Machine Learning Approaches to Improve European Subpopulation Ancestry Inference for Genome Wide Association Studies on Wegener's Syndrome (Granulomatous Polyangiitis) Patients

Discipline: Life Sciences
Subdiscipline: Genetics

Leen Arnaout[*1]; Rowland Pettit[2]; Jinyoung Byun[2] and Christopher Amos[2], *(1)Boston University, (2)Baylor College of Medicine*

Abstract: Wegener's syndrome is an auto-immune, respiratory-system blood vessel inflammation disease, with a mortality rate of >90%, affecting 3/100,000 Europeans. Genome Wide Association Studies are used to identify genetic markers associated with Wegener's syndrome, to guide early-detection efforts. To avoid false positives from ancestry-based genetic differences, studies are done within genetically-homogeneous ancestral subpopulations. Previous approaches inferred ancestry as distances between unknown-ancestry individuals and centroids of known-ancestry populations. However, incorrect ancestry may be discerned for them when we lack control samples with similar ancestry/markers. Therefore, we investigated if Machine Learning models can improve such ancestry stratification's accuracy by discerning how genetic patterns influence subpopulation membership.

A HapMap dataset of 24,705 ancestry-informative markers for 952 controls of 7 known European subpopulations was obtained, and split into training and testing sets. Using Python 3.6's sklearn library, we trained two models, supervised k-nearest neighbor (k-NN) and unsupervised k-means clustering, then used them to classify test data. Analysis was repeated after data dimensionality was reduced using Principal Component Analysis (PCA). Accuracy was calculated as percent agreement between the dataset's original labels and the model's classification.

Pre-PCA, k-means clustering's accuracy was 38%, while k-NN's was 22.3%. PCA improved accuracy: k-means clustering accuracy was 46%, outperformed by k-NN with 91%. With larger datasets and seeding subpopulation clusters manually, k-means accuracy can be improved. K-means is reliable, with subpopulation grouping similar to researchers', but with slight differences, like separating previously-grouped-together Sardinians from South Europeans. Scientists may combine genetically/geographically-proximal groups if they are too small to infer trends from alone.

Using Nitrogen Isotopes in Amino Acids Preserved in Corals and Surficial Sediments to Reconstruct Euphotic Zone N Sources and Trophic Structure.

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Evelyn Kuhnel[*1]; WingMan (Charlotte) Lee[1]; Ava Kreider-Mueller[2]; Mark Altabet[2] and Lin Zhang[1], *(1)Texas A&M University at Corpus Christi, (2)University of Massachusetts Dartmouth, School of Marine Science and Technology*

Abstract: Nitrogen (N) is a limiting nutrient for productivity in open ocean and regulates atmospheric CO_2 sequestration into deep ocean. Different N sources and trophic positions in the surface ocean have unique N isotope ratios ($\delta^{15}N$), which are imbedded in sinking particles and transported into deeper ocean. Sinking particles are consumed by corals and buried in sediments, the unique $\delta^{15}N$ produced in the euphotic zone are thus recorded in coral skeletons and sediments. Compound-specific $\delta^{15}N$ of individual amino acids (AA) can be used to retrieve these information. The $\delta^{15}N$ of phenylalanine (Phe) retains the baseline $\delta^{15}N$ of N sources, unaffected by trophic transfer, while glutamic acid (Glu) demonstrates significant ^{15}N enrichment with each trophic transfer. In this study, AAs in corals from the South China Sea and sediments from the Gulf of

California (GoCA) were liberated via acid hydrolysis, purified through ion-exchange resin, then separated and collected using an Ion-Exchange Chromatography for $\delta^{15}N$ analysis. The $\delta^{15}N$ of Phe and Glu in GoCA sediments were 12.35‰ and 24.88‰. The trophic position of GoCA sample was 2.51, suggesting that the sediments mainly derived from primary and secondary producers. The $\delta^{15}N$ of Phe (12.35‰) was higher than the average global ocean nitrate value (~5‰), indicating that the nitrogen source was upwelled from a deeper basin affected by water-column denitrification. Coral samples are being analyzed. Our results demonstrate that the $\delta^{15}N$ of Phe and Glu recorded in sediments and corals can be used to reconstruct the N sources and trophic positions in surface ocean.

Tentacle Development in Pedal Lacerates of the Cnidarian *Exaiptasia Pallida*(Aiptasia) Is Influenced By Symbiotic State

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Elizabeth Wirsching*; Jason Presnell and Virginia Weis, *Oregon State University*

Abstract: The tropical sea anemone *Exaiptasia pallida* (Aiptasia) forms a symbiotic relationship with dinoflagellate algae of the family Symbiodiniaceae, the same algae found in corals. Aiptasia is an ideal model organism because they are low maintenance, able to be rendered without their algae (aposymbiotic) and kept in this aposymbiotic (Apo) state indefinitely, and rapid proliferation through asexual pedal laceration. Pedal lacerates, small bits of tissue pinched off from the pedal disc, grow into an adult polyp. Symbiotic (Sym) pedal lacerates develop into fully formed polyps in ~15 days. However, little is known about the early stages of lacerate development and if the symbiotic state affects this. It is hypothesized that Apo pedal lacerates will develop slower than Sym pedal lacerates due to a lack of nutritional input given by the algae. To test our hypothesis, we characterized the spatio-temporal patterns of new tentacle formation in both Apo and Sym pedal lacerates for a 20-days by combining brightfield microscopy and confocal fluorescence microscopy. Our data show that new tentacles orient around the oral disc similarly in both Apo and Sym pedal lacerates. Additionally, Apo pedal lacerates develop tentacles before Sym pedal lacerates up to the 8 tentacle stage but were then surpassed by Syms. Tentacles tended to develop in pairs, usually in a *trans* orientation for the first 8 tentacles, followed by *cis* orientation for the remainder. Overall, Aiptasia pedal lacerates present an effective experimental system for studying the cellular and molecular mechanisms underlying symbiosis onset, maintenance, and breakdown.

Localizing Opsin Gene Expression in the Visual System of the Copepod *Labidocera Madurae*

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Kristina Theam*; Mireille Steck and Megan Porter, *University of Hawaiʻi at Mānoa*

Abstract: Copepods are the basis of many marine food webs, serving as the essential link between photosynthetic phytoplankton and larger, heterotrophic marine sea creatures. Despite their ecological importance, not much is known about how their visual systems function. While most copepod species have a singular three-partite eye, the Pontellid copepods have modified this eye type, forming three separate eyes: two dorsal and one ventral. The dorsal eyes are especially unique due to the presence of an enlarged lens, scanning abilities, and an unusual photoreceptor setup. Additionally, the genus *Labidocera* is sexually dimorphic—males tend to have much larger dorsal eyes than females. Because of the uniqueness of *Labidocera* eyes, it is valuable to analyze their opsin gene expression, as opsins are proteins that mediate light detection in animal visual systems. It is hypothesized that opsin gene expression will differ between the ventral and dorsal eyes, and between male and female eyes. Three opsin genes were previously isolated from *Labidocera madurae*, a species local to Hawaiian waters. These genes were used to create mRNA riboprobes, which label sites of gene expression through the process of *in situ* hybridization. Confocal microscopy work showed that the most highly expressed opsin gene was detected in three distinct regions in the dorsal eyes of adult females. The other two opsin genes were not detected in the dorsal eyes of adult females. Further work on the confocal must be done to examine gene expression in the ventral eye of females, as well as in adult male eyes.

Investigating the Female Reproductive Anatomy of Viviparous Surfperches (Embiotocidae) Using a Medical Diagnostic Technique

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Shereen Lam*, *California State University Fullerton* and Kristy Forsgren, *California State University, Fullerton*

Abstract: Viviparous surfperches give live birth to offspring after retaining the developing offspring within the ovary. Female surfperches are unique in that they have a single ovary that presumably is connected to the genital opening which is located on the ventral side of the fish. Unfortunately, little else is known about female surfperch reproduction and reproductive anatomy. By employing a specialized medical diagnostic tool called diffusible iodine-based contrast-enhanced computed tomography, in conjunction with digital reconstruction using computer segmentation software, we hypothesize that the female reproductive tract anatomy can be elucidated and described. Our research focuses on four surfperch species: dwarf perch (*Micrometrus minimus*), shiner perch (*Cymatogaster aggregata*), walleye surfperch (*Hyperprosopon* *argentuem*), and black perch (*Embiotoca jacksoni*). We anticipate confirming that the genital opening is directly connected to the ovary through the labyrinth of the female reproductive tract. It is imperative to gain a better understanding of the female reproductive anatomy in order to expand our knowledge about surfperch reproductive mechanisms. Our research could provide insight on the ability of females to store sperm for extended periods of time and sperm competition.

Are Dwarf Perch (*Micrometrus minimus*) Born Sexually Mature?

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Taylor Naquin* and Kristy Forsgren, *California State University, Fullerton*

Abstract: Surfperch are internally fertilizing, viviparous marine fishes. It has been reported that dwarf perch (*Micrometrus minimus*) are born sexually mature, but no empirical data exists to support this claim. We hypothesize that gonadal histology will provide the evidence necessary to determine the reproductive status of newborn male dwarf perch. Dwarf perch sampling across several seasons will also enable us to determine if dwarf perch are born sexually mature only during a subset of the breeding season. To investigate, we performed paraffin wax histology on dissected gonads and used a rotary microtome to section the tissues (n=21). After staining with hematoxylin and eosin, we have characterized spermatocyte development to determine the stage of sexual reproduction at the time of capture. Mature sperm are present in testes from males caught later in the breeding season. Our research will provide additional information on the reproductive timing and life history of this unique group of viviparous marine species.

Oyster and Mussel Biomass and Condition Index on Single Versus Multi-Habitat Restoration in Newport Bay, CA.

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Mayra A. Silva*; Ariana M. Sanchez; Kaysha Kenney and Danielle Zacherl, *California State University, Fullerton*

Abstract: Oyster beds form complex habitats that enhance biodiversity, improve filtration quality, and protect coastal areas from wave erosion. Sedimentation can obstruct the gills in oysters and other bivalves, however, adjacent eelgrass beds may act to mitigate the problem. Declines in the native Olympia oyster, *Ostrea lurida*, prompted creation of a Living Shorelines Project in Newport Bay, CA that restores both eelgrass and oysters and examines if restoring both habitats together returns more benefits versus restoring each habitat in isolation. We hypothesized that oyster health would be optimized when restored adjacent to eelgrass. To compare oyster health on the restoration treatments, we calculated their average Condition Index (CI). Ten excavation samples of surface shell were taken from both an oyster bed and an oyster bed upshore from eelgrass one year following restoration. From those samples, each bivalve was measured for length, width, total weight, shell weight, and tissue weight, then dried in a vacuum oven for 22 hours at 100°C and remeasured for dry weight. The CI of the bivalves was calculated to compare the relative health of bivalves from each restoration treatment. Preliminary data show that *Ostrea lurida* biomass CI was higher when restored alone, while non-native mussels, *Muscalista senhousia,* had higher biomass on oyster beds restored upshore from eelgrass; their CI was unaffected by restoration treatment. These data have important implications for future Living Shorelines restoration design if we want to maximize oyster success.

Spatial Distribution of Structurally Complex *Modiolus Modiolus* Beds in the Northeast Atlantic Continental Shelf; Impacts to Community Structure and Potential Needs for Habitat Protection

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Jezella Peraza* and Burton Shank, *California State University, Monterey Bay*

Abstract: *Modiolus modiolus* (horse mussels) are important marine bivalves because of their significant role in creating biogenic, structurally complex habitats, however, their spatial distribution is poorly documented. Much of the Northeast Atlantic continental shelf lacks such structurally complex habitats that can serve as nursery grounds for juvenile fish and invertebrates. Thus, *Modiolus* beds may increase the productivity of demersal and benthic assemblages but are susceptible to disturbance from mobile fishing gear (trawls, dredges, etc.). The purpose of this research is to use an existing archive of underwater imagery that covers much of the Northeast Atlantic continental shelf to identify regions with existing *Modiolus* beds, describe the size and spatial structure of *Modiolus* beds, and document faunal assemblage associated with these beds compared to adjacent habitats. Following a broad-scale search for the presence of *Modiolus* beds, individual *Modiolus* beds were selected for detailed analysis of benthic coverage and faunal assemblages using multivariate and spatial statistical methods. Within the study domain, *Modiolus* beds were found primarily east of Cape Cod, Massachusetts along the Great South Channel. Direct evidence of disturbed *Modiolus* beds was common, presumably from mobile fishing gear. Image analysis has also provided a large image library that can be used to train machine learning algorithms to identify *Modiolus* and efficiently perform extensive searches across the remaining archive of the Northeast Atlantic continental shelf. Improving our knowledge of the potential distribution and ecological role of *Modiolus* beds may help inform management through habitat protection and possibly enhance ecosystem services.

Surface Chlorophyll Variability in the Southern Ocean

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Isis Guadalupe-Díaz*, *University of Puerto Rico, Río Piedras Campus* and Nicole Lovenduski, *University of Colorado Boulder*

Abstract: The Southern Ocean (SO) supports diverse biological species and unique food webs, making it both economically important for commercial fishing, and uniquely biodiverse. As primary producers, phytoplankton form the base of the marine food web, and their abundance or deficiency influences the entire marine ecosystem. Chlorophyll, a pigment used for light harvesting during photosynthesis, is a key indicator of phytoplankton biomass. The SO is the windiest and roughest ocean basin, which makes it difficult to obtain on-site observations of chlorophyll concentration and thus phytoplankton abundance. To address this issue, the Saildrone company launched an unmanned surface vehicle in the Southern Ocean in 2019 that successfully circumnavigated Antarctica and collected information about physical and biogeochemical ocean properties, including chlorophyll. Here, we quantify the spatial and temporal variability in Southern Ocean surface chlorophyll using the Saildrone observational data stream. We find high chlorophyll concentrations near iron rich regions of the SO (e.g. near islands and continental shelves), consistent with previous studies. The chlorophyll variance is higher in winter than in other seasons, and the Pacific Ocean sector exhibits the longest decorrelation length scale in chlorophyll (532 km). We further validate the Saildrone chlorophyll observations with estimates of surface ocean chlorophyll collected by the MODIS satellite, though cloudiness often obscures the satellite observations. Our study provides a first view of Southern Ocean chlorophyll collected on an uninterrupted autonomous vehicle and shows promise for possible future autonomous observations.

Evaluating Copepod Behavioral Responses to Sinking Marine Snow Particles

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Rhonda Papp*[1]; Christian Briseño-Avena[2] and Jennifer Prairie[1], *(1)University of San Diego, (2)University of San Diego, Department of Environmental and Ocean Sciences*

Abstract: Marine snow and copepods are important components of the global carbon cycle. Marine snow (aggregates of detritus, phytoplankton, and inorganic matter) help remove CO_2 from the surface ocean by slowly sinking into the deep ocean, where it remains for thousands of years. Because marine snow is one of the primary food sources for copepods (a common type of zooplankton), it is important to understand interactions between them from the point of view of the organisms. While there is some information on copepods reacting to the chemical plumes left behind by sinking marine snow, little is known about copepod reactions to mechanical stimuli from sinking marine snow coming from above.

Here, we explore how marine snow particles elicit motor responses, such as escape, attack, or capture in the copepod *Calanus pacificus*. We conducted a series of laboratory experiments using high-speed cameras to film tethered copepods in a tank with marine snow sinking from above. We then used MATLAB to quantify the reaction distance to the marine snow particles and classify the types of reactions in copepods. We will present our observations of different copepod behaviors and accompanying motion patterns of individual set of appendages, including but not limited to: active vs. passive movements, jumping, and feeding, among others. Observing how copepods react and use their appendages when exposed to marine snow can improve our understanding of copepod-marine snow interactions, which has implications for larger scale trophic dynamics, and in turn the global marine carbon cycle.

Quantifying Physical Changes to Marine Snow Particles As a Result of Copepod Interactions

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Leah Ring*[1]; Jennifer Prairie[1] and Christian Briseño-Avena[2], *(1)University of San Diego, (2)University of San Diego, Department of Environmental and Ocean Sciences*

Abstract: The ocean plays a critical role in Earth's carbon cycle, as the largest sink for actively cycled carbon. Organic matter is transferred to the deep ocean in the form of sinking particles known as marine snow that are comprised of phytoplankton and other organic material. Marine snow is known to be an important food source for many types of zooplankton, including copepods, and studies have suggested that zooplankton feeding on marine snow may result in the fragmentation and deformation of these particles. However, there have been no previous observations on the physical changes to these particles immediately following copepod interactions given the small scale (micrometers) at which they occur.

In this study, we aimed to determine how the size, shape, and number of marine snow particles are affected by interactions with copepods. To address this objective, we used a high-resolution camera to image a copepod as it manipulates and feeds on marine snow that was descending from above. MATLAB was used to quantify each particle's shape (using metrics of eccentricity and circularity) and size (in terms of area) over time. Then these metrics were compared before, during, and after the copepod interaction. Here, we will present results demonstrating that, after direct interaction with the copepod, marine snow generally fragments into smaller, less round particles. This finding suggests that copepod interactions may

have implications for the settlement rates of marine snow since smaller and less round particles sink slower, thus affecting the transport of carbon to the deep ocean.

Using Ecosystem Modeling Software to Explore Micro-Plastic Pathways through the Antarctic Peninsula Food Web

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Karina Halliman*, *University of California San Diego* and Tammy Russell, *Scripps Institution of Oceanography*

Abstract: Since plastic production began, it's increasingly used for the durable properties, sanitation and cost, yet along with this growing trend, marine plastic pollution increases as well. A growing concern of marine plastic debris are microplastics (< 5mm), which enter into the environment straight from manufacturing or through the breakdown of larger plastic pieces. Microplastics are widespread and ubiquitous throughout marine environments and have been found in marine wildlife diets. Little research has been done on how microplastics get into or move through the food web. The potential exposure and accumulation of marine plastic contaminants poses a concern for organisms in higher trophic levels of the food web. Recent research has found microplastics in the remote area of the Southern Ocean, and concentrations reported are greater than expected. This region is already under tremendous stress from climate change. The fastest warming area in this region, the Western Antarctic Peninsula (WAP), is experiencing the retreat of permanent ice shelves and diminishing winter sea-ice extent and concentration. To address the growing concern of microplastics, we are investigating microplastic-food web pathways in this vulnerable ecosystem using an existing ecosystem model with Ecopath with Ecosim (EwE). We hypothesize that Antarctic krill (*Euphausia superba*) are a main pathway of microplastics in the Antarctic food web, due to their sheer biomass in the WAP and their ability to efficiently filter feed through the water column. Understanding microplastic pathways and potential bioaccumulation to higher trophic level species will aid in understanding potential impacts of human plastic pollution.

Monitoring Microphytobenthos Biodiversity in Intertidal Mudflats of the South San Francisco Bay

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Emilia Lepe* and Sherry Palacios, *California State University, Monterey Bay*

Abstract: Microphytobenthos (MPB) are aggregations of diatoms, bacteria, protozoa, and fungi, referred to as biofilms, and are the primary energy source for consumers, such as water birds, fish, and invertebrates, accounting for 50% of their diet. Monitoring the biodiversity of the MBP is crucial in understanding how restoration efforts affect primary production and energy flow in intertidal mudflat ecosystems. Biofilms secrete a cohesive substance (Extracellular Polymeric Substances: EPS) that not only contributes to the stability of sediments but also biogeochemical cycling. The presence of EPS along with fine sediment size of the mudflats makes traditional sampling methods, such as the use of a handheld spectrophotometer, difficult to execute. In order to reduce difficulty, there has been increased interest in utilizing remote sensing imagery to monitor the microphytobenthos. Our project objectives are to increase understanding of how physical and biological elements drive changes in biofilm biodiversity. Using the MicroPhytoBenthos Optical Model (MPBOM), we aimed to remotely identify phytoplankton taxonomic class within intertidal mudflats of the South San Francisco Bay. Multispectral data of the South Bay from the Sentinel-2 satellite was collected then input in the Geographical Information System (GIS) software QGIS. QGIS was used to run the MPBOM model due to its raster calculator and Python console features. We anticipate our results will show that biofilm biodiversity is lost with increased coastal development, freshwater input, and sea-level rise. These results may provide guidance in restoration efforts and supply us with information to improve current phytoplankton classification models for multispectral remote sensing.

The Impact of Ocean Temperature and Oxygenation on Benthic Foraminiferal Size in the Southern California Borderlands

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Sonali Langlois*[1]; Hannah M. Palmer[2] and Tessa Hill[2], *(1)Santa Rosa Junior College, (2)University of California, Davis*

Abstract: Due to human activity, oceans across the world are becoming more acidic, and ocean oxygenation is decreasing with important impacts to seafloor ecosystems. Benthic foraminifera are protists that live on the ocean floor and produce calcareous shells. Over time these shells accumulate in the sediment in distinct layers going back thousands of years. This makes them an excellent tool for understanding historic changes in the ocean. Multiple hypotheses exist regarding the relationship between shell size and environmental conditions, including temperature and oxygen. Here we test the hypothesis that larger shells are produced in cooler, more oxygen depleted environments. We analyze variability in the size and shape of foraminifera from the Southern California Borderlands from three cores collected from 1194 m to 1818 m water depth.We quantify the length, width, and surface area of the shells of two foraminifera species (*Bolivina spissa* and *Quinqueloculina* sp.) through time from 2000 to 5,500 ybp and compare changing patterns in foraminiferal size to the foraminiferal assemblage and benthic oxygen and carbon isotope record. Preliminary results show that the size of *B. spissa*

shells increases in more recent shells while the size of *Quinqueloculina* shells increases in older shells. Understanding past changes in the ocean allows us to better predict the impact of future ocean changes as humanity continues to alter the world around us.

Spatial and Temporal Variability of Cephalopods in the Diet of Longnose Lancetfish across the Central North Pacific

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Rachel Chen*, *University of California San Diego*; Elan Portner, *National Oceanic and Atmospheric Association Southwest Fisheries Science Center* and Anela Choy, *Scripps Institution of Oceanography*

Abstract: Food web dynamics in the central North Pacific Ocean (CNP) are changing, with declines observed in the size, abundance, and distribution of both predators and primary producers. Despite serving as the trophic connection between primary producers and top predators, few studies describe mid-trophic animals and their responses to environmental pressures. Cephalopods (such as squids and octopods) are well represented within the forage community used by open ocean predators but are poorly studied because most evade capture by trawling. Using diet data from the longnose lancetfish (*Alepisaurus ferox*) collected during 2009-2019, we quantify variability in the diversity of cephalopod prey in the CNP and their horizontal and vertical distributions. Lancetfish are a commonly caught predator in the Hawaiian deep-set longline fishery that consume a broad assemblage of cephalopods while foraging throughout the water column (approximately 0-2000m). This predator provides an opportunity to sample cephalopods living in both shallow and deep habitats, which may exhibit differential responses to environmental pressures. To explore whether the habitat depth of cephalopods helps explain variation in response, we examine spatial patterns in the distribution of the most abundant shallow- (e.g. *Argonauta argo*) and deeper-dwelling cephalopods (e.g. *Japetella diaphana*). We also present time series of temperature, oxygen, and primary productivity to explore how changes at the base of the food web might affect cephalopod abundance. Our research aids in understanding how predators foraging across different depths may face differential changes in prey availability as a reflection of the prey responses to environmental pressures.

Corals Thermotolerance in American Samoa

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Silvia Vasquez*, *California State University, Monterey Bay* and Cheryl Logan, *California State University Monterey Bay*

Abstract: Coral has been known to adapt and acclimate after heat stress. In addition, pollution can also be a stressor for coral. Heat and pollution stress can act together, therefore, we are interested to view a cross-tolerance enhancing or preventing growth by analyzing the amount of differential gene expression. In this study, we experiment with Acropora hyacinthus exposing fragments to high, medium, and low temperatures, similar to the natural temperature experienced in their home, American Samoa. A total of 24 samples were collected from three different colonies varying levels of pollution starting with the least polluted, Faga'tele, Faga'alu, and Coconut Point being the most polluted. We investigating the transcriptome response of colonies before and six after exposure to heat (35℃) or control (29 °C) conditions. Our findings can suggest similarities or differences in gene expression at different conditions. In results, samples exposed to both high heat and high pollution levels expressing similar up- and down-regulated genes can support a cross-tolerance. By analyzing the ratios between up- and down-regulated genes in each treatment, we can estimate when the coral has a higher possibility of adapting/acclimating or a negative effect in its natural condition. The significance of this research is to provide policymakers with valuable information they can use to set limits or manage water waste in American Samoa affecting the health of corals.

Pollicipes Polymerus and *Mytilus Californianus* and Their Roles As Foundation Species

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Cody Henrikson*; Sean Craig and Claire Windecker, *Humboldt State University*

Abstract: Foundation species play important ecological roles in their communities, providing physical habitats necessary for other organisms to inhabit and mediate harsh conditions that would otherwise make the facilitation of other organisms impossible. The roles that intertidal foundation species play in their communities need further study to examine how foundation species alter physical factors (habitat space, temperature, etc.) and biological factors (competition, predation, etc.) to facilitate other species. In the rocky intertidal zone along California's outer coast, *Mytilus Californianus,* the Californian ribbed mussel is an important foundation species that facilitates numerous invertebrates, some of which live in and among the byssal threads that attach these mussels to the substrate. The interwoven network of byssal threads traps debris and forms a sediment-laden habitat for other species, such as isopods, crabs and annelids, which in turn are important sources of food for marine birds. Stalked barnacles (*Pollicipes polymerus),* also found in the mid-intertidal zone, may act as an additional foundation species even though they compete for space with mussels. Through destructive sampling of beds in the field, this study examined how the identity of the dominant foundation species *(M. californianus* vs. *P. polymerus)* impacts species richness and abundance. Multiple factors (including tidal height, bed depth, foundation species ID, and sediment biomass trapped) were found to affect the species richness and abundance within these beds. Hence, the ecology of these foundation species include multiple factors which need further dissection in order to fully understand how foundation species enhance the richness of marine intertidal communities.

Density and Abundance Patterns of Native and Non-Native Oysters *Ostrea Lurida* and *Crassostrea Gigas* over Time in San Diego Bay, California

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Jada Smith*; Joann Lam; Trina Miller; Madison Panzino; Nicholas Torres; Alisa Hernandez; William J. Hoese and Danielle Zacherl, *California State University, Fullerton*

Abstract: Oysters, foundational species in bays and estuaries, provide complex habitat for marine species. *Ostrea lurida,* the only oyster native to the U.S. west coast, experienced significant population declines during the 1900s and has not recovered since, while *Crassostrea gigas*, a non-native oyster, was introduced for aquaculture and has since recruited to estuaries outside of aquaculture. *C. gigas* populations may negatively impact native *O. lurida*. Over the past decade, *C. gigas* densities and abundances increased dramatically in Newport Bay, CA, suggesting that this global invader's populations may be increasing throughout southern California. We hypothesized that *C. gigas* density and abundance have increased and *O. lurida* density and abundance have declined from 2013-2020 in San Diego Bay, CA. We calculated density and abundance at Chula Vista Wildlife Reserve (CV), Grand Caribe (GC), and Glorietta Bay (GB) at tidal elevations ranging from -0.3 to +1.81 m MLLW. One-way ANOVAs with *post-hoc* comparisons were used to analyze change in *O. lurida* and *C. gigas* density across years at tidal elevations > and ≤ +0.38 m MLLW. *C. gigas* density and abundance increased at higher tidal elevations at 2 of 3 sites (CV, GB). *O. lurida* density and abundance decreased at lower tidal elevations at 2 of 3 sites (CV, GC). However, *O. lurida* population declines did not coincide with *C. gigas* population increases in space and time. Further studies may elucidate whether population dynamics of *O. lurida* and *C. gigas* are linked over time within San Diego Bay.

Processing Oceanographic Data for Analysis of El Niño Southern Oscillation (ENSO) Impacts on Pacific Bigeye Tuna Catch

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Elyse Bonner*, *Tuskegee University* and Réka Domokos, *National Oceanic and Atmospheric Administration (NOAA)*

Abstract: Bigeye tuna *(Thunnus obesus)* is a pelagic fish species caught using longline and purse seine fishing techniques. The El Niño Southern Oscillation (ENSO) likely impacts Bigeye tuna catch variability, especially along the equator, where sea-surface temperatures are anomalously high during El Niño and low during La Niña. Equatorial fishing grounds are strongly influenced by the ENSO cycle, the effects of which on Bigeye tuna distribution, abundance, and catchability are important to understand for stock management purposes. Temperature plays an important role in determining Bigeye tuna horizontal and vertical distribution due to their preferred ocean temperature ranges. To examine the effects of the ENSO on Bigeye tuna distribution along the equator, the area of 12.5°S-12.5°N and 105°E-75°W was selected and data were gathered from 1990 – 2017 for this project. The variables processed for the study were: Sea Surface Temperature, Sea Surface Temperature Anomaly, Sea Level Anomalies, Mixed Layer Depth, Absolute Geostrophic Velocity, Geostrophic Velocity Anomalies, Chlorophyll-a, Pacific Decadal Oscillation, Multivariate ENSO Index, Southern Oscillation Index, and Oceanic Niño Index. Each variable was altered to the correct spatial and/or temporal resolution and recentered to the desired grids along the equator. These data were processed in separate raster files and converted to 5x5 raster bricks for analysis. The data will be instrumental in identifying environmental impacts on the distribution, biomass, and/or catchability of Bigeye tuna. The results of these analyses can be used to help predict fisheries performance under certain environmental conditions and provide crucial information for managerial decisions in the future.

Comparison of Deep-Sea Faunal Composition between Inactive and Active Hydrothermal Vents at the EPR 9°50'N Using High-Resolution Imagery

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Michael J Meneses*[1]; Lauren N Dykman[2]; Daniel J Fornari[2]; Jason B Sylvan[3] and Lauren S Mullineaux[2], *(1)University of California, Santa Barbara, (2)Woods Hole Oceanographic Institution, (3)Texas A&M University, College Station*

Abstract: Recent volcanic activity within the past decade, including a large-scale eruption in 2005-2006, provides an opportunity to study transient and ephemeral biology of hydrothermal vent communities at the East Pacific Rise (EPR) near 9°50'N. Because most of the submersible dives have focused on communities at active vents, there is a scarcity of data regarding the diversity, abundance, and composition of invertebrate fauna at inactive vent sites, primarily from lack of observational coverage both off-axis and along axis. Inactive vents are considered "extinct" when they are no longer hydrothermally active with no visible effluent into the bottom water, thereby removing the major energy source required to maintain the chemosynthetic ecosystems seen at active vents. High-resolution imagery taken by *DSV Alvin* during a recent research cruise in 2019 (AT42-21) reveals the presence of benthic megafauna living on and around a newly-discovered

inactive, off-axis vent called "Lucky's Mound" (9.7903°N, 104.2870°W). Due to the significant changes in environmental conditions caused by the lack of hydrothermal fluids, we expect to see a significant change in the composition and distribution of species inhabiting Lucky's Mound when compared to that of active vents located in the EPR axial trough roughly ~530 m from Lucky's Mound. Our study analyzes still-images and 4k video to quantify and identify species that inhabit Lucky's Mound and compare differences in species composition between Lucky's Mound to V-Vent, a nearby active vent located at 9.7879°N, 104.2829°W.

Ten Years of Domoic Acid Surveillance in Stranded Marine Mammals of Monterey Bay 2009-2019

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Bianca Ramirez*; Karolina Wirga and Robin Dunkin, *University of California, Santa Cruz*

Abstract: *Pseudo-nitzschia australis*, a naturally occurring diatom, produces domoic acid (DA), a neurotoxin that can result in acute or chronic neurological symptoms and death in marine mammals. In this study, we report on the prevalence of domoic acid in 13 stranded marine mammal species in Monterey Bay between 2009 and 2019. During this period we performed necropsies and quantified DA levels from 172 fresh dead or moderately decomposed animals. Of these, 79.7% had DA present in at least one body fluid. In animals with detectable levels of DA, concentrations spanned 5 orders of magnitude (0.5 ng g^{-1} to 285978.4 ng g^{-1}). The majority of strandings occurred in spring, concomitant with most Harmful Algal Bloom (HAB) events. However, DA was detected in animals that stranded throughout the year, indicating domoic acid is likely widespread in the environment even outside of HAB events. Our data indicate widespread domoic acid exposure for marine mammals in Monterey Bay regardless of species or season. Further, 80.5% of California sea lions had DA present in at least one sample and of these, many had levels consistent with acute (19.5%) or chronic (16.1%) DA toxicosis as identified in a prior study (Goldstein et al. 2007). Given the chronic neurological effects and reproductive harm of DA on marine mammals as well as increasing frequency of HAB events, the results of this study indicate DA exposure is an unquantified and potentially large health concern for marine mammals in this region.

Comparison of Microfibers Found in the Digestive Tract and Gills of the Sardine Fish, *Sardina Pilchardus*

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ashley Rauda* and Andrea Huvard, *California Lutheran University*

Abstract: A microfiber is a microscopic strand of plastic measuring under 5mm long. Our clothes are the main source of microfibers since strands primarily fall off when we wash our clothes. These fibers end up in the ocean through our washing machines and are ingested by living organisms, like fish. The aim of the present study is to investigate the quantity of microfibers found in the digestive tract compared to the gills of the Sardine fish, *Sardina pilchardus.* While comparing the microfibers in the digestive tract and the gills of the fish, it was expected that there would be more microfibers found in the digestive system. The fish were dissected and the gills and digestive tract of each were removed to be mashed up and filtered. The microfibers were counted and sorted by color. Results determined that in terms of quantity, more microfibers were found in the digestive tract compared to the gills. However, after conducting a t-test it was determined that the results were not significant since the p-value was 0.13 ($p > 0.05$). In conclusion, there was no statistical difference between the quantity of microfibers in the digestive tract compared to the gills of the *Sardina pilchardus.* Although there was no statistical difference found, it is significant that of the forty-nine fish that were sampled, every single fish had multiple microfibers. This fact shows the extreme pollution of the ocean these microfibers have caused which may be damaging to the fish as well as their ecosystem.

Evaluating Automated Image Analysis for Pinniped Assessments

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Nilanjana Das*[1]; Elizabeth Josephson[2] and Kimberly Murray[2], *(1)Stockton University, (2)National Oceanic and Atmospheric Administration*

Abstract: Aerial photographic surveys have long been used to monitor gray and harbor seal populations, but extracting data from those images is a time-intensive process. Just one image from a haul-out or pupping site may contain over one hundred seals, which must be manually counted and categorized by sex or age. This project aimed to automate this image analysis and obtain population estimates more efficiently through machine learning, specifically with the software VIAME (Video and Image Analytics for Marine Environments). Survey images from gray seal pupping sites on Monomoy and Muskeget Islands off of Cape Cod, Massachusetts were manually annotated to identify pups and adults, after which the annotations were used to generate a trained detector through deep learning. After 4 iterations of this process, the detector's probability of correctly identifying a pup or adult of this species on sandy substrates is 0.87. Going forward, this detector will be further refined to provide accurate estimates of gray and harbor seal abundance in various environments in a fraction of the time it would take using traditional methods.

The Impact of Harvest on the Success of Northwestern Pacific Hatcheries

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Alexis Hernandez*; Floyd Clark and James Graham, *Humboldt State University*

Abstract: Salmon are an important source of sustenance for many, and are significant to many tribes of Humboldt County, located in the American Pacific Northwest. Since the construction of the Trinity Dam in 1957 on the Trinity River, there have been noticeable adverse effects on the population of the local salmonid species, and a hatchery built upon that same river has since then been established to mitigate the loss of habitat. We investigated annual reports provided to us by the Trinity River Hatchery, and found fluctuations of highs and lows, in the number of salmonids produced, released, and re-caught by the hatchery. We further observed harvest rates of salmonids by tribal and non-tribal entities, to determine if the hatchery was efficient in restoring the salmonid population within the Trinity River, and whether overfishing was a notable contribution to the decline in salmonids within the Trinity River. With the lack of feasible data provided by the reports we analyzed, it was clear more data needed to be collected before concluding anything, but it was certain that better methods to track harvest rates needed to be implemented to prevent future drastic declines in salmonid populations.

Strong Spatial Variability in the Distribution of Plastic Debris on Guam Beaches

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Ahmyia Cacapit*, *University of Guam* and J.P. Walsh, *University of Rhode Island Graduate School of Oceanography*

Abstract: Marine plastic poses an ecological and economic concern to island communities by negatively impacting their aesthetic quality and wildlife. Around Guam, marine plastic is a well-known problem; however, the distribution around the coast has not be measured. This study aimed to identify patterns and processes of plastic distribution for three size classes: large microplastics (1-5 mm), mesoplastics (5-25 mm), and macroplastics (>25 mm). Eight beaches around Guam's coasts were visually surveyed on three shore-perpendicular transects at each site, from the wet/dry line to the backshore. On each transect, a visual count was made, and photographic stations were conducted at the upland/vegetation transition, high-tide line, and upper swash zone. The amount of plastics visually observed across all sites ranged from 8-2397 plastic particles, with the highest number occurring at South Pago Bay with 127.5 particles/m^2. At all sites, microplastics were the dominant count (70%), and mesoplastics accounted for 20%. Based on photograph counts, plastic particles were found more frequently in the backshore (57%) than at the high-tide line (41%) and swash zone (<2%). Most surprising was the significant variability in the plastic abundance; generally, higher plastic counts were seen on the eastern beaches. Interestingly, the North Pago Bay site had notably less plastic than South Pago Bay, indicating strong local variability, possibly due to oceanographic influence. The irregular distribution of plastic abundance found in this study, suggests proximal (e.g., transport, dumping and littering) and larger-scale (e.g., windward vs leeward and ocean circulation) factors are important.

An Initial Ecological Characterization of Mesopelagic Fauna at Johnston Atoll and Musicians Seamounts

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Jason Gronich*[1]; Adrienne Copeland[2]; Michael Ford[3] and Amanda Netburn[2], *(1)California State University, Monterey Bay, (2)National Oceanic and Atmospheric Administration, Office of Ocean Exploration and Research, (3)National Oceanic and Atmospheric Administration, National Marine Fisheries Service*

Abstract: The mesopelagic zone (200-1000 m) of the ocean hosts a wide variety of organisms in a concentrated layer known as the deep scattering layer (DSL). Much of the mesopelagic zone in the Central North Pacific remains unexplored, rendering management plans for the region incomplete. To combat this knowledge gap, the NOAA Office of Ocean Exploration and Research used the NOAA Ship *Okeanos Explorer* to conduct two expeditions in the region, one to Johnston Atoll and the other to the Musicians Seamounts. During these expeditions, a remotely operated vehicle collected video and CTD environmental data while the ship collected active acoustic data. This project combined and analyzed those three data sets to create a mesopelagic ecological characterization of Johnston Atoll and Musicians Seamounts. The initial characterization included a full inventory of mesopelagic fauna, the differences in abundance between functional groups, and a comparison between abundance of mesopelagic fauna within the DSL and outside of the DSL. Additionally, the abundance of functional groups compared to the environmental factors of salinity, temperature, and oxygen concentration was investigated. Generally, there were more sightings per minute of gelatinous organisms than any other category and more overall sightings per minute within the DSL than outside the DSL at Musicians Seamounts. Overall, there were significant linear relationships between the abundance of functional groups and the environmental factors of salinity, temperature, and oxygen concentration. These initial characterizations will better inform management decisions for the region during future investigations into the mesopelagic zone of the ocean.

Detection and Quantification of *Enterococcus* Spp. in a Recreational Beach with an Identified Point Source of Fecal Pollution and Antimicrobial Resistance

Discipline: Life Sciences

Subdiscipline: Microbiology

Gabriel J. Vázquez-Badillo*; Lourdes Delgado-Ruiz and Odalys S. Alvarez-Perez, *Inter American University of Puerto Rico*

Abstract: The Environmental Protection Agency has established regulations based on the detection and quantification of enterococci as an indicator of fecal pollution to maintain recreational water quality. Enterococci are members of the intestinal microbial community of mammals and are considered opportunistic pathogens that cause disease. *Enterococcus* spp. is classified as a causative agent of nosocomial infections. There has been increasing concern about the antibiotic resistance genes (ARGs) of these bacteria. The objective of this research is the quantification of enterococci in a recreational beach with an identified point source of fecal pollution (FP) in the northwest coast of Puerto Rico and the detection of class 1 integron-integrase genes (*Intl1*). *Intl1* plays a major role in the spread of ARGs, therefore it is important to understand their presence in the environment. Our hypothesis establishes that coastal waters impacted by FP represent a reservoir for enterococci and ARGs. The quantification of enterococci was performed using the membrane filtration technique and the m-Enterococcus agar. The isolates were confirmed using bile esculin and 6.5% NaCl agar. The antimicrobial susceptibility test was implemented using chloramphenicol and penicillin discs. Optimization of *Intl1* detection was performed using specific primers for the amplification of *Intl1* regions. We detected fecal enterococci in water samples, some isolates showed resistance to antibiotics. These isolates were cultured for the detection of *Intl1*. Our preliminary results showed that coastal waters impacted by anthropogenic activities represent an environment for the dissemination of fecal enterococci and transfer of ARGs.

Downregulation of RNA-Mediated Antibiotic Resistance with Biosynthetic Antisense Molecules

Discipline: Life Sciences
Subdiscipline: Microbiology

Raphael Angelo Zambrano*; Lizette Silva; Aaron Stibelman and Melissa Takahashi, *California State University, Northridge*

Abstract: The development of antibiotic resistance in pathogens remains to be a major health concern requiring a novel approach. Among known resistance mechanisms bacteria utilize, small RNAs (sRNA) are transcribed due to stress, interfering with the translation of significant proteins. We are exploring a method to inhibit RNA-regulated antibiotic resistance by studying MicF, an sRNA produced by *Escherichia coli* in response to the presence of antibiotics. MicF represses the translation of outer membrane protein F (OmpF) by binding to the 5’ untranslated region (UTR) of *ompF* mRNA coded from a different region of *E. coli* chromosome, thus reducing antibiotic uptake. We hypothesize that synthetically designed antisense molecules sequestering MicF will increase permeation of a panel of antibiotics by preventing OmpF inhibition. Antisense molecules were screened using a cell-free transcription-translation system and a fluorescence reporter, measuring *ompF* expression over a period of time. Systematically testing our designs, we confirmed that our approach interferes with MicF regulation of *ompF*. In addition, we identified sequences effectively sequestering MicF and recognized integral regions of MicF that repress translation. We then proceeded to observe if the effectiveness of successful candidate molecules extended in live bacteria. Transformed *E. coli* including the successful sequences with an inducible promoter were subjected to minimum inhibitory concentration (MIC) tests for multiple antibiotics. Our results show a decline in MIC levels for induced bacteria, suggesting that antibiotic uptake increased in the presence of the antisense molecules. We expect that biosynthetic molecules will be recognized as a novel strategy to improve antibiotic efficacy.

Comparative Genomic Analysis of 42 Environmental *Vibrio Vulnificus* Isolates from the Northern Gulf of Mexico

Discipline: Life Sciences
Subdiscipline: Microbiology

Ceejay Saenz*, *Texas A&M University Corpus Christi* and Jeffrey W. Turner, *Texas A&M University-Corpus Christi*

Abstract: *Vibrio vulnificus* is a Gram-negative bacterium and an opportunistic pathogen, known for causing necrotizing fasciitis, a potentially deadly disease in humans. Through sequence polymorphism of the 16S rRNA gene and the virulence-correlated gene (*vcg*), distinct clinical and environmental ecotypes have been identified and confirmed with whole-genome sequencing. The comparative analysis of clinical and environmental genomes can aid in the identification of virulent genes. However, a large public collection of nonpathogenic genomes is needed. To support this effort, we sequenced 42 environmental isolates from the northern Gulf of Mexico (NGOM). Isolates were recovered from seven locations in the Texas coast between August 2006 and July 2007 and confirmed as *V. vulnificus* with matrix-assisted laser desorption ionization-time of flight (MALDI-TOF) mass spectrometry. Genomic DNA was extracted with a QIAamp DNA minikit and quantified with a Qubit double-stranded DNA (dsDNA) broad-range (BR) assay kit. Sequencing was completed using the Illumina MiSeq 500-cycle kit (v2) following standard FastQ-only generation protocols to produce 250-bp paired-end reads. Overlapping paired reads were merged using FLASH, adapter sequences, low-quality bases were trimmed using Trim Galore, and draft genomes were assembled using SPAdes. Overall, the size of the draft assemblies ranged from 4,778,453 to 5,412,903 bp, the number of contigs ranged from 36 to 252, and the N50 value ranged from 59,128 to 704,086 bp. Current research is focused on the comparative analysis of clinical and environmental genomes with the goal of identifying genomic features that define clinical strains.

The Characterization of Novel Onygenalean Fungal Isolates

Discipline: Life Sciences
Subdiscipline: Microbiology

Kaitlyn Parra* and Bridget Barker, *Northern Arizona University*

Abstract: In an inquest to identify the causative agent of a suspected disease affecting the endangered black footed ferret in Aubrey Valley, AZ, USA, novel fungal isolates were found. Prairie dogs were used as an indicator of disease by analyzing prairie dog lungs harvested from the region. The lungs were used to culture out any fungi in the lungs and genetic analysis was used to identify the species of fungi. The genetic analysis using Sanger Sequencing determined nine novel species from the fungi grown. Whole genome and phylogenetic analysis were performed on novel isolates. The analysis revealed a novel clade containing five of the isolate. Only three of the five isolates were successfully regrown from the original experiment. It is hypothesized the three novel isolates are all distinct species and are pathogenic. To assess the speciation of the isolates, we quantified macro and micro morphology and the growth rate. The macromorphology was studied using five different growth mediums and the colony growth patterns were characterized. To describe micromorphology, a slide culture method was developed. Growth rate was determined through radial growth experiments on two media types. Through these experiments, the three strains have been characterized with distinct morphologies and growth rates. With the initial use of genomic analysis and now old culturing methods, the project combines contemporary techniques with classic mycological methods to identify the role the novel isolates play in the ecosystem.

Distinct Group of NDM-1 Producing *Acinetobacter* spp. Strains Leading the Increase in NDM-1 Emergence in Argentina

Discipline: Life Sciences
Subdiscipline: Microbiology

Déja Rodgers* and Maria Ramirez, *California State University, Fullerton*

Abstract: **Background**:

Multidrug resistant Gram-negative bacterial infections caused by carbapenemase-producing organisms are the most problematic. The most widely disseminated carbapenemase is the New Delhi Metallo-β-lactamase (NDM-1). In the present work, we attempted to understand the emergence, genetic and phenotypic characteristics of NDM-1 *Acinetobacter* spp. isolates recovered in Argentina.

Materials/Methods:

Forty non-epidemiologically related NDM-1 *Acinetobacter* isolates were recovered during the years 2014-2017 in Argentina. Whole genome sequencing was performed using an Illumina NextSeq500. Annotation and genomic analysis using Prokka and CARD, roary, ISfinder and ISseeker were carried out. The Neighbor-Joining tree was generated using MEGA and visualized using iTOL. Phenotypic assays in selected representative strains were also performed.

Results:

Results revealed that all *A. baumannii* genomes (n=33) belonged to ST25 and were closely related. In the non- *baumannii* genomes $bla_{\text{NDM-1}}$ was located in the Tn*125* transposon on a plasmid. However, in the *A. baumannii* genomes, Tn*125* was located in the chromosome. A novel resistance gene island (RI) carrying the cephalosporinase gene, $bla_{\text{PER-7}}$, and several other antimicrobial resistance determinants was found on a plasmid in a subset of *A. baumannii* strains. The majority of the strains did not exhibit surface-associated motility, but all were able to resist desiccation for at least seven days. Macrocolony biofilms analysis revealed different structural characteristic and all strains resist peroxidase treatment.

Conclusions: The emergence of an NDM-1-positive clone in a complex genetic background including $bla_{\text{PER-7}}$ and a new RI in *A. baumannii* in Argentina highlights the importance of molecular surveillance programs for CR *Acinetobacter* strains.

Does Plasmid Conjugation Prevent Cheaters from Outcompeting Cooperative Plant Pathogens during Experimental Infections?

Discipline: Life Sciences
Subdiscipline: Microbiology

Reilly Jensen*; Priscila Guzman and Thomas Platt, *Kansas State University*

Abstract: Microbe-microbe interactions occurring within the microbiome of hosts can have significant consequences on the within-host success of pathogens. In this study, we examine how plasmid conjugation shapes the dynamics of competition between a plant pathogen and avirulent cheaters. *Agrobacterium tumefaciens* is a tumor inducing plant pathogen impacting several crop plants. These bacteria genetically transform plant cells by inserting a portion of their tumor inducing (Ti) virulence plasmid, called the T-DNA, into the plant's genome. Following transformation, plant cells produce opines which the pathogen can consume as a public good. Some agrobacteria lack the Ti plasmid but are nonetheless able to catabolize opines. Because these strains are not burdened by the costs associated with infecting plants, yet reap the benefits of opine public goods, they are predicted to outcompete the pathogen on infected hosts. Consistent with this, we have observed that these cheater strains outcompete cooperative strains during experimental infections in which each strain is initially half of the population. We are studying the conditions under which conjugation of the Ti virulence plasmid can alter the outcome of competition between agrobacterial cooperators and cheaters during experimental infection of common sunflower, *Helianthus annuus*, plant hosts. Our hypothesis is that when cheaters are rare, plasmid conjugation will convert cheaters into cooperators quick enough to prevent cheater invasion. We are evaluating this hypothesis using both wildtype and conjugation mutant cooperators with the prediction that the mutants will be vulnerable to invasion to cheaters while the wildtype strains will prevent cheater invasion via conjugation.

Pulmonary Dendritic Cell Subset Interactions with *Cryptococcus Neoformans*

Discipline: Life Sciences
Subdiscipline: Microbiology

Brenden Determann II*; Karen L. Wozniak; Ashlee Hawkins and Benjamin Nelson, *Oklahoma State University - Stillwater Campus*

Abstract: *Cryptococcus neoformans* is an opportunistic fungal pathogen acquired by inhalation that causes cryptococcal meningitis. This disease results in over 180,000 annual deaths in patients with AIDS. Innate phagocytes in the lung can kill *C. neoformans,* or it can evade killing and replicate intracellularly. Intracellular survival is thought to be responsible for dissemination of *C. neoformans* from the lung to the brain, causing meningitis. Dendritic cells (DCs) are innate phagocytes that can kill *C. neoformans* in vitro, and these cells are recruited to the lungs during cryptococcal infection. Two subsets of conventional DCs are described in the murine lung: $CD11b^+$ and $CD103^+$. Based on our data with other innate phagocytes, we hypothesized that pulmonary DC subsets have different interactions with *C. neoformans*. We first purified DC subsets from murine lungs and analyzed DC-cryptococcal interaction. Flow cytometry confirmed interaction of each DC subset with *C. neoformans.* Antifungal assays showed that neither DC subset has antifungal activity in vitro. Further studies will examine cytokines produced by the DC subsets and intracellular morphology following uptake of *C. neoformans* by each DC subset. Also, RNA sequencing will be used to identify genes that are up- or down-regulated in DC subsets following cryptococcal interaction. Understanding mechanisms of DC antifungal activity or fungal immune evasion will provide new therapeutic targets for cryptococcal meningitis.

Evolution of Antibiotic Resistance in *Klebsiella Pneumoniae* biofilms

Discipline: Life Sciences
Subdiscipline: Microbiology

Alexandra Hough*, *Fresno State* and Tricia Van Laar, *California State University, Fresno*

Abstract: *Klebsiella pneumoniae* is a gram-negative bacterium causing significant multi-drug resistant infections. A major virulence factor in *K. pneumoniae* is biofilm formation. Biofilm infections can be very difficult to treat as these protective communities often allow bacteria to only tolerate antibiotics. Recent research suggests previously sensitive cells within a biofilm can develop resistance to an antibiotic after continued exposure. The objective of this study is to determine if previously sensitive *K. pneumoniae* can develop antibiotic resistance while inside a biofilm, which has important implications for clinical therapy.

Biofilms of *K. pneumoniae* were formed on glass discs and treated with 5 and 100 times the minimum inhibitory concentration (MIC) of kanamycin (Kan). After 24-hour bidiurnal treatment periods, biofilms were disrupted and plated on 0x, 5x, 100x MIC Kan LB agar plates. Cells in biofilms treated with 5x MIC Kan developed resistance to that concentration in a single day. Cells in biofilms treated with 100x MIC Kan developed resistance to that concentration within 4 days. Cells from untreated biofilms never developed antibiotic resistance.

We then extracted and sequenced whole genomic DNA from the biofilms. We used the breseq bioinformatics program to identify single nucleotide polymorphisms such as S20C, L344Q, and R109C among other single nucleotide substitutions.

The knowledge that *K. pneumoniae* in biofilms can evolve antibiotic resistance in as little as 24 hours has significant clinical implications and can inform physicians to closely monitor their infected patients. By characterizing genes contributing to resistance, we can potentially identify novel targets for anti-*K. pneumoniae* therapy.

The Role of the Phosphodiesterase Rega on the Translocation of the Transcription Factor Gtac in *Dictyostelium*

Discipline: Life Sciences
Subdiscipline: Microbiology

Kierra Dixon* and Jeffrey Hadwiger, *Oklahoma State University*

Abstract: When starved for nutrients the amoebae *Dictyostelium* forms a multicellular aggregate that undergo morphogenesis to create a fruiting body. The aggregation process is mediated by extracellular cAMP signaling between cells, allowing cells to communicate and migrate to each other. When cells are stimulated with cAMP the receptors on the surface activate G proteins, MAP kinases (MAPKs), and cAMP dependent protein kinases (PKA) and trigger several responses including the translocation of a transcription factor, GtaC, from the nucleus to the cytoplasm. During stimulation, cells produce a transient burst of cAMP by activating adenylyl cyclases and inhibiting the phosphodiesterase RegA. RegA is an important regulator of development because cells lacking RegA have a rapid developmental phenotype and cells overexpressing RegA have a delayed developmental phenotype. Mutations that affect the phosphorylation of RegA by MAPKs or PKA can affect the rate of development. RegA function in the translocation of GtaC is unknown but GtaC contains sites that could potentially be phosphorylated by MAPKs and PKA. To test the impact of RegA function on the translocation of GtaC a GFP-GtaC reporter assay was used to monitor the location of GtaC in a variety of *regA* mutants stimulated by cAMP. A vector containing the reporter construct was transformed into *regA* mutants. The mutants were examined for the reporter shuttling using confocal microscopy. The shuttling of the reporter in the *regA* mutants resembled that of wild-type cells suggesting RegA is not a critical regulator of GtaC translocation.

Assessing the Skin Microbiome of Inverse Psoriasis

Discipline: Life Sciences
Subdiscipline: Microbiology

Miguel G. Rodriguez-Reyes*[1]; Jennifer Chung[2]; Jethro Johnson[2] and George Weinstock[2], *(1)University of Puerto Rico at Mayaguez, (2)The Jackson Laboratory for Genomic Medicine*

Abstract: Psoriasis is a chronic inflammatory skin disease affecting 8 million Americans and 125 million people worldwide. Plaque psoriasis is the most common type; while inverse psoriasis is a rare subtype that develops in skin folds and only happens in a quarter of people with psoriasis. The cause of psoriasis is unknown; however, microbiome factors are linked to the disease. Although the skin microbiome has been studied in the context of plaque psoriasis, it has never been studied in inverse psoriasis. We hypothesize that a distinct skin microbiome at inverse sites may play a role in the etiology of inverse psoriasis. Therefore, this study aims to characterize the skin microbiome of inverse psoriasis and identify differences between lesion and non-lesion sites in inverse psoriasis. Twenty-eight individuals were enrolled into three cohorts: those with both plaque and inverse psoriasis, those with only plaque psoriasis, and healthy. Nine inverse body sites were sampled using skin swabs. After DNA extraction, the variable V1-V3 16S rDNA region was PCR-amplified and sequenced using Illumina MiSeq. Sequence reads were clustered into 1,635 Operational Taxonomic Units with 463 unique taxa, being *Staphylococcus* and *Corynebacterium* the most abundant genera. It was found that the microbial composition between cohorts and body sites is different. Community structure is similar in lesion and non-lesion sites; however, intrasample diversity is decreased in lesion sites. Four potential protective bacteria against inverse psoriasis were identified. This first-ever microbiome-inverse psoriasis study establishes a base for elucidating the etiology of the disease and the development of therapeutics.

A Selection for Hyper-Competent *B. Subtilis* mutants

Discipline: Life Sciences
Subdiscipline: Microbiology

Alexander Webb*[1]; Jason Webb[1] and Prof. Briana Burton[2], *(1)University of Wisconsin, Madison, (2)University of Wisconsin-Madison*

Abstract: Natural competence is the ability for bacteria to produce proteins that mediate transport of extracellular DNA into the cytoplasm and integrate it into their genome. In *B. subtilis*, ComEC is the putative membrane protein that transports DNA across the cell membrane. Despite decades of research, our understanding of the mechanism underlying this process is limited. A selection for hyper-competent *comEC* mutants will be performed to identify residues critical for DNA uptake, which will lead to new hypotheses regarding ComEC function. Mutant *comEC* libraries will be produced by mutagenic PCR of *comEC*, followed by transformation of the PCR products into *B. subtilis* at an ectopic site. Wildtype *comEC* alleles will be removed from the libraries by transforming an antibiotic resistance marker into the endogenous *comEC* locus exclusively, leaving only mutagenized *comEC* copies in the libraries. The libraries will be transformed with another antibiotic resistance maker to select for mutants with functional mutant *comEC* alleles. Finally, these libraries will be transformed and selected one last time. They will be plated in low enough cell numbers that only hyper-competent variants (with inherently higher transformation efficiency) would be expected to grow compared to the wildtype strain. The surviving colonies will be sequenced to identify the causal *comEC* mutations, and the resulting amino acid changes will be mapped onto putative ComEC structures to inspire novel hypotheses and testing for ComEC function. Preliminary data confirms that the mutagenic PCRs were successful, showing that our selection process is viable because *comEC* mutant library generation is possible.

Detection of Siderophore Producing Bacteria in Puerto Rican Soils

Discipline: Life Sciences
Subdiscipline: Microbiology

Miguel Rodriguez Anavitate*, *University of Puerto Rico at Mayagüez* and Carlos Ríos-Velázquez, *University of Puerto Rico at Mayaguez*

Abstract: During the industrial revolution asbestos, a fibrous silicate mineral, was a common material used in constructions due to its incredible properties. Unfortunately, long term inhalation of asbestos fibers has been linked with lung diseases. Previous research has shown that trace amounts of iron in asbestos may be responsible for its toxicity since iron can promote reactive oxygen species to develop, which can lead to cellular damage. A possible way to treat asbestos-filled sites would be to remove the iron. To achieve this, a geomicrobiological solution using siderophores has been proposed. Siderophores are small chelating molecules produced by microorganisms capable of trapping iron in the environment. The focus of this research is to isolate and characterize siderophore-producing bacteria (SPB). SPB have been identified using

Blue CAS agar which turns from blue to orange in presence of siderophores. Soil samples were collected from the municipality of Cabo Rojo. To isolate SPB, serial dilutions until 10^{-6} were performed to the samples and grown on CAS media for 72 hours at 37°C. Colonies with orange halos were isolated for further molecular and microbiological characterization. Determination of UFC/g showed the samples ranged from 1.55×10^{-4}UFC/g (where 9% SPB was identified) and 4×10^{-2} UFC/g (where 100% SBP was identified). Spectrophotometry is currently being used to quantitatively determine siderophore production by measuring the absorbance of supernatant of bacteria grown on iron-limited media with CAS reactant. This research could help develop methods of utilizing bacteria as tools to decontaminate asbestos-filled sites.

Effects of Systemic Immunity on Diurnal Stomatal Movement of *Arabidopsis thaliana*

Discipline: Life Sciences
Subdiscipline: Microbiology

Marral Pourmoghadam*; Lisa David and Sixue Chen, *University of Florida*

Abstract: Plants respond to attack by pathogenic bacteria by eliciting long-distance mobile signals that travel to uninfected systemic tissue so that the remote tissues can prepare or "prime" itself for potential pathogen attack. We investigated Systemic Acquired Resistance (SAR), a long-distance signaling response in *Arabidopsis thaliana* elicited by the pathogenic bacteria Pseudomonas syringae pv tomato DC3000, and the effect on guard cells, the cells that form and control stomata aperture. We found that the SAR immune response in uninfected remote tissue led to reduced stomatal apertures, which may provide protection against pathogen invasion. SAR immune deficient mutant non-expressor of pathogen response 1 (npr1) did not exhibit the narrowed stomatal apertures in response to "priming" by SAR signals. Later experiments were conducted to test the integrity of the priming effects on the diurnal cycle of the stomatal apertures of the Col-0 primed and control leaves. Leaf surface images were obtained by light microscopy and stomata apertures were measured from 3 biological replicates of hourly time points throughout the day to discover the overall effect of SAR signals on stomata aperture when the guard cells are also receiving diurnal signals to open and close the stomata.

Morphological Effects of Systemic Immunity during Development of Wild Type and npr1 Mutant *Arabidopsis thaliana*:

Discipline: Life Sciences
Subdiscipline: Microbiology

Andres Lorenzo*; Ivan Grela; Lisa David and Sixue Chen, *University of Florida*

Abstract: Although plants lack the specialized immune cells found in animal systems, they are not left defenseless against bacterial infections. Plants have an immune response called Systemic Acquired Resistance (SAR), which sends long-distance mobile signals throughout the plant to “prime” uninfected leaves for pathogen defense. We found that the stomata of primed leaves responded differently than those of our control plants. Stomatal response is important as they are used by bacteria to gain access inside the apoplastic spaces of leaves, which they colonize. We used the *Arabidopsis thaliana* knockout mutant of one important protein that controls SAR, *npr-1* (Non-Expresser of Pathogenesis Related protein1) to investigate how the differences in stomata of primed to the control plants affect their growth and development. The npr1 mutant lacked the stomatal priming response of the Columbia wild type plants, so we compared their growth and development to that of the wild type plant. The physiological data collected after priming the plants and post-infection by the bacterial pathogen *Pseudomonas syringae* were leaf count, rosette diameter, and dry weight. We found significant differences in growth measurements of primed vs control wild type Arabidopsis, and also differences between wild type and *npr1* plants. We conducted Chlorophyll and Malondialdehyde (MDA) Assays to assess the level of health and stress in the wild type and npr1 mutant in control and primed plants.

Isolation and Characterization of Potential *Rhizobium Sp.* from Legumes in Puerto Rico

Discipline: Life Sciences
Subdiscipline: Microbiology

Gabriela Figueroa-Crespo* and Carlos Ríos-Velázquez, *University of Puerto Rico at Mayagüez*

Abstract: Nitrogen is one of the most important and limiting elements in plant production. Nitrogen fixation by microorganisms is the only natural way of reducing nitrogen into a usable form for plants. *Rhizobium* are symbiotic bacteria that fixate large amounts of atmospheric nitrogen reducing it into ammonia to be used by its host plant. Studying the *Rhizobium’s* nitrogen fixation mechanism can lead to optimizing plant productivity and yield without using chemical fertilizers. Nodules from *Cajanus Cajan, Arachis hypogaea*, and *Macroptilium lathyroides* from the west regions of Puerto Rico were analyzed. Using a *Rhizobium* isolation protocol from Agah, 2013, nodules found in the roots were harvested, dissected and plated on yeast extract mannitol agar with congo red dye for the isolation of potential *Rhizobium* bioprospects. Candidates were incubated in the dark and little to no absorption of congo red dye was indicative of *Rhizobium.* The isolates were subjected to macroscopic and microscopic morphological analysis to determine which corresponded to *Rhizobium* traits. 18 Gram-negative variable sized rods of *Rhizobium* bioprospects were isolated. Physiologically, they expressed variability in mobility, catalase and oxidase production. Molecularly, 16S rDNA amplicons will be sent to be sequenced and confirm the identity of the bioprospects. Currently primer specific n*odC* and n*ifH* amplifications are being completed to identify the presence of genes characteristic of the Rhizobium genus. The main objective is to correlate the diversity of

Rhizobium species relative to host plant and location as well as finding ways to optimize its nitrogen fixation capabilities for agricultural use.

Study of Ribosome Specialization in *Leishmania* Parasites Using Polysomal Profiling and CRISPR-Cas9 Gene Editing Technology

Discipline: Life Sciences
Subdiscipline: Microbiology

Andrea Perez*[1]; Sneider Gutierrez Guarnizo[2]; Kai Zhang[1]; Elena Tikhonova[3]; Zemfira Karamysheva[1] and Andrey Karamyshev[3], *(1)Texas Tech University, (2)Universidad de Antioquia, (3)Texas Tech University Health Sciences Center*

Abstract: *Leishmania* species cause leishmaniases that affect around 12 million people worldwide. To develop better treatments, it is necessary to uncover the molecular mechanism of parasite adaptation during the host change from sand flies to vertebrates.When parasite switches from the insects to warm blooded mammals, it is exposed to dramatic stresses including temperature rise, change in pH and nutrition. However, the molecular mechanism that support adaptation and survival of parasite during this transition is poorly understood. Our data based on polysomal profiling and proteomic approaches demonstrate substantial changes in the composition of translational apparatus during heat stress. We have found that ribosomes lost 30 proteins at 37°C that are typically present at 27°C and gained 6 additional proteins including ribosomal protein L36 during heat shock. Specialized ribosomes support translation of heat induced transcripts when general translation is repressed due to stress. We established CRISPR-Cas9 technology to edit its genome, which allows to knock-out or tag genes in a short period of time. L36 gene knock-out and N-terminal tagging were successfully achieved using the technique. Both wild type and *L36* KO grew at the same rate at optimal temperature (26°C), however, *L36* KO cells were very sensitive to the heat stress (37°C) in comparison with wt cells supporting that this specialized ribosome component plays an important role in parasite survival during the heat stress. Our data support the hypothesis that ribosomes undergo a change in the composition to support selective translation during the heat shock and transmission to mammalian host.

Abnormal Ion Concentration in Cystic Fibrosis Lungs Impact Rhamnolipid Production in *Pseudomonas Aeruginosa*.

Discipline: Life Sciences
Subdiscipline: Microbiology

Casandra Salinas*; Marianna Patrauchan and Michelle King, *Oklahoma State University*

Abstract: *Pseudomonas aeruginosa* causes severe acute and chronic infections in immunocompromised patients, most known for infecting the lungs of Cystic Fibrosis (CF) patients. CF patients have a dysfunctional chloride channel, which results in a disruption of ion homeostasis, including Ca and Fe. With the disease progression, the lung capacity decreases limiting gas exchange. *P. aeruginosa* is able to adapt and survive in the host environment. Understanding the mechanisms of such adaptations will aid in discovering innovative treatments against infections. One of the pathogen's many virulence factors is its ability to swarm, which contributes to the formation of biofilms and relies on the production of biosurfactant rhamnolipid. The latter also aids in the evasion of the host immune response. Previously, we have demonstrated that the elevated concentrations of Ca, Fe, NaCl, and MgCl impact swarming behavior. We **hypothesized** that the chemical conditions in the CF lungs affect the regulation of rhamnolipid biosynthesis. We aimed to determine the impact of these conditions on the expression of *rhlA*, required for production of rhamnolipid. For this, we used a promoter construct (P*rhlA*-*gfp* fusion), containing *rhlA* promoter upstream of *gfp*. Thus far, we have determined that the presence of elevated Ca and Fe increased *rhlA* promoter activity. Our data also indicate a loss of *rhlA* promoter activity when the cells carrying the construct are exposed to 5% CO_2. This abolishment of the *rhlA* promoter activity occurs even at elevated Fe and Ca. These results show multifactorial nature of *P. aeruginosa* rhamnolipid regulation.

Role of Interferon Lambda during Usutu Virus Infection in Mice

Discipline: Life Sciences
Subdiscipline: Microbiology

Claudia Perez* and Nisha Duggal, *Virginia Polytechnic Institute and State University*

Abstract: Usutu virus (USUV) is spread by mosquitoes and can cause neuroinvasive disease in humans, similar to related virus West Nile virus (WNV). USUV has spread from Africa into Europe, and there are increasing reports of neuroinvasive disease caused by USUV in Europe. USUV has the potential to become endemic in the Americas, as was the case with WNV. Previously, we have found that African and European USUV strains drastically differ in pathogenesis in a mouse model. Interferons (IFN) are a component of the innate immune system that defend against viruses. IFN lambda is expressed at the blood brain barrier, which defends against neuroinvasive viruses. We hypothesized that USUV would be more pathogenic in mice deficient in IFN lambda response. C57BL/6 (WT) and IFN lambda receptor knock-out (KO) mice were infected with two strains of USUV and treated with an antibody against IFN alpha receptor to render them susceptible. Blood and brain tissue samples were collected and tested for virus level via plaque assay. We found significant differences in viral level between the WT and KO mice with one USUV isolate, suggesting the importance of IFN lambda. There were also significant differences in viral level between the African and European USUV isolates at multiple timepoints, as previously observed. Additionally, one KO mouse succumbed to illness (20%) while all WT mice survived. In conclusion, IFN lambda may play a role in USUV infection and pathogenesis. Future studies will investigate the mechanism of USUV strain-specific differences in pathogenesis.

The Role of Wrky Transcription Factors in Virus Host Interactions

Discipline: Life Sciences
Subdiscipline: Microbiology

Esmeralda Alcala* and Susan Schroeder, *University of Oklahoma*

Abstract: The change in climate across the world has been a concern for the agricultural industry especially when it comes to drought. The common response so far has been to genetically modify the plants (GMOs) but there are many concerns with this practice. An alternative method is to stimulate the plant's immune system by infecting it with a plant specific virus which will handle drought stress better than an uninfected plant. To test this method, we analyze the gene expression of plants dealing with drought conditions through a group of transcription factors unique to plants called WRKY (named after the main amino acids in the sequence). In this study, the WRKY genes of interest are from the tomato plant, Solanum lycopersicum. The WRKY genes of interest are from the Solanum lycopersicum tomato plant, which we infected with Tobacco Mosaic Virus (TMV) or Satellite Tobacco Mosaic Virus (STMV). Tracking the common WRKYs expressed after a plant is infected helps us understand the specific WRKYs activated for each virus. We hypothesize that the commonly expressed WRKY factors in different virus infections might also be responsible for drought tolerance.

Identification of Antibiotic Resistant Bioprospects Present in Metagenomic Libraries from the Sub Tropical Dry Forest Reserve in Puerto Rico

Discipline: Life Sciences
Subdiscipline: Microbiology

Diego Mendez Aviles*, *University of Puerto Rico at Mayaguez* and Carlos Ríos-Velázquez, *University of Puerto Rico at Mayagüez*

Abstract: In the early 1900's, infectious diseases were the major causes of death in the United States. The discovery of antibiotics alleviated the infectious diseases crisis. However, due to the misuse of antibiotics, multi-drug resistant microorganisms have emerged once again. This highlights the importance of utilizing new approaches to identify the resistance mechanisms that bacteria utilize to circumvent antibiotics. One such approach is Metagenomics, a culture-independent technique which has demonstrated to be a powerful tool for the discovery of novel activities. The purpose of this research was to identify antibiotic resistant bioprospects in an uncommon environment using a culture-independent strategy. A functional metagenomics approach was used to screen for clones capable of tolerating aminoglycoside antibiotics from a metagenomic library generated from the Puerto Rican Guanica Dry Forest (GDF). The Minimal Inhibitory Concentration of kanamycin, a broad-spectrum aminoglycoside antibiotic, was determined on the surrogate host *Escherichia coli* Epi300, used to generate the library with GDF DNA cloned into the pCC1FOS vector. The MIC obtained for Epi300 was 11 μg/μL, and the metagenomic library was grown in LB medium supplemented with 1X–4X MIC of kanamycin. A total of 114 kanamycin-resistant clones were isolated. 35 clones were randomly selected for analysis and the library's fosmid was confirmed molecularly in all clones. 5 distinct kanamycin resistant clones were identified by restriction analysis. These findings demonstrate the presence of naturally occurring antibiotic resistance mechanisms in this environment and presents the opportunity to characterize the gene(s) responsible for the resistance by Tn mutagenesis and in silico analysis.

Simulated Microgravity Decreases T Cell-Associated Cytokine Production By Murine Lung Leukocytes

Discipline: Life Sciences
Subdiscipline: Microbiology

Caroline Carter*[1]; Harlan Jones[2]; Kelsey Bettex[2] and Colette Ndjom[2], *(1)University of Texas at Arlington, (2)University of North Texas Health Science Center*

Abstract: In 2024 NASA will launch a new moon base that will allow humans to live long term in space in preparation for exploration to Mars. Long-term spaceflight is known to negatively impact an astronaut's health. In particular, space-induced alterations in immune function has been shown to be a leading risk factor. To date, little is known of the impact that microgravity (MG) may have on resident lung leukocyte responses. Thus, the purpose of the current study was to establish a ground-based experimental model to simulate the effects of MG effect on lung immune function.

We hypothesize that simulated MG suppresses CD4 T-cell cytokine production by murine lung leukocytes.

Studies were conducted in which total murine leukocytes were exposed to MG conditions using a tabletop clinostat able to apply continuous rotation (75 RPMs). After 24 hours of rotation, leukocytes were stimulated in vitro through anti-CD3 mediated activation of T cells subsets to assess their cytokine production.

Results shown that exposure to simulated MG resulted in a significant decrease in T helper cell 1 (Th1), T helper cell 2 (Th2) and T helper 17 (Th17)-associated cytokines. Using this ground-based experimental design, studies suggest a global adverse effect of simulated MG on lung leukocytes.

Statistical analysis of the data supports our hypothesis that simulated MG suppresses both anti-inflammatory and inflammatory cytokines.

In Vitro and In Vivo Activity and Tolerability of BX795 As an Antiviral Agent Against Herpes Simplex Virus-2 Genital Infection

Discipline: Life Sciences
Subdiscipline: Microbiology

James Hopkins; Farreh Qatanani* and Deepak Shukla, *University of Illinois at Chicago*

Abstract: Herpes simplex virus type 2 (HSV-2) is among the most common sexually transmitted diseases in the world. It can cause lesions around the genitals that are both physically and emotionally painful. Acyclovir (ACV) is the most common treatment for an HSV-2 infection, but there is emerging resistance to the drug. BX795 is a small molecule inhibitor of TANK-binding kinase 1 (TBK1), and was found to suppress HSV-1 ocular infection through an off target effect. In this study, we propose that BX795 would inhibit HSV-2 infection. We show that BX795 is able to suppress HSV-2 infection in both *in vitro* and *in vivo* models, by inhibiting AKT phosphorylation which is important for HSV-2 replication. In tissue culture a significant decrease in infectious virions was observed after treatment with BX795. This decrease upon BX795 treatment was seen at both the viral transcriptional levels and viral protein levels by quantitative reverse transcription polymerase chain reactions (RT-qPCR) and Western blots. After treatment we discovered that there was a decrease in AKT phosphorylation which is important for the HSV-2 life cycle. After infection with HSV-2 vaginally in mice, we found that there were less infectious virions in the BX795 treated mice. Our results indicate that BX795 is able to successfully inhibit HSV-2 infection and could be a promising antiviral against rising ACV resistance.

Group B Streptococcus Influences Apical Microvilli and Membrane Vesicle Biogenesis in Host Cells

Discipline: Life Sciences
Subdiscipline: Microbiology

Jan Mikhale Cajulao* and Lily Chen, *San Francisco State University*

Abstract: *Streptococcus agalactiae*, also known as Group B Streptococcus (GBS), is a gram-positive cocci shaped bacterium causing neonatal sepsis, meningitis, and pneumonia. GBS utilizes several strategies to colonize host tissues, among them are secreted virulence factors. In this study, we explored the effect of GBS exposure on HeLa cells and found that GBS secreted factors rearrange the HeLa cell cytoskeleton, destroy the HeLa cell monolayer, and reduce apical microvilli and microvilli dependent membrane vesicle shedding. HeLa cell monolayers were exposed to GBS, or cell-free supernatant for 4 hours. Afterwards, samples were processed for scanning electron microscopy (SEM) or processed to enumerate HeLa cell detachment. Monolayers exposed to GBS or GBS supernatant were destroyed. SEM analysis revealed that HeLa cells exposed to GBS or GBS supernatant had reduced and withered apical microvilli and reduced surface membrane vesicle content. GBS supernatant also caused HeLa cells to exhibit a spheroid morphology. We believe these phenomena are due to GBS secreted factors causing significant cytoskeleton rearrangements. This study demonstrates a form of GBS pathogenicity that does not require live bacteria or physical contact with host cells and provides an avenue to explore alternative treatment options for GBS infection.

Differentiation of Potentially-Pathogenic Strains of Vibrio Vulnificus through Polymerase Chair Reaction (PCR) of the Vcge Locus

Discipline: Life Sciences
Subdiscipline: Microbiology

Alvaro Ortola Tortosa*; Vinoshna Sama and Gregory Buck, *Texas A & M University - Corpus Christi*

Abstract: *Vibrio vulnificus* is an asporogenous, halophilic Gram-negative comma-shaped bacteria that is found in marine and estuarine waters. This organism may cause gastroenteritis, septicemia or necrotizing fasciitis through cuts in skin; the latter condition has high morbidity and mortality. Corpus Christi is a coastal community with a large population of individuals who may be susceptible to vibriosis due to predisposing health conditions in the population such as diabetes, liver disease or hemochromatosis. Corpus Christi is especially vulnerable to potentially high levels of vibriosis during the warmer months, due to storm surges as a result of hurricane season. Two allelic forms of the *vcg* gene, whose function is currently not known, may be seen: *vcgC* predominates in clinical isolates and *vcgE* is mostly seen in environmental isolates. This study investigates the potential use of the *vcgE* gene in *Vibrio vulnificus* as an indicator for high levels of the organism in the aquatic ecosystem. DNA was extracted from *V. vulnificus* samples previously gathered from areas surrounding Corpus Christi for analysis, PCR assays were performed, and visualized on a 2% agarose gel with 0.5 µg/mL ethidium bromide. Preliminary data indicate that *vcgE* can be used to detect *Vibrio* isolates and distinguish from isolates containing *vcgC*. Further experiments are currently underway to optimize PCR conditions for definitive results.

Presence of Antibiotic-Resistant Bacteria in Manure Samples from Puerto Rico

Discipline: Life Sciences
Subdiscipline: Microbiology

Shanaika Jaced Vargas Rivera*; Luciane Jimenez Rodriguez and Elizabeth Padilla Crespo, *Inter-American University of Puerto Rico*

Abstract: The use of antibiotics in agriculture is a significant contributor to drug-resistant infections in clinical cases. About 80% of the antibiotics produced in the USA are used in agricultural applications for disease prevention, treatment, and improved animal growth. Antibiotic use in humans has shown to select for resistant strains, and the same pattern is observed with livestock. Antibiotics are known to remain bioactive in soils for several months. Also, these drugs have weak adsorption in the animal body, with 90% of the administered dose secreted in excrement and urine, which can also harbor viable drug-resistant bacteria. Consequently, large quantities of antibiotics and resistant strains can spread throughout agricultural topsoil or plantations (when manure is used as fertilizer); thus, becoming a significant public health concern. We hypothesize that antibiotic-resistant bacteria are present in chicken and cow manure in a farm in Camuy, P.R. To isolate drug-resistant bacteria, samples were serially diluted and plated on Nutrient Agar containing 0.05 - 25 ug/mL of ampicillin, and 3.5-15 ug/mL of tetracycline. DNA was extracted from strains that exhibited growth and interrogated via PCR with primers targeting *tetA* and *blasSHV* resistance genes. Isolates from both manure samples showed positive amplification. These findings confirm viable antibiotic-resistance bacteria in our samples, and that their genes are present. Future efforts aim to fully characterize the isolated strains, assess the presence of other resistance genes, and possible ways of dissemination in the samples collected. These efforts will provide a better glimpse of their potential threat to public health.

The Effects of Cytidine Deamination on Retroviral Evolution

Discipline: Life Sciences
Subdiscipline: Microbiology

Mary-Benedicta C. Obikili*; Karen Salas Briceno; Alexya N. Aguilera and Susan Ross, *University of Illinois at Chicago College of Medicine*

Abstract: *A3G* is a member of the mammalian apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like (*APOBEC3*) family. There are 7 *APOBEC3* genes in primates: *A3A, A3B, A3C, A3DE, A3F, A3G*, and *A3H*, while mice have a single *A3* gene. APOBEC3 proteins are single-strand DNA cytidine deaminases, changing cytidine-to-uracil residues in retrovirus (-) strand DNA and thus causing G-to-A mutations that inhibit infection in the coding strand. However, some mutations could be beneficial to the virus and help it evade the antiviral effects of A3G, the immune system or anti-viral drugs. Another protein, Uracil DNA Glycosylase (UNG) removes uracil from chromosomal DNA, leaving gaps which are filled by DNA repair enzymes. Here we tested whether A3G selects for retroviruses that are A3G-resistant *in vivo* and whether UNG plays a role in repairing A3G-mutations. To test this, plasma was obtained from four different strains of mice infected with murine leukemia virus (MLV): A3 knockout (KO), UNG KO APO KO, A3 KO A3G+, and UNG KO A3 KO A3G+. The plasma was used to infect two cell lines expressing GFP or A3G-GFP and virus titers were obtained. We found that plasma viral titers most of the mice were higher on GFP cells compared to A3G-GFP cells. This was expected, since A3G inhibits MLV infection. However, in one sample from an A3G-expressing mouse, the titers on A3G-GFP 3T3 and GFP-3T3 were similar, suggesting that the viruses gained beneficial mutations that counteract A3G. We are sequencing these viruses to determine whether they have acquired A3G-resistance mutations.

Competence of *S. Pneumoniae* Encapsulated within Aqueous Micro-Droplets.

Discipline: Life Sciences
Subdiscipline: Microbiology

Catarina Bromatti*; Trinh Lam and Donald A. Morrison, *University of Illinois at Chicago*

Abstract: *Streptococcus pneumoniae* is a Gram-positive bacterium responsible for pneumonia, meningitis, and bloodstream infections. *S. pneumoniae* acquires external DNA by the transformation mechanism after becoming competent by the stimulation of a competence-stimulating peptide (CSP). The acquired foreign DNA can lead to antibiotic resistance or other new traits. We previously showed that competence can be developed by individual cells isolated inside 10-μm-diameter droplets, but we did not establish the absolute level of competence in this new restrictive environment. In this project, we investigated the fraction of *S. pneumoniae* cells that can become competent when isolated in the microdroplets by using a droplet microfluidic device with three inlets: an inlet for 5% surfactant in FC-40 oil, and two aqueous inlets of a mixture of competent cells and 6-kbp Nov^R donor DNA, and CSP cocktail, respectively. The pure donor DNA molecules can convert nearly all competent cells into Nov^R recombinants, providing a direct measure of competent cells. The results showed that transformation efficiency, and thus competence level, within droplets was equivalent to the control cells that had not been confined, demonstrating that the encapsulation of cells in droplets did not affect competence level. This use of microdroplets will allow us to observe competent cell behavior directly under the microscope, followed by the recovery of recombinants from the imaged droplets by selective plating with Novobiocin.

Supported by LASGANAS, and the National Institute of Allergy and Infectious Diseases (NIH-NIAID), number 5R21AI133304-02.

Pyorubin Extraction from *Pseudomonas Aeruginosa* Secretions and Assessment through SDS-PAGE and MALDI-TOF

Discipline: Life Sciences
Subdiscipline: Microbiology

Aldo Trejos*; Brent Beadell; Nathan Lanning, PhD and Edith Porter, MD, *California State University, Los Angeles*

Abstract: *Pseudomonas aeruginosa* is a Gram-negative, rod shaped bacterium, which can cause pneumonia and other infections. Different phenotypes of *P. aeruginosa* can secrete not only numerous proteins but also various pigments such as pyocyanin and pyorubin, among others. Pyocyanin has been well studied. Its cytotoxic activity against airway epithelial cells has been of interest in the search for novel anticancer drugs. In contrast, the cytotoxicity of pyorubin is still undetermined. Our laboratory has a pyorubin-producing *P. aeruginosa* strain and the objective of this study was to extract and purify pyorubin from *P. aeruginosa* secretions as a first step in the characterization of this pigment and its cytotoxic activity. Exploiting the much lower molecular weight of pyorubin compared to secreted proteins and its color, we were able to purify pyorubin by subjecting bacterial secretions to native polyacrylamide gel electrophoresis (native-PAGE), eluting the pigment from the gel by overnight incubation in water, and concentrating the pigment by lyophilization. Silver-stained SDS-PAGE showed only traces of low molecular weight proteins. MALDI-TOF analysis revealed the masses 209.7 and 231.6 (m/z), which are consistent with reported masses of chemically modified subcomponent of pyorubin, aeruginosin A. The pyorubin extract can now be evaluated for cytotoxic activity. This is the first step and if found to have cytotoxic activity, further pyorubin purification using centrifugal filtration will be carried out. This research may lead to the discovery of novel cytotoxic drugs. Funding for this study was provided by NSF CHE 1919722 and NIH RISE GM061331.

Consequence of Sars-Cov-2 Coronavirus Infection on Fetal Outcomes

Discipline: Life Sciences
Subdiscipline: Microbiology

Corey Simpson*; Joe Westrich and Candace Mathiason, *Colorado State University*

Abstract: The COVID-19 pandemic originated in Wuhan, China in December of 2019. The World Health Organization (WHO) immediately issued statements regarding reported cases of pneumonia and shortly thereafter identified the pathogen as a novel coronavirus, denoted SARS-CoV-2. As of July 2, 2020, there have been 10.7 million confirmed cases, 516,000 of which have resulted in death. Of these cases, 10,537 have been identified in pregnant women. The impact of these infections on pregnancy and fetal outcomes remains unknown. It is known that modulation of the maternal immune response at the maternal-fetal interface, as well as fetal deprivation of nutrients or oxygen can lead to neurologic and physical fetal abnormalities. By collating novel reports on SARS-CoV-2 and other related severe coronavirus infections (Middle Eastern Respiratory Syndrome [MERS] and Severe Acute Respiratory Syndrome [SARS]), we aim to generate a comprehensive review on the topic of coronavirus infections and pregnancy outcomes. Investigation of the impact these maternal infections have on the developing fetus is imperative to our understanding of the implications to the long-term health of babies born to SARS-CoV-2-infected mothers.

Characterization of Tiny Earth Isolate 308 and Its Antibiotic Production Against the Crown Gall Pathogen *Agrobacterium Tumefaciens*

Discipline: Life Sciences
Subdiscipline: Microbiology

Hector Navarro* and Enid Gonzalez-Orta, *California State University, Sacramento*

Abstract: *Agrobacterium tumefaciens* is a soil-borne plant pathogen that can infect a wide variety of major crops. This disease limits nursery production of fruit and nut trees and causes an estimated annual loss of $23 million in California. There are many strategies to manage crown gall, yet this disease remains a prevalent issue. Students participating in the Tiny Earth Network at Sacramento State isolated bacteria from soil at the university's arboretum in search of antibiotic producing strains. One strain, Tiny Earth Isolate 308 (TE308), killed an *A. tumefaciens* strain isolated from a California walnut orchard. Further analysis of the 16s rRNA sequence reveals the strain to be *Bacillus*. The genus *Bacillus* produces many antimicrobial peptides. Therefore, we hypothesize that TE308 has the potential to be used as a biocontrol agent for *A. tumefaciens*. We investigated what genes take part in the biosynthesis of antimicrobial compounds in TE308 by extracting genomic DNA to use as a template in a series of polymerase chain reactions (PCR). We used specific primers to target putative antimicrobial associated genes for amplification. These included the genes responsible for the synthesis of the following compounds: bacilysin, iturin, surfactin, bacillaene, bacillibactin, and amylocyclicin. Results show the presence of the gene responsible for the lipopeptide, surfactin, in the genome of TE308. Continued genomic characterization is expected to uncover additional genes associated with antimicrobial compounds. Future work includes sending TE308 for whole genome sequencing followed by bioinformatic analysis using bioinformatic programs, like AntiSMASH to search for biosynthetic gene clusters.

A Carbon-Rich Permeable Reactive Barrier Enhances the Bacterial Community to Remove Nitrate from Groundwater

Discipline: Life Sciences
Subdiscipline: Microbiology

Claudio Amaya Santos[*1]; Nicole Schrad[2] and Chad Saltikov[2], *(1)Saint Peter's University, (2)University of California, Santa Cruz*

Abstract: Nitrate concentration in groundwater has risen to dangerous levels due to inorganic fertilizer and animal manure leaching into the water supply. Nitrate contamination is linked to health problems, such as methemoglobinemia, and can cause eutrophication in the environment. In this study, we analyzed microbial sequencing data from a column experiment that simulated nitrate-contaminated groundwater conditions. Adding a horizontal carbon-rich permeable reactive barrier (PRB) to a column enhanced microbial denitrification compared to a native soil control column. We analyzed the 16S rRNA genes to understand the microbial community makeup for each column. We also analyzed the nitrous oxide reductase gene (*nosZ*) to understand whether or not the bacteria in each column are able to perform the last step of denitrification. We hypothesize the samples with a PRB will have the highest number and diversity of *nosZ* gene reads and species that are most abundant in the PRB samples will also be the species that have the *nosZ* gene. Our initial 16S beta diversity analysis results demonstrate that the PRB changes the community makeup by depth compared to the control. *Sphingobium* and *Novosphingobium* communities were found in a higher abundance in the columns with the PRB. We expected these species to also have the *nosZ* gene. This research lays the foundation for understanding the connection between denitrification rates and microbial communities within soil. This foundation is essential for future research aiming to reduce the nitrate contamination in groundwater.

Discovering Novel Members of the Thermophilic Ammonia Oxidizing Archaea in Hot Spring Metagenomes

Discipline: Life Sciences
Subdiscipline: Microbiology

Yingshan Bi*[1]; José de la Torre[2]; Rebecca Salcedo[2]; Gonzalo Arcidiácono[3] and Saul Cortez-Alvarado[2], *(1)University of California, Berkeley, (2)San Francisco State University, (3)University of California, Santa Cruz*

Abstract: Ammonia-oxidizing archaea (AOA) plays an essential role in the global nitrogen cycle, controlling the rate of ammonia oxidation in nitrification. AOA have been found in a wide variety of terrestrial and aquatic environments, including extreme environments such as hydrothermal systems. Our laboratory has cultivated and sequenced the genomes of over 15 thermophilic AOA (ThAOA) from hot springs around the world. Genomic analyses show that these ThAOA genomes are extremely similar to each other, even though cultivation-independent molecular approaches indicate a diverse population of ThAOA in these hot springs. In this project, we have designed a computational approach to identify genomic sequences from uncultivated lineages of ThAOA in metagenomes from a variety of hot springs. For each metagenome, we used BLAST to identify individual reads matching the genome sequence reference ThAOA from that environment. We used a custom script to extract reads matching the reference between 90% and 96% nucleotide identity over an alignment length of at least 150 bp. Matching paired reads were then assembled using metaSPAdes and annotated using an in-house pipeline. Phylogenetic analyses using single-copy genes (e.g. 16S ribosomal RNA gene, or genes for the archaeal ammonia monooxygenase), or 122 concatenated archaeal marker proteins will be used to determine the evolutionary relationship of these assembled genomes to known AOA lineages. We predict that the application of our culture-independent approach will allow us to identify a greater diversity of ThAOA, which in turn will help us better understand the ecology and evolution of these important microorganisms.

Characterization of Mouse Schlafen 14 upon Viral Infection

Discipline: Life Sciences
Subdiscipline: Microbiology

Lilia Olmstead*, *The University of Texas at El Paso* and Manuel Llano, *University of Texas at El Paso*

Abstract: The Schlafen (SLFN) family of proteins have been suggested to have important functions in cell proliferation, immune cell development, and antiviral response. It has already been found that Schlafen 11 can be characterized as an interferon-stimulated gene that has the capability of controlling the synthesis of proteins by regulating tRNA abundance. Through this mechanism, Schlafen 11 has been shown to impair human immunodeficiency virus 1 (HIV-1) infection and flaviviruses. This presentation will aim to characterize the mouse derived protein mSLFN14 to see its effects upon viral activity by evaluating viruses such as HIV-1, Vesicular Stomatitis Virus (VSV), and West Nile Virus (WNV). Experiments were first carried out with gene cloning by creating a mSLFN14 expression plasmid. The resulting DNA was sequenced and analyzed for any mutations with High-Throughput Sequencing (HTS). Upon finding no mutations, A-172 cell lines were generated expressing mSLFN14 or an SLFN11-specific shRNA (KD). The cell lines were infected with HIV-1 and p24 levels were measured 4 days later in the cell supernatant by ELISA; p24 values were normalized to the values found in KD cells for each cell line. The preliminary results revealed that mSLFN14 restricts viral infection by displaying significant anti-viral activity compared to the KD. It is expected that this work will have the potential to expand our knowledge on viral functionality and the anti-viral activity of proteins of the Schlafen protein family, an area poorly exploited.

Computational Identification of Mitochondrial Orthologs in the Alpha-Proteobacterium *Sinorhizobium Meliloti* That Contribute to Symbiosis

Discipline: Life Sciences
Subdiscipline: Microbiology

Rodrigo Cuellar*, *Skyline College* and Joseph Chen, *San Francisco State University, San Francisco*

Abstract: Mitochondria are unique organelles present in almost all eukaryotes, as they contain their own genomes, produce a number of their own proteins, and reproduce independently from the host cell. These characteristics form the basis of the endosymbiosis theory, which suggests that mitochondrion developed from a free-living bacterium taken up by the proto-eukaryote. Molecular data, including genomic analysis, indicate that the ancestral mitochondrion is closely related to alpha-proteobacteria. *Sinorhizobium meliloti*, a representative member of the *Rhizobiales* order in the *Alphaproteobacteria* class, colonizes compatible legumes and fixes nitrogen for the plant host in an endosymbiotic relationship similar to that seen for mitochondria. We hypothesize that *S. meliloti* and mitochondria share ancestral and homologous proteins that allow both to interact successfully with their hosts. To identify such candidates, we performed literature and database searches for mitochondrial proteomes across diverse species. We then used bioinformatics tools, including BLAST, to screen for homologs of mitochondrial proteins in *S. meliloti*. During the screen, proteins with homologs in other bacteria, including alpha-proteobacteria not known to participate in symbiosis, will be eliminated. We expect that mitochondria and *S. meliloti* would share a limited set of proteins, some of which may impact host-symbiont relationships. Future projects will build on the list of proteins generated to determine their molecular activities in *S. meliloti*, to obtain a better understanding of the complex coordination underpinning symbiosis.

The Search for Fungi in Ancient Permafrost

Discipline: Life Sciences
Subdiscipline: Microbiology

Keenan Manpearl*, *California State University, Northridge* and Rachel Mackelprang, *California Statue University Northridge*

Abstract: Permafrost, or permanently frozen soil, contains large amounts of undecomposed carbon. As it thaws due to climate change, microorganisms degrade the carbon and “breath” it into the atmosphere as carbon dioxide and methane. Thus, it is becoming of increasing importance as global temperature rises. Current research investigating microbial communities in permafrost has mainly focused on bacterial and archeal communities, leaving eukaryotic populations largely understudied. To determine how fungi contribute to microbial communities, characterize fungal diversity, and ascertain whether permafrost age impacts diversity, we performed metagenomic sequencing of microbial communities in permafrost of varying ages. We extracted fungal reads from the metagenomes by comparing sequences to databases of known genes and performing taxonomic classification. Initial analysis found substantial taxonomic diversity, with high abundances of Ascomyota and Basidiomycota. Ongoing research is focused on identifying how taxonomy varies across age categories. By analyzing the fungal DNA found in these samples, we are gaining novel insights into the microbial communities in this important environment and how they may respond to permafrost thaw.

Characterization of *Caenorhabditis Elegans* Skin Microbiome and the Effects of Naturally-Correlated Bacteria on Nematode Undulatory Behavior

Discipline: Life Sciences
Subdiscipline: Microbiology

Nadia Haghani*[1]; Molly Matty[2] and Sreekanth Chalasani[1], *(1)University of California, San Diego, (2)Salk Institute*

Abstract: Popularization of microbiome research has led to an expansive understanding of microbial ability to affect host behavior. While the gut microbiome holds the spotlight, the skin microbiome and cuticle interactions with external microbes remain understudied in the model nematode, *Caenorhabditis elegans*. There is frequent implication of the existence of a skin microbiome; researchers adopt harsh bleaching and wash protocols to remove surface-adherent bacteria from the cuticle. The purpose of this research is to characterize the *C. elegans* skin microbiome and quantify bacterially-induced changes to host undulatory behaviors. I will quantify worm locomotory and swimming behaviors with changes to the worm microbiome, specifically a change from laboratory bacterium *Escherichia coli* to the natural microbiome termed *CeMBio*. Using 16s rRNA sequencing, we plan to characterize the skin microbiome of the nematode and test worm conditions hypothesized to elicit a noticeable effect on microbial colonization of *C. elegans*. These conditions include manipulations to washing protocols and additional worm cuticle mutants, Dpy, Srf, Bus, and Bah mutants known to affect the worm cuticle. I expect the analysis of this sequencing data to corroborate implications of bacterial adherence to *C. elegans* cuticle and the existence of a skin microbiome. These studies can provide a deeper understanding of how environmental microbes elicit behavioral changes in animals and provide insight to the impact of environmental microbes on an animal’s first line of defense--the skin. In the future, I would like to better understand the ecological significance of the worm cuticle and its evolutionary relationship with microbes.

Genomes and Transcriptomes of Enterohemorrhagic *Escherichia coli* (EHEC) O113:H21 Strains 4 and EH41 Representing Two Clonal Complexes with Disparate Disease Manifestation

Discipline: Life Sciences
Subdiscipline: Microbiology

Isaiah Goertz*; Sam Zaia; Ricardo Martinez; Anna Allué-Guardia; Sara Koenig and Mark Eppinger, *University of Texas at San Antonio*

Abstract: Enterohemorrhagic *Escherichia coli* (EHEC) of serogroup O113:H21 are a globally disseminated lineage of Shiga toxin (Stx)-producing *E. coli* (STEC), characterized by the production of a potent phage borne cytoxin. In this study we analyzed representative strains of the two major phylogeographical clonal complexes. Infections with ST-820 complex isolates circulating in Australia only have caused severe human disease, such as hemolytic uremic syndrome (HUS), conversely ST-223 isolates prevalent in the US and elsewhere rarely cause human disease, but are frequent contaminants of produce. To discern if there is a particular genotype associated with the hypervirulent ST-820 lineage, we sequenced and functionally characterized the transcriptomes of strains 4 (ST-223 and) EH41 (ST-820). Genomes were sequined to closure through MinION and Illumina Next Generation Sequencing (NGS) technology followed by the whole genome sequence typing (WGST) of the core and accessory plasmids. Pathways involved in phage mobilizing and ultimately production of Stx were comprehensively analyzed by RNASeq. Integrating the genome and virulence information in this lineage is critical for the identification of potentially hypervirulent subpopulations. The catalogued virulence gene inventory and our pathogenicity assessment in Stx-production traits supports the notion of an increased pathogenic potential of ST-820 strains, in accordance with the strain-associated epidemiological metadata. The identified genome signatures are readily available for biosurveillance and risk assessment to ultimately improve public health.

The Phylloplane: Another Habitat Where Purple Non-Sulfur Bacteria Thrive.

Discipline: Life Sciences
Subdiscipline: Microbiology

Bianca N. Lopez Rosado* and Elizabeth Padilla Crespo, *Interamerican University of Puerto Rico*

Abstract: Purple non-sulfur bacteria (PNSB) are among the most energetically versatile of all prokaryotes. These group carry out anoxygenic photosynthesis under anaerobiosis in the presence of light. The aim of this study was to isolate PNSB from plant leaf surfaces, since we hypothesize these metabolic versatile bacteria can also be associated in the phylloplane. To accomplish this goal leaves of the *Nymphaeaceaesing* family were aseptically collected and used as inoculum in enrichments with Pfennig's medium (mineral medium that is suitable for most PNSB) under light and anaerobic conditions. After 2 weeks enrichments were positive for PNSB growth, subsequently, DNA was extracted and interrogated via PCR with primers targeting the anoxygenic photosynthesis biomarker gene *pufLM.* PCR results were positive, and the resulting amplicons were cloned and sequenced. Phylogenetic analysts indicated the presence of *Rhosopseudomonas* and *Rhodoplanes* sp. in our samples, interestingly these groups have been previously described in the literature as associated with plant leaves and rhizosphere. Future efforts are also focused in obtaining pure bacterial isolates from these samples, in order to better understand the bacterial communities inhabiting aquatic plant species, especially these anoxygenic phototrophs.

Isolation and Characterization of Surfactant Producing Bacteria for Potential Use in Bioremediation Applications

Discipline: Life Sciences
Subdiscipline: Microbiology

Yareliz Pellot-Soto* and Elizabeth Padilla-Crespo, *Interamerican University of Puerto Rico, Aguadilla Campus*

Abstract: Biosurfactants are natural surface-active agents produced by bacteria, yeast, and fungi. These biomolecules reassemble detergents and have broad applications that are relevant to the bioremediation, pharmaceutical, cosmetics, and food industry, among others. Biosurfactants represent an alternative to chemically synthesized surfactants, by having lower toxicity, higher biodegradability, and environmentally friendly potential. In the area of bioremediation, biosurfactants can be employed in enhanced oil recovery efforts, restoration of oil-contaminated environments, and for cleaning of oil-storage tanks. Biosurfactants are also used in agriculture as natural pesticides; other biomedical applications include synthesis of nanoparticles with antimicrobial properties. In this study we isolated bacteria from hydrocarbon contaminated soil, since we hypothesized their presence in those samples. We applied a strategic screening methodology that encompassed various techniques: using CTAB-Methylene blue agar, hemolysis test (on blood agar plates), the drop collapse assay, the microplate test, and the oil spreading assay. We successfully established a collection of 20 isolates that show biosurfactant production; which exhibit a variety of morphologies and diversity. Currently, the objective is to screen which bacterial isolates produce rhamnolipids, a specific type of surfactant known for its efficacy in bioremediation of organic and heavy metal polluted sites. Future efforts are aimed to establish a consortium of biosurfactant-producing bacteria that can aid in bioremediation efforts of oil and fuel impacted ecosystems.

Determining Programmed Translation Frameshifts in Streptomyces Bacteriophages

Discipline: Life Sciences
Subdiscipline: Microbiology

Carolina Menchaca* and Lee Hughes, *University of North Texas*

Abstract: Programmed translational frameshifts are naturally occurring phenomena that allow the production of two peptide products from one mRNA transcript. Tailed bacteriophages have well-studied frameshifts in their tail assembly chaperone (TAC) genes. Production of the TAC gene in many phages is known to result in two products: a short, abundant tail assembly chaperone protein, and a longer version produced at a small rate. The strongest identified regulatory factor of translational frameshifts is the “slippery sequence” which typically follows a 5’-XXXYYYX-3’ structure. BryanRecycles, a cluster BD1 phage discovered in Denton, Texas has a bioinformatically-identified TAC frameshift and also has a potential translation frameshift in its DNA primase gene. We have identified the DNA primase gene as a possible frameshift due to a significant amount of coding potential in a -1 frame starting before the stop codon of the genes, similar to that of TAC. We performed PCR to amplify the target genes, and isolated them via designed primers that would exclude digestion of restriction endonuclease SmaI. We then inserted the TAC/DNA primase PCR products into pUC18 plasmid vector which was introduced to chemically-competent DH5α E. coli via plasmid recombination using pUC18. The proteins were then extracted and purified via column chromatography and have been further analyzed using SDS-PAGE/western blot. We will be using the TAC as a positive experimental control and use the same procedures for isolating, then identifying whether or not DNA primase has a translational frameshift. This set of procedures could be used in determining frameshifting in other bacteriophage genomes.

Ecology and Distribution of Nitrogen Fixing Bacteria

Discipline: Life Sciences
Subdiscipline: Microbiology

Jesenia Rosa Miranda*, *Inter American University of Puerto Rico, Aguadilla Campus* and Elizabeth Padilla-Crespo, *Interamerican University of Puerto Rico, Aguadilla Campus*

Abstract: Biological nitrogen fixation is a process exclusively accomplished by the prokaryotic world. Nitrogen fixing bacteria are both symbiotic and free living. Rhizobium takes atmospheric nitrogen and reduces it to ammonia making it available for plant utilization; in return the bacteria receives organic compounds from the plant host. On the other hand, free-living Rhizobium cells make a lifestyle as a saprophyte (on dead organic matter), although Nitrogen fixation by free-living cells has been described under certain conditions. Most studies look at Rhizobium spp. presence and diversity isolated from root nodules of legume hosts, while only a limited number have focused on their direct isolation from soils. In this study we investigated the presence of Rhizobium in soil samples from urban, costal, and agricultural areas; we hypothesize these bacteria also are present at these sites. To achieve our goal, 1 gr of sample was serially diluted (10-1 to 10-5) and plated on Yeast Mannitol- Congo red agar. More than 20 bacterial strains were isolated across all samples, and characterized by classic microbiology techniques, and via PCR using group specific (16S-23S rRNA) and process specific (nifH, nitrogenase reductase) primers. Of special interest, was the positive amplification in assays targeting genes from Rhizobium tropici. To our knowledge only one study has previously described, or reported, R. tropici in samples from Puerto Rico. Future efforts will be invested to know more about the ecology and distribution of Rhizobium spp. (especially R. tropici) in our samples, and the possible use of these strains as biofertilizers.

Characterization of Phosphate-Solubilizing Bacteria Isolated from Agricultural Soil and Their Efficiency on the Growth of Pigeon Peas (Cajanus Cajan)

Discipline: Life Sciences
Subdiscipline: Microbiology

Efrain J. Gerena Rodriguez*, *Inter-American University of Puerto Rico, Aguadilla campus* and Elizabeth Padilla-Crespo, *Interamerican University of Puerto Rico, Aguadilla Campus*

Abstract: This study aimed to isolate phosphate-solubilizing bacteria (PSB) from soil and rhizosphere of pigeon peas (Cajanus cajan) in conventional farms. Pigeon peas is a cuisine staple in Puerto Rico, and therefore an agricultural relevant product, linked with food security. Phosphate and Nitrogen are the macronutrients most essential for plant growth, but approximately 95-99% of the natural phosphorus in soil is present in insoluble form, not accessible for the crops. There are groups of bacteria capable of solubilizing phosphate for plant uptake, representing an alternative to commercial fertilizers, we hypothesize these bacteria are present in the roots of Cajanus cajan. To achieve this goal, samples were homogenized in a mortar, serially diluted and plated on the NBRIP-BPB medium and Pikovskayas Agar. These media contain insoluble phosphates; thus, colonies exhibiting a halo/clear zone are potential phosphate solubilizers. PSB bacteria were isolated from all samples. Following, the effects of PSB on pigeon peas were observed in a randomized block trial in triplicates. Legume seeds were planted and then inoculated with 5 mL of PSB cell suspension (2.0 × 10 8 CFU/mL).Preliminary, results suggest that while some strains do exhibit plant growth promoting capabilities, other lower it. The negative effect of on seeds germination/ and plant-growth with bacteria inoculants that do exhibit good PS indexes on agar plates, may reflect a phytopathogenic effect. More trials will be performed and a more in-depth better picture of potential microbial biofertilizers that enhance crop yield health.

Transposition Unit IS1294-*bla*$_{CMY\text{-}2}$ Responsible for Beta-Lactam Antibiotic Resistance Found on a Conjugative Plasmid in an Environmental *Escherichia coli*

Discipline: Life Sciences
Subdiscipline: Microbiology

Karina Navarro Alvarez*; Amelie Garenaux and Luis Mota-Bravo, *University of California, Irvine*

Abstract: The increase in resistance to antibiotics observed in *Escherichia coli* constitutes a world-wide health issue. Knowledge about the presence of transposition units mobilizing resistance genes between DNA molecules in environmental isolates is scarce. To study the role of environmental *E. coli* as a source of plasmid-borne and clinically relevant resistance genes, *E. coli* (SW3750) was obtained from Aliso creek, Laguna Beach, CA identified using MALDI-TOF. Its resistance profile assessed by Disk Susceptibility Test, plasmid extraction with MIDI-prep, and conjugation experiment done using *E. coli* DH10B as recipient. The plasmids were sequenced using Oxford-Nanopore and Illumina, assembled using Unicycler and Geneious, annotated with PATRIC and ISFinder, and compared with the NCBI GenBank database using BLAST. SW3750 was resistant to β-lactams (including penicillins and third-generation cephalosporins). It carried 9 plasmids. Two genes coding for β-lactamases, $bla_{TEM\text{-}1B}$ and $bla_{CMY\text{-}2}$ were found on Plasmid-1(115,675bp) and Plasmid-2(67,073bp) respectively. Plasmid-2 and Plasmid-3 (65,057bp, no resistance gene detected) were transferred together via conjugation. The resulting transconjugant was resistant to the same β-lactam antibiotics as SW3750. The analysis of the $bla_{CMY\text{-}2}$ region of IncI2-type Plasmid-2 revealed the presence of an IS1294-$bla_{CMY\text{-}2}$ transposition unit that has been found in clinical *E. coli* isolated from humans and animals in many continents, but this is the first report of this transposition unit in an IncI2-type plasmid and in an environmental *E. coli.* In conclusion, environmental *E. coli* are a source of mobile genetic elements that are able to mobilize ARGs such as $bla_{CMY\text{-}2}$ throughout the world in clinical isolates.

Investigating Bacteriophage Identity and Function in Cheese Microbiomes

Discipline: Life Sciences
Subdiscipline: Microbiology

Galilea Guerrero*[1]; Cong Dinh[2]; Brooke Anderson[2] and Rachel Dutton[2], *(1)University of California, Santa Cruz, (2)University of California, San Diego*

Abstract: Microbiomes have colonized virtually every surface on Earth, from soil to our gastrointestinal tract, and are of great ecological and medical importance. Bacteriophages are influential members of microbial communities and have the ability to alter microbiome composition and activity. In order to truly understand community dynamics and function, we must investigate the identity and role of the phages present. We studied the biofilms that form on the surface of a cheese due to their ability to be modeled in a laboratory setting. We investigated the identity, function, and persistence of the phages found in natural rind cheese by analyzing phage sequences from a metagenomic coassembly. DNA sequences from cheese rind samples taken at different time points in 2011 and 2017 were co-assembled with metaSPAdes. The resulting contigs were processed and subsequently binned using CONCOCT. Bacterial and eukaryotic taxonomy was assigned using Kraken2, while VIBRANT was used to identify phage sequences and assign functions. These analyses inform us about the functional impact of phages in a naturally-ocurring microbial community and their influence on community composition. While it is possible that specific phage or phage-derived functions are not consistently selected for in this community, we hypothesize that some phage functions, and potentially some specific bacteriophage, will persist in this community over years due to the important consequences that phage may have in a microbiome.

Analysis of Vocalization in Mice with Phelan-Mcdermid Syndrome

Discipline: Life Sciences
Subdiscipline: Neurosciences

Urooj Ansari*, *Hunter College* and Elodie Drapeau, *Icahn School of Medicine at Mount Sinai*

Abstract: Phelan McDermid Syndrome (PMS) is a genetic neurodevelopmental disorder caused by disruption on Chromosome 22. While many genes can be affected by this disruption, haploinsufficiency of the SHANK3 gene has been identified as the cause of PMS syndrome. Symptoms of PMS include developmental delays including autism and delayed speech. We hypothesized that mice with deletion of all SHANK3 isoforms would have communication deficiencies. Ultrasonic vocalizations of two different batches of mice were recorded at 6 and 12 days old. The 6-day cohort consisted of mice that have never been separated from their mother. Being younger and smaller, they are sensitive to the cold, calling their mothers as a result. In the 12-day cohort, the mice already participated in daily testing and were separated from their mothers. They were resistant to the cold and called less as a result. Upon analysis of 3 minute recordings of each cohort, no phenotypic difference was seen in the 12 day old mice. In the 6 day old group, however, the KO genotype had the least number of calls and shortest calling time, while the WT had the most number of calls and a longer calling time. In conclusion, the 6-day-old group supported the hypothesis of communication deficiencies while the 12-day-old group did not. A potential cause may be the 12-day-old group was familiar with human contact and had already experienced daily maternal separation while the 6-day-old batch had not. For future studies, both age cohorts should be studied with naive mice.

The Role of Increased GluA1 AMPA Receptor Expression in the Basolateral Amygdala on Stress-Enhanced Fear Learning

Discipline: Life Sciences
Subdiscipline: Neurosciences

Daniel Weatherill; Sonya Waston; Michael Conoscenti; Yuqing Huang* and Michael Fanselow, *University of California Los Angeles*

Abstract: Post-traumatic stress disorder (PTSD) has a 6.8% lifetime prevalence among adult Americans (9.7% among females and 3.6% among males). One promising model for studying PTSD is the rodent Stress-Enhanced Fear Learning (SEFL) model, which captures many phenotypes of PTSD, including non-associative enhancement of fear learning. Research has demonstrated that an increase in expression of alpha-amino-3-hydroxy-5-methylisoxazole-4-proprionic acid receptor (AMPAR) in the basolateral amygdala (BLA) correlates with both associative fear learning and non-associative SEFL. We hypothesize that increased GluA1 expression either within the postsynaptic density or within recycling endosomes of neurons in the BLA plays a critical role in SEFL expression either by enhancing the induction or expression, respectively, of the long-term potentiation (LTP). In order to test for a causal relationship between increased GluA1 expression and enhancement of fear learning following acute stress, antisense oligonucleotides targeting GluA1 were infused bilaterally into the BLA of rats 1 hour following SEFL or control-treatment and again 1 hour prior to fear conditioning in a new context the following day. Preliminary results demonstrated that knocking down GluA1 expression blocked the ability of acute stress to enhance subsequent new fear learning. In addition, we will compare surface-, total-, and PSD-levels of GluA1 in synaptoneurosome samples extracted from SEFL or control-treated rats to subcellularly locate the increased GluA1 expression following SEFL via the Wes (automated Western blot) assay. Further understanding of the subcellular localization of increased GluA1 expression following acute stress will shed light on which molecular signaling pathways may be successfully targeted for treatment of PTSD.

The Effect of Glia-Secreted Factors on Neural Excitability

Discipline: Life Sciences
Subdiscipline: Neurosciences

Van-Khanh Tran*; Husniye Kantarci and Brad Zuchero, *Stanford University*

Abstract: The nervous system enables us to formulate thoughts, process emotions, and respond to our physical environment. The ability of a neuron to respond to environmental stimuli is called excitability. My project studies the mechanism by which glial cells--a cell type which constitutes over half of the nervous system--modulate neural excitability.

Since neurons and glia are physically intermingled in the nervous system, our lab used immunopanning techniques to obtain pure cultures of dorsal root ganglion neurons (DRGs) and Schwann cells (SCs), a type of glial cell. This novel technique enables us to study the behavior of neurons in the absence of glia. I verified the purity of the DRG neuron and SC cultures using immunohistochemistry. I then compared the excitability of pure, untreated neurons and neurons treated with Schwann cell conditioned media (SCCM) using RNAscope in situ hybridization. I tested for the expression of genes encoding sodium channel proteins (NaVs), which allow neurons to conduct action potentials that propagate neural signals. I tested for the genes encoding NaV1.6, 1.7, and 1.8 since these NaVs are associated with the pain response of DRG neurons.

The immunopanned DRG cultures were composed of 97.4% neurons based on immunohistochemical data, thus confirming successful cell type isolation. RNAscope experiments revealed that neurons treated with SCCM--as opposed to non-treated neurons--had a two-fold change in expression of NaV1.6 and 1.8, and a seven-fold change in expression of NaV1.7. These results suggest that glia secrete a factor which up-regulates the transcription of NaV proteins, thereby increasing excitability.

Identification of Odor Blends Used By *Caenorhabditis Elegans* for Recognition of Bacterial Food By Gas Chromatography Mass Spectrometry

Discipline: Life Sciences
Subdiscipline: Neurosciences

Emily Rainge*; Elizabeth Glater; Charles Taylor and Joseph Lopez, *Pomona College*

Abstract: *Caenorhabditis elegans* (*C.elegans*) are worms that inhabit bacteria-rich environments such as rotting fruit and plant matter. They use their sense of smell to make choices about what bacterial species they are good food sources and which are pathogenic. The goal of this project is to investigate what blends of chemical cues *C.elegans* olfactory systems use to distinguish among different bacteria. This presentation will report what volatiles we found are present in the air above samples of two strains of *E.coli*, *OP50*, and *HB101*. Both these strains are common food sources for *C.elegans* in the laboratory. In addition, several studies have shown that *E.coli HB101* is a more nutritious source of food for *C.elegans* than *E.coli OP50*. We will use gas chromatography mass spectrometry to detect volatile organic chemicals found in headspace above these two *E.coli* strains. Preliminary results have shown that the headspace of both strains contain indole, but *OP50* headspace contains dimethyl disulfide while *HB101* headspace contains 1-Butanol and 2,4-Di-tert-butylphenol. Our next goal is to investigate whether worms use these chemicals to distinguish between *OP50* and *HB101*.

Reward Conditioning: Acquisition and Extinction of Virtual Reality Conditioned Area Place Preference

Discipline: Life Sciences
Subdiscipline: Neurosciences

Arleen Perez* and Emma Childs, *University of Illinois, Chicago*

Abstract: Computerized tasks based on conditioning place preference (CPP) methodology has offered the opportunity to study about learning mechanisms involved in conditioned reward in humans. In this study, we examined the acquisition and extinction of a CPP for virtual environments associated with monetary reward ($). We hypothesized that participants would have a higher preference for the virtual environment paired with higher $ based on time spent and self reported ratings on liking and preference. We collected data from healthy human participants (N=15) who completed a computerized CPP task where they controlled an avatar. Throughout the study, participants completed 6 conditioning trials where one room was paired with high $ and another with low $. The acquisition of CPP was assessed by measuring the time spent in each virtual room during an exploration test and by using self-reported ratings of room liking and preference. After this, there was 4 successive exploration tests of the virtual environments to assess retention and extinction of CPP. Participants exhibited a CPP for the virtual room paired with high $ over the one paired with low $. They also reported preference for the high $ room and significant liking over the low $ room. These findings show that individuals show transient behavioral and subjective preferences for a virtual environment that is paired with monetary reward. Variations of this study may be effective in studying different brain mechanisms and brain substrates that are involved in reward conditioning and to explore how drugs may influence reward conditioning.

Role of Fear in Hippocampal Place Cell Activity

Discipline: Life Sciences
Subdiscipline: Neurosciences

Denisse Morales-Rodriguez*; Dr. Seetha Krishnan and Mark Sheffield, *University of Chicago*

Abstract: As an animal navigates through an environment, hippocampal place cells fire at different locations in space. These place cells are thought to form a cognitive map, providing the animal with the memory of locations visited and aiding in precise navigation. A visited location can be associated with an emotion, such as fear associated with the location of a predator. Remembering the emotion associated with a location is necessary for an animal's survival; however, it is unknown whether place cells play a role in encoding these emotions or if they are purely associated with space alone. To answer this, we will employ a contextual fear conditioning (CFC) paradigm whereby mice navigating an environment will receive mild electric tail shocks. In preliminary studies, it has been demonstrated that mice quickly learn to associate this environment with the fearful stimulus. We will record neural activity from hippocampal place cells before and during CFC, as well as during memory recall by utilizing two-photon microscopy. The activity of these place cells will then be compared to place cells formed in a control environment, which we believe will be distinct from each other. This experiment will provide the understanding of whether emotions associated with an environment affect place cell firing.

Discovering Correlations between Parameter Values and Output Characteristics of Computational Motoneuron Models

Discipline: Life Sciences
Subdiscipline: Neurosciences

Cynthia Krejczman* and Tomasz Smolinski, *Delaware State University*

Abstract: Spinal motoneurons that are activated for a prolonged period of time seem to undergo changes in their electro-chemical properties. Looking into these changes can help explain what happens to motoneurons after disease or injury. To capture and describe these changes, we propose adjusting the parameters of a computational model of a motoneuron, under control and continuously activated (treated) conditions, to characterize correlations between the model's parameters and two of its output characteristics: current threshold and input resistance. The treated group of the computational models simulates motoneurons being treated in a "wet lab" with high potassium solution, mimicking prolonged activation. "Good" computational models replicate two behavioral characteristics of a real motoneuron: (1) when injected with electric current, the model exhibits spiking behavior, and (2) the amplitude of the current threshold, and the corresponding input resistance, are within acceptable ranges.

Our simulations are executed in NeRvolver, a program that constructs models and changes their parameters using an evolutionary algorithm, and runs experiments using the NEURON simulation environment. Step current injections are applied to see which amplitude results in the spiking behavior of a neuron until (a) there is spiking activity ("good" model), or (b) the maximum acceptable current is reached, and there is no spiking ("bad" model). We propose to focus on subsets within the data, using fuzzy logic, to determine what causes a model to be "bad" versus "good," and how relationships between the "goodness" of a model and certain parameter values can be used to treat damaged motoneurons.

Association between Brain and Physical Function in Older Adults Compared to Young Adults

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jennifer Art*; Yong Woo An and Yangmi Kang, *New Mexico State University*

Abstract: Older adults often experience a deterioration of mobility and performance capability, leading to higher risk of fall. This functional decline may be associated with changes in brain function. However, investigation into the link between neural activation in the brain and physical function in older adults is limited.

In this study, electrocortical activation at the prefrontal (Fz), primary motor (Cz), and somatosensory (Pz) cortices was collected using electroencephalogram (EEG) during physical function tests related to daily-living activity in twenty older adults (OLD) compared to twenty younger adults (YOUNG). Physical function scores (PFS: maximum score 100) were used to determine functional decline. Power spectral analysis was used to calculate EEG power in theta (4-8 Hz) and alpha-2 (10-12 Hz) frequency bands.

Preliminary results (4 OLD, 4 YOUNG) showed lower PFS in the OLD than the YOUNG ($p = 0.003$) but no significant group differences for electrocortical activation ($p > 0.05$). However, there were slight trends toward decreased theta and alpha-2 power at Fz and Cz in OLD participants. The lower theta power at Fz and Cz may indicate attenuated neural activity related to attention and decision-making, and error detection processes respectively, while lower alpha-2 power in these areas may imply compensatory neural activity during physical function tasks.

The results confirm physical function declines with age but were not conclusive with regard to changes in brain function due to small sample size. Further research with a larger sample size is needed to determine the association between electrocortical activation and functional decline.

The Effect of Brain Iron Deficiency Found in Women

Discipline: Life Sciences
Subdiscipline: Neurosciences

Heidi de Leon* and Michael Wenger, *University of Oklahoma*

Abstract: From the onset of menstrual cycle, through the child-bearing years, a large number of women worldwide are challenged by iron deficiency (ID). The effects of ID include deficits in cognitive performance, attenuation of brain dynamics, and declines in physical performance and productivity. However, following menopause there is sparse literature on the relationship between iron status and both cognitive performance and brain health. Furthermore, to date, there are no studies considering such relationship. We propose a cross-sectional study that focuses in quantifying relationships among measures of systemic iron, regionally-specific brain iron, behavioral cognitive performance, and brain dynamics. To determine eligibility to participate in the study we will screen a total of 420 women between the ages 40 to 60. Women who meet the enrollment criteria will then be scheduled for a structural MRI scan, in order to obtain region-specific estimates of brain iron and volume, and three sessions of behavioral testing with concurrent EEG. Gathering MRI information will help us track the progress of the brain's ID and the behavioral testing will help us understand the effects of ID in behavioral performances. We hypothesize that ID levels are affecting mechanisms in areas in the brain such as myelination, neurogenesis/synaptogenesis, neurotransmitters, and energy which affect perception, memory, and cognition performances. This experiment has not yet been completed, but we expect our findings to demonstrate women with lower ID levels performing lower in the behavioral testing sessions than women with higher ID levels in the brain.

Characterization of the Effects Third Trimester-Equivalent Ethanol Exposure on Parvalbumin Interneurons in the Retrosplenial Cortex of Adolescent Mice.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Megan Barber*; Clark Bird; Glenna Chavez and Fernando Valenzuela, *University of New Mexico*

Abstract: Prenatal ethanol exposure causes a wide array of persistent cognitive deficits. Alterations in the function of inhibitory interneurons play a role in the cognitive effects of developmental ethanol exposure. Studies indicate that a single binge-like ethanol exposure during the third trimester-equivalent of human pregnancy causes apoptotic cell death of interneurons in the retrosplenial cortex (RSC). The RSC plays a central role in visuospatial processing and in the storage and retrieval of hippocampal-dependent episodic memories. In this study, we examined the long-term consequences of the RSC interneuron cell death induced by third trimester-equivalent ethanol exposure. We characterized the impact of ethanol exposure on the number of parvalbumin positive (PV+) interneurons using stereology techniques. Mice were exposed to air or ethanol vapor for 4 hr at postnatal day 7 (peak blood ethanol concentrations in pups were near 400 mg/dl). Mice were then left until adolescence (postnatal days 45-60) when we prepared parasagittal brain section using a cryostat. We found that the density of RSC PV+ interneurons was (mean cells per µm2 ± SEM): control = 0.0001413 ± 1.269x10-5 (6 mice from 6 litters); ethanol 0.0001217± 3.644x10-5 (5 mice from 5 litters); p=0.36 by t-test). This findings suggest that third trimester-equivalent ethanol exposure does not cause alterations in the number of RSC PV+ interneurons. Ongoing studies are examining the impact of this effect on the function of the RSC.

Towards Efficient and Precise *In Vivo* Genome Engineering

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jeffrey Inen*; Ryan Richardson; Marilyn Steyert; Bekir Altas; Andrea Romanowski and Alexandros Poulopoulos, *University of Maryland School of Medicine*

Abstract: Human development is underscored by the complex interactions between multiple cell types over space and time. In order to better understand these processes and to better translate this understanding for therapeutic success, it is paramount that we develop models that can faithfully recapitulate these intricacies. In contrast to *in vitro* models, autochthonous, *in vivo* models preserve the endogenous tissue and its complex microenvironment while leaving the immune system intact. Despite the application of CRISPR/Cas9 mediated genome editing to develop these models faster, cheaper, and with greater throughput, homology directed repair (HDR) remains a notoriously inefficient process in mammalian cells. This inefficiency challenge is particularly salient for direct *in vivo* applications where enrichment strategies commonly used *in vitro* cannot be used. While many investigators have previously optimized various aspects of CRISPR/Cas9 mediated HDR, most of these optimizations were performed separately and in a variety of different contexts. In this study, using two independent systems, we examine the combined effect of Cas9 and donor template variants that were all previously shown to separately improve HDR efficiency. Our findings show that while a high fidelity Cas9 does not improve knock-in (KI) over Wt, the combination of Cas9 (Wt) fused to Ctip, an enzyme critical in the endogenous HDR pathway, and an homology mediated end joining (HMEJ) donor template leads to 20-25 fold increase in total KI efficiency and a 40% increase in biallelic modification. Finally, we explore the use of this technology in neural progenitors directly in the embryonic mouse brain.

Novel Role of Receptor Tyrosine Phosphatase in Neurodevelopment

Discipline: Life Sciences
Subdiscipline: Neurosciences

Saovleak Khim*; Uriel Jean-Baptiste; Andrea Romanowski; Bekir Altas and Alexandros Poulopoulos, *University of Maryland School of Medicine*

Abstract: Brain development relies on temporal and spatial regulations, the synchrony of molecules that act in concert to direct proper neuronal wiring. Subsequently, circuit-specific remodeling results in functional brain circuitry. We utilize synthetic biology, in utero electroporation, and in vivo genome editing to reveal circuit-specific wiring endophenotypes and measure their severity using a novel index to quantify circuit miswiring seen in disorders on the Autism and Schizophrenia spectra. Here, we identify the PTPR family of receptor tyrosine phosphatases that are enriched in growth cones of callosal projecting axons during development. Each may have a role in guiding axonal growth in various brain regions. Our study uses internally controlled in vivo CRISPR knockouts (KO) and overexpression (OE) to observe the effects of these PTPRs on circuit formation in the mouse. PTPRδ KO resulted in a loss of corticoperirhinal and cortico-striatal projections, regions important for sensory processing, memory, cognition, and executive functions. In contrast, PTPRδ OE led to ectopic arborization of axons from the corpus callosum, crucial for integration of information from left and right hemispheres. We believe that endogenous PTPRδ is temporally and spatially regulated during development at defined regions along the corpus callosum. PTPRδ may bind with its substrates to act as an “exit” sign that signals axons to leave the white matter axon highway to innervate their grey matter targets. Further studies are underway to explore how different subfamilies and variants of PTPRs function to coordinate proper wiring in the developing brain.

The Role of Fractalkine in Microglia Function during Early Stages of Diabetic Retinopathy

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alicia Pietramale*; Derek Rodriguez and Astrid Cardona, *University of Texas at San Antonio*

Abstract: Diabetic Retinopathy (DR) is a severe complication of *diabetes mellitus* and the leading cause of blindness in the working age population. The CDC estimates the number of DR patients will double from 7.7 to 14.6 million by 2050. Individuals who suffer from DR experience progressive vision loss suspected to be the result of neuronal cell loss in the retina. Neuronal damage associated with local and systemic inflammation that arises from uncontrolled high blood sugar and damages the retinal vasculature. Research using diabetic mouse models has suggested that microglia, the resident phagocytes of the retina, play a role in inflammatory-mediated damage to the retina. Microglial pro-inflammatory actions are downregulated when fractalkine (FKN), a signal released from neurons, binds to the microglia CX3CR1 receptor. We hypothesize that enhancing the CX3CR1/FKN interaction will reduce neuronal damage to the retina. This study aims to ameliorate microglia by delivering FKN, in an adeno-associated viral vehicle, to the eyes of diabetic mouse models through intravitreal injections; and, analyze the retina for neuronal damage. Preliminary results, from ELISA assays, reveal that FKN is effectively delivered and sustained in the brain of 4-week diabetic mice. We anticipate delivery of FKN to the diabetic retina before disease onset will ameliorate neuronal damage. This project provides a preclinical model to test the effects of FKN administration to diabetic patients as an alternative therapeutic preventative for DR.

Adolescent Stress Induces Long-Lasting Loss of Excitatory and Inhibitory Synapses from the Posterior Parietal Cortex

Discipline: Life Sciences
Subdiscipline: Neurosciences

Mona Fariborzi* and Gyorgy Lur, *University of California, Irvine*

Abstract: In humans, adolescent stress is known to induce enduring effects in the posterior parietal cortex (PPC). Rodent experiments show that stress leads to a decrease in the number of synapses in several brain regions. Yet, the precise mechanistic details of these persistent stress effects have remained elusive. To determine the cause of the long-lasting effects, we quantified the density of excitatory and inhibitory synapses in the PPC directly after stress and following a month-long recovery period. We concurrently tested depression, anxiety and cognitive behaviors. We found that stress persistently reduced the number of excitatory synapses in the PPC. The number of inhibitory synapses were reduced directly after stress, however the reduction did not last after a month. Furthermore, we observed impaired performance in the y-maze directly after stress but this effect did not persist. Our data indicated that after stress, this effect was not due to depression or anxiety, however we did find decreased neophobia in stressed mice. These data suggest that reduced performance in the y-maze was likely due to the loss of both excitatory and inhibitory synapses, and recovered with the recovery of inhibition in the PPC.

Ambiguity Aversion in Mice with Elevated Anxiety-Related Behavior

Discipline: Life Sciences
Subdiscipline: Neurosciences

Julia Brock*; Anne Andrews; Merel Dagher; Sara Erwin and Katie Perrotta, *University of California, Los Angeles*

Abstract: Individuals with anxiety disorders have a greater tendency to view emotionally ambiguous information as negative. We use the elevated plus maze (EPM), an approach-avoidance test, to investigate anxiety-related behavior in mice. For this study, we will explore the use of fear conditioning, an associative learning paradigm, to assess anxiety-related behavior in particular to ambiguous information. In the fear conditioning paradigm, mice learn to associate an unconditioned stimulus (e.g. a shock) with a conditioned stimulus/cue (e.g. a tone). Male mice naturally freeze in response to footshock. With training, mice also learn to freeze in response to the conditioned cue, even in the absence of footshock. The conditioned cue can be made ambiguous, such that it is not always associated with a shock. I hypothesize that mice with elevated anxiety-related behavior will exhibit increased freezing behavior to ambiguous cue-pairings. I will use genetic and environmental models of anxiety. Mice constitutively lacking the serotonin transporter (genetic model), which is the primary target for SSRIs, exhibit increased anxiety-related behavioral phenotypes. I hypothesize that these mice, compared to their wildtype counterparts, will show increased freezing behavior to ambiguous cues. I also hypothesize that chronically stressed mice will exhibit elevated freezing behavior to ambiguous cue pairings, and those treated with the SSRI escitalopram will show attenuated anxiety-related behavior and freezing to ambiguous cues.

Loss of ErbB4 in PV+ Interneurons Leads to Altered Morphology of Pyramidal Neurons

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alejandro Nuno*[1]; Antara Majumdar[2] and Jessica Cardin[2], *(1)Yale University, (2)Yale School of Medicine, Department of Neuroscience*

Abstract: GABAergic interneurons expressing Parvalbumin (PV) play an important role in the development of cortical circuits in the brain as inhibitory neurons. The tyrosine kinase ErbB4 is critical for GABAergic maturation during development and perturbation of ErbB4 or its ligand Nrg1 results in altered neural development. Indeed, both Nrg1 and ErbB4 have been implicated in schizophrenia. However, little is known about how loss of ErbB4 in GABAergic cells affects the maturation of their synaptic targets, excitatory pyramidal neurons (PNs). To examine the developmental impact of the ErbB4 deletion, we crossed an Lhx6-iCre mouse line to a conditional ErbB4 line resulting in ErbB4 being selectively expressed only in PV cells, allowing for a PV-specific deletion of ErbB4. We used Cre- and Flp-dependent viral tools to visualize and reconstruct individual layer 5 and layer 2/3 PNs in the visual cortex in control and mutant animals. We analyzed total dendritic length (TDL) and density of dendritic spines, markers of excitatory inputs, along various dendritic stretches defined by region in the neuron. We found a significant difference in spine density at the apical tufts of layer 5 PNs and found a significant difference in TDL of layer 2/3 and layer 5 PNs. This finding points to an altered number of cortical and thalamic excitatory inputs to layer 5 PNs following ErbB4 deletion from PV cells, suggesting that proper ErbB4 activity is important for the formation or maintenance of long-range connections. This finding is significant as it points to a potential neurodevelopmental pathophysiology in schizophrenia.

TRPM8 Activity Is Necessary for Motor Neuron Survival in *Xenopus laevis* Embryos Raised at Cold Temperature

Discipline: Life Sciences
Subdiscipline: Neurosciences

Andrea Navarrete Vargas*[1]; Olesya Visina[2]; Kira Spencer[1] and Laura Borodinsky[1], *(1)University of California, Davis, (2)Shriners Hospitals for Children*

Abstract: Motor neuron degeneration is a major characteristic of several neurodegenerative disorders such as Amyotrophic Lateral Sclerosis (ALS). Previous studies in the lab demonstrated that animals grown at cold temperature exhibit higher number of motor neurons and lower number of apoptotic spinal cord cells than siblings grown at warm temperatures. We hypothesize that the cold-sensitive channel TRPM8 regulates the rate of motor neuron apoptosis in developing *Xenopus laevis* spinal cord neurons. To test this hypothesis, two-cell stage embryos were injected with TRPM8 or control morpholino then raised at corresponding temperatures (16℃ and 22.5℃). Transverse sections of stage 40 spinal cord were then processed for immunostaining to detect expression of HB9, a motor neuron transcription factor, and for TUNEL which

fluorescently detects apoptotic cells. We observed that TRPM8 knockdown leads to an increase in TUNEL-positive cells within the spinal cord of larvae grown at cold temperature from a mean of 0.7 ± 0.3 apoptotic cells in controls to a mean of 7 ± 1 apoptotic cells/10 mm of spinal cord in TRPM8-deficient larvae. Additionally, TRPM8 knockdown results in an increase in apoptotic motor neurons shown by an increased percent of both HB9 and TUNEL positive cells from a mean of 1 ± 1% in controls to 34 ± 7% in the TRPM8 morpholino group, in turn leading to a decrease in HB9-positive cells. These data support my hypothesis that TRPM8 is necessary for the prevention of apoptosis of spinal cord neurons, specifically motor neurons, in animals raised at cold temperature.

"Dissecting the Mechanisms Underlying Attraction to Cat Sensed Cues: Worms and Cats Aren't Much Different"

Discipline: Life Sciences
Subdiscipline: Neurosciences

Brianna Ramos* and Gareth Harris, *California State University Channel Islands*

Abstract: **Significance:** Organisms across the phyla are capable for sensing an array of sensory cues to control or shape complex behavioral responses to survive in a complex environment consisting of an array of attractive and dangerous cues. Mammalian systems extensively use olfactory and gustatory behavior to fine tune these sensory-dependent decision-making behaviors. Despite understanding the importance of behavioral responses to cues in the form of odors in shaping behavior. The underlying mechanisms that mediate these responses at the level of sensation, processing, integration and modulation of these sensory dependent responses are not fully understood. To understand these mechanisms, we discovered the use of the invertebrate worm, *C. elegans* to characterize the attraction and repulsion to mammalian sensed odorant cues.

Hypothesis/Experimental Methods: We use the worms ability via chemotaxis assay to attract to catnip oil cues and repel from cat sensed repellants to dissect the neural mechanisms, at the levels of genes (molecular substrates) and neurons architecture involved in these sensory dependent chemotactic behaviors to mammalian sense cues. We have identified specific sensory neurons, sensory transduction mechanisms, including G-proteins, cyclic nucleotide gated ion channels, specific core interneurons and multiple neurotransmitter systems that regulate odor-dependent attraction and repulsion behavior to cat sensed odor cues. We therefore provide a platform to use *C. elegans* as a model for studying olfactory-dependent pathways to attractive and repulsive cues that have been shown to be attractants and repulsion to mammalian systems. This allows characterization of the neural mechanisms that shape olfactory behavior and decision-making in higher systems.

A Xenotransplantation Model to Study the Differentiation and Migratory Patterns of Human Cortical Interneurons

Discipline: Life Sciences
Subdiscipline: Neurosciences

Eric Garcia*[1]; Quetzal Flores[2] and Mercedes Paredes[2], *(1)Pomona College, (2)University of California, San Francisco*

Abstract: The human neocortex is responsible for higher cognitive functions, which are made possible by the balance of excitatory and inhibitory neurons, also known as interneurons. Disruptions in interneuron development can cause hyper-excitability in the brain, resulting in cognitive dysfunction. This raises fundamental questions regarding the origins of interneurons, as understanding the development of this neuronal population would have implications for interneuron-related diseases, including epilepsy, autism and schizophrenia.

The human ganglionic eminence (hGE), a transient structure in the embryonic brain, produces the majority of cortical interneurons. We aim to use human-to-mouse transplantation to characterize the neurogenic and gliogenic potential of hGE-derived cells. Preliminary results suggest that hGE progenitors possess extensive migratory potential and develop into mature neurons. We hypothesize that transplanted hGE cells retain a high rate of proliferation, migration, and differentiation even upon human-to-mouse transplantation.

In our study, we isolated hGE-derived progenitors and infected them with an interneuron-specific lentivirus expressing GFP. These cells were then injected into the cortex of immunodeficient, neonatal mice and subsequently analyzed at various times post-transplant. At 1 month post-transplant, high migratory properties of GFP-expressing transplanted cells were observed and video recorded using time-lapse microscopy. At 7 months post-transplant, immunohistological experiments reveal that transplanted hGE cells differentiated and expressed mature interneuron subtype markers. Our results suggest that xenotransplants offer an efficient model for long-term human cortical development, which will inform potential therapeutic applications to neurodegenerative disease.

Utilizing Deeplabcut 3-D Pose-Estimation Technology for Optimized Behavior Quantification in Rodent Models

Discipline: Life Sciences
Subdiscipline: Neurosciences

Aranis Muniz Perez*; Stephanie Degges; Matthew Wanat and Claire Stelly, *University of Texas at San Antonio*

Abstract: Our lab investigates the patterns of mesolimbic dopamine signaling in several models of behaviors motivated by appetitive and aversive stimuli. When testing these behaviors, we measure dopamine signaling via fast-scan cyclic voltammetry, while behavior is recorded via responses on the operanda and/or a top-view camera. Behaviors not captured by the operant chamber are then manually scored. Alternatively, we use commercially available video tracking systems, though the accuracy with these systems is dependent upon the contrast between the subject and the background. As such, our methods are not optimized for effective, high-throughput behavior quantification. We propose utilizing DeepLabCut, a deep learning-based pose estimation algorithm, as a potential solution for difficulties encountered by our current lab methods for behavioral quantification. Users train a deep neural network for the algorithm to track user-defined labels on a specified model accurately across novel videos with variable contrasts. We have begun to train a neural network that will be able to accurately track rodent behaviors, and are currently gathering videos that demonstrate the desired behaviors to be tracked. However, the program is limited to shorter videos with minimal occlusions of user-defined labels. We are identifying whether or not these limitations will hinder the algorithm's application to our lab. Ultimately, we aim to utilize DeepLabCut to track diverse behaviors in our rodent models for increased time-efficiency and improved behavior quantification.

Constraint Induced Movement Therapy Improves Recovery of Certain Sensorimotor Functions in Experimental Traumatic Brain Injury

Discipline: Life Sciences
Subdiscipline: Neurosciences

Laila Khorasani*[1]; Afshin Paydar[1] and Neil Harris[2], *(1)University of California, Los Angeles, (2)David Geffen School of Medicine*

Abstract: Traumatic brain injury (TBI) is a form of brain damage inflicted by external forces, and can potentially cause severe deficits in sensorimotor capability. Unilateral TBI leads to unequal motor deficits, impacting the limb contralateral to injury site more severely. Following TBI, overuse of the unaffected limb suppresses usage and recovery of the affected limb. Constraint Induced Movement Therapy (CIMT) as a rehabilitation encourages usage of the limb that is impacted by brain damage by restraining the limb that is unaffected by the injury. TBI studies in humans and rodents have shown that CIMT improves long term motor function, particularly when combined with other therapies. Based on this background, we hypothesize that CIMT will improve sensorimotor recovery after TBI in rats. In order to test this, we induced an experimental unilateral TBI in rodent subjects, administered CIMT restraint for 2 weeks, and utilized behavioral and immunohistochemical methods to assess the efficacy of CIMT. Our behavioral testing included horizontal ladder, cylinder, and cheerio eating tasks that measure gait, limb asymmetry, and fine manipulation skills respectively. Preliminary behavioral findings indicate that CIMT enhances fine sensorimotor function in the long term. We anticipate this will also be supported on the cellular level by using silver and phosphorylated c-jun staining to indicate axonal damage and regeneration throughout brain tissue. In addition to supporting our hypothesis that CIMT shows potential as a reliable treatment for TBI patients, conclusions from this study can also indicate regions of connectivity in the brain throughout recovery after TBI.

Assessing the Role of Dorsal Hippocampal Circuits in Reinforcement and Expression of Opioid-Induced Contextual Memory

Discipline: Life Sciences
Subdiscipline: Neurosciences

Rossana Sandoval* and Jose Morón-Concepcion, *Washington University in St. Louis*

Abstract: The formation and maintenance of drug-paired contextual memory precipitates craving and relapse to opioid misuse following re-exposure to contexts in which the drug has been routinely taken, even after long periods of abstinence. Previous studies have demonstrated that the CA1 region of the dorsal hippocampus (dCA1) is involved in morphine-induced contextual memory formation and retrieval, but it remains unknown if the dCA1 is necessary and sufficient in the formation and expression of reward-paired contextual memories. We hypothesize that the dCA1 is necessary for the expression of opioid-context memory and stimulation of the dCA1 is sufficient to trigger real-time and context-dependent reward-seeking behavior. To determine the necessity of the dCA1 during cue-induced drug-paired memory retrieval, we chemogenetically silenced the dorsal hippocampus following morphine conditioned place preference. Our preliminary findings show that silencing the dCA1 may attenuate the retrieval of morphine context-dependent memories. To determine the sufficiency of the dCA1 in reward-seeking behavior, optogenetic activation was utilized to stimulate the dorsal hippocampus via excitatory opsins during cued and un-cued real-time place conditioning. Our results show that direct stimulation of the dCA1 is sufficient to drive a behavioral preference for the stimulation-paired compartment in real-time but unable to drive lasting memory formation, uncovering the possible role of the dCA1 in the reinforcement of reward-paired contexts. Together, our findings illuminate the role of the dorsal hippocampus in the formation of reward-associated memories. Further investigation will allow us to determine the necessity of the dorsal hippocampus in the maintenance and recall of contextual opioid-paired memories.

The Cellular and Molecular Mechanisms Central to the Development of Ethanol Tolerance in Drosophila Melanogaster

Discipline: Life Sciences
Subdiscipline: Neurosciences

Pratik Adhikari; Alexander DelToro* and Fred Wolf, *University of California, Merced*

Abstract: Alcohol is one of the most widely abused drugs, yet the molecular mechanisms involved in simple behavioral adaptations like tolerance, preference, and reward are still not well known. Our goal is to uncover molecular mechanisms for behavioral plasticity that are initiated by the first exposure to ethanol. Individuals nearly always require repeated exposures to ethanol to elicit an alcohol use disorder (AUD). How do the early molecular events relate to AUDs? A current hypothesis is that drug induced changes in gene expression alter the molecular landscape for the next drug exposure: each repeat exposure will act on neurons with changed properties and changed gene expression responses. We identify genes that are regulated by the first ethanol exposure and determine their role in ethanol-induced behavioral plasticity. Ethanol activates the Mef2 transcriptional activator to induce Hr38, and the Sirt1 histone/protein deacetylase terminates Hr38 to promote tolerance. Furthermore, the three genes function in the same neurons, the mushroom body a/b neurons, to promote ethanol tolerance, preference, and reward. Our findings suggest that ethanol uses a rapid and transient regulation of the expression of specific genes to allow a coherent molecular program to drive behavioral plasticity.

Cortical Reorganization with Age-Related High Frequency Hearing Loss in the Auditory Cortex of the Rhesus Macaque

Discipline: Life Sciences
Subdiscipline: Neurosciences

Diana Polhac* and Gregg Recanzone, *University of California, Davis*

Abstract: Humans with high frequency hearing loss due to aging often complain of consistent tinnitus, a symptom characterized by ringing in the ears without external sensory stimuli. The effect of this symptom on a patient's life can range from a nuisance to impairment of daily activities. Changes in brain physiology underlying this condition remain unknown. Studies in young animals with ear damage indicate that there is an overexpression in the auditory cortex of the edge frequency that the animal can still hear, leading to the possibility that this reorganization underlies tinnitus. The objective of this study is to investigate differences in activity of individual neurons between reorganized and non-reorganized areas of the auditory cortex in alert male macaques. To investigate this hypothesis, I am comparing activity of neurons in young (10-year-old), middle-aged (22-year-old) and geriatric (26-year-old) monkeys to tone stimuli of different frequencies and durations using standard extracellular recording techniques. The data in this abstract reflect findings with a 26-year-old male. Inside a sound booth, the macaque passively listened to sounds emitted in pseudo-random order from a speaker contralateral to the electrode. Tones were presented at the frequency neurons responded best to for 0.1, 1, 10, and 100 seconds. An electrode was lowered into the brain to extracellularly record single auditory cortical neurons. Preliminary results indicate high frequency hearing loss results in edge frequency enhancements in macaques. Further, neurons in the reorganized region have significantly different response properties than those in non-reorganized cortex, which may explain the phantom tinnitus percept.

First Trimester Equivalent Binge-like Alcohol Exposure in Mice

Discipline: Life Sciences
Subdiscipline: Neurosciences

Deva Reign* and Eileen Moore, *San Diego State University*

Abstract: Prenatal alcohol exposure (PAE) can disrupt the development of an embryo/fetus, and cause growth retardation, impairments, among other deficits. The outcomes are referred to as Fetal Alcohol Spectrum Disorders (FASD). Mouse models of first-trimester equivalent binge-like PAE have reported detrimental impact on offspring brain size with disproportionate effects on the olfactory bulbs. Our study aimed to determine if such exposure would also impact olfactory detection. We assessed body weight, activity level, and brain weight in mice, as prior research has shown these to be affected in rodents with PAE. On gestation days 7, 9, 11, and 13, female C57BL/6J mice were intraperitoneally injected with 3 g/kg ethanol (20% v/v) or an equivalent volume of saline. Offspring's weight was measured on postnatal days (PND) 10 and 20, locomotor activity was monitored in open field chambers on PND 22. Mice were tested using an olfactory habituation paradigm on PND 23. On PND 24 mice were euthanized and brains were extracted to determine brain weight. Data were analyzed with independent t-tests. Results considered significant at $p<.01$. Results showed mice with PAE weighed significantly less than controls on PND 10 and 20. Brains from alcohol-exposed mice weighed significantly less than controls. Results indicate that first-trimester equivalent alcohol exposure impacted the growth and development of both the body and brain. Future studies will look at additional behaviors on other mouse strains. Funded by a grant from the National Institute of General Medical Sciences (NIGMS) of the National Institutes of Health (NIH): SDSU MARC U*STAR 5T34GM008303.

The Effects of Glyphosate-Based Herbicides on Grooming Behavior As an Index of Anxiety-like Behavior in Rats

Discipline: Life Sciences

Subdiscipline: Neurosciences

Hector Haddock-Martinez*[1]; Demetrio Sierra-Mercado[2]; Mauricio Cáceres-Chacón[3]; Melissa Rivera-López[3]; Osmarie Martínez-Guzmán[4] and Cesia Román[5], *(1)University of Puerto Rico Rio Piedras Campus, (2)Dept. of Anatomy & Neurobiology,University of Puerto Rico, Medical Science Campus, San Juan, PR,, (3)University of Puerto Rico School of Medicine, (4)Dept. of Anatomy & Neurobiology,University of Puerto Rico, Medical Science Campus, (5)The Residential Center of Educational Opportunities of Mayagüez*

Abstract: Glyphosate-based herbicides (GBH) were initially considered safe because they act by inhibiting a metabolic route not present in mammals. Unfortunately, their use has recently been correlated with increased diagnosis of movement and anxiety disorders. Studies in rodents have shown that high dose GBH causes decreased locomotion and increased anxiety-like behavior, which correlates with decreased dopamine in the striatum. However, these studies have focused on traditional behavioral measurements to reach these conclusions. Grooming is one of the most frequently performed behavioral activities in rodents. Moreover, this behavior involves an evolutionarily conserved sequencing pattern that is processed by various parts of the brain, including the striatum. Converging lines of evidence suggest that grooming can be correlated with levels of anxiety. Therefore, we aim to evaluate the effects of prolonged GBH consumption on grooming behavior. Male Sprague Dawley Rats had access ad libitum to GBH-contaminated drinking water (0.7mg/l), whereas control rats received filtered drinking water. After prolonged exposure to GBH (22 weeks), animals were placed in an Open Field Test and later in a Fear Conditioning Paradigm for traditional behavioral assessments. Video recordings of each session for both paradigms will now be reviewed and analyzed to determine changes in grooming behavior between control and experimental groups. Specifically, we will quantify the number of grooming bouts, as well as total time grooming via manual observation of each video. We hypothesize that prolonged exposure to GBH will increase grooming behavior in rats, consistent with increased levels of anxiety.

***In Vitro* regulation of the *Kiss1* promoter By VAX1 and SIX3**

Discipline: Life Sciences

Subdiscipline: Neurosciences

Nay Chi P. Naing*; Shanna N. Lavalle and Pamela L. Mellon, *University of California - San Diego*

Abstract: Kisspeptin neurons in the hypothalamus are critical regulators of the hypothalamic-pituitary-gonadal (HPG) axis. Dysregulation of the HPG axis can cause negative effects in reproduction, such as idiopathic hypogonadotropic hypogonadism (IHH). Homeodomain transcription factors such as VAX1 and SIX3, are necessary for reproductive processes in mice. The loss of a single *Vax1* or *Six3* allele results in decreased *Gnrh1* mRNA expression and various degrees of subfertility. We investigated the role of VAX1 and SIX3 in regulating the mouse *Kiss1* promoter in immortalized kisspeptin neurons derived from the anteroventral periventricular nucleus (AVPV) or the arcuate nucleus (ARC) of a female mouse. We found that overexpression of VAX1 represses the *Kiss1* promoter in both AVPV and ARC cell lines. The optimal concentrations of VAX1 in mediating this repression in AVPV and ARC cell lines were 200 ng and 50 ng respectively. We are currently in the process of conducting a dose-response for SIX3 to determine if it regulates the *Kiss1* promotor. These experiments will help further our understanding of *Kiss1* gene regulation and the roles of homeodomain transcription factors within the HPG axis.

The Role of Autophagy and Proteasome Function in the Degradation of Tdp-43 Protein in *C. Elegans*

Discipline: Life Sciences

Subdiscipline: Neurosciences

Yuriy Khlopas*; Kimberly Nu-tall; Helena Puccini de Castro; Shagufta Khatoon; Rogelio Alvarado and Cindy Voisine, *Northeastern Illinois University*

Abstract: Proteostasis, the process by which a cell maintains protein synthesis, folding, and clearance is critical for survival; however, the fidelity of this process declines with age. Disturbances in proteostasis contribute to many age-related neurodegenerative diseases, such as amyotrophic lateral sclerosis (ALS), leading to the accumulation of misfolded proteins. The majority of patients with this disease accumulate an aggregated form of the ALS associated protein TDP-43 in neurons, suggesting a disruption in proteostasis. Important mechanisms like autophagy and proteasome function normally degrade accumulated proteins that are toxic to cells. Here, we are using the nematode *C. elegans*to examine how the protein TDP-43 challenges proteostasis by impairments in folding and clearance. *C. elegans*short life cycle, transparency, and conservation of genes with human orthologues provides advantages for experimentation. In this study, key genes responsible for autophagy and proteasome function will be identified by comparing the gene expression patterns of neuronally expressed TDP-43 with wild type worms. Investigating clearance of TDP-43 and genes responsible for its degradation will contribute to our understanding of the pathology of neurodegenerative diseases.

Development and Characterization of Ganglionic Eminence Self-Organizing Single-Rosette Spheroids

Discipline: Life Sciences

Subdiscipline: Neurosciences

Juan Gonzalez Valdivieso*; Maria Varela; Andrew Tidball and Jack Parent, *University of Michigan - Ann Arbor*

Abstract: Cerebral organoids are an increasingly utilized tool in neurodevelopmental modeling, both structurally and functionally. However, multiple rosette structures in standard organoid models introduce high levels of variability between organoids. A novel version of this *in vitro* approach has recently addressed this issue, via the Self-Organizing Single-Rosette Spheroid (SOSRS) method. While our dorsal patterned excitatory neuron SOSRS express normal cortical layer markers such as CTIP2, SATB2 and Reelin and exhibit functional electrophysiological properties, the development of ventral patterned SOSRS to generate inhibitory cortical neurons is still needed. Such a model requires further analysis of its regional subsets due to their differential aspects and region-specific qualities. Here, we generate highly reproducible Ganglionic Eminence (GE) SOSRS with the addition of smoothened agonist (SAG) and XAV, and characterize them via an array of immunohistochemical, molecular and functional assays. We report that our GE SOSRS express typical ventral markers including NKX2.1, GABA, and somatostatin as well as glial markers GFAP and OLIG2. These findings provide promise for the future application of dorsal/ventral fusion SOSRS as a more comprehensive and reproducible *in vitro* brain model to study neurodevelopmental mechanisms and pathologies.

Sex Differences in the Neural Circuits Underlying Voluntary Exercise

Discipline: Life Sciences
Subdiscipline: Neurosciences

Nashra Jamil[*1]; Margaret k. Tanner[1]; Aleezah Balolia[1]; Kelsey Bonar[1]; Alyssa A. hohorst[1]; Kelsey Abrams[1]; Esteban C. Loetz[2] and Benjamin N. Greenwood[2], *(1)University of Colorado Denver, (2)University of Colorado Denver, Department of Psychology*

Abstract: Females are more likely than males to develop stress-related psychiatric disorders, but the majority of stress resilience studies focus on males. We have observed that female rats benefit from the stress resilience effects of exercise more readily than male rats. Female rats also develop habitual exercise behavior more easily than males. This is important, because clinical studies indicate that maintaining habitual exercise is key to unlocking the stress-protective effects of exercise. The goal of this study was to determine if there are sex differences in the neural circuits underlying the development of habitual exercise. Identifying these differences could reveal why females are more responsive to the stress-protective effects of exercise. Fluorescent in situ hybridization for the neural activation marker cfos revealed that fewer days of exercise are required to activate a brain region implicated in habit (dorsal lateral striatum; DLS) in female rats, compared to males. Moreover, temporary inactivation of the DLS with a GABAA/GABAB agonist prior to a bout of exercise revealed that voluntary exercise behavior becomes dependent on the DLS in females (4 days) much earlier than it does in males (4 weeks). In contrast, males rely on the dorsal medial striatum (DMS, a region implicated in goal-directed behavior) early in the acquisition of exercise behavior (4 d). We have identified sex differences in the neural circuits controlling the development of habitual exercise. Future research will investigate whether the DLS contributes to the rapid stress resilience produced by exercise in females.

Myelin Sheath Repair Is Regulated By Protease Activated Receptor 2

Discipline: Life Sciences
Subdiscipline: Neurosciences

Ms. Delaney Liskey[*]; Hyesook Yoon, Ph.D.; Chanil Choi, Ph.D. and Isobel Scarisbrick, Ph.D., *Mayo Clinic*

Abstract: Multiple sclerosis (MS) is a chronic inflammatory condition of the central nervous system (CNS) that affects millions of individuals worldwide. The myelin sheath facilitates signal transduction along the axons in the brain and spinal cord, and when it is mistakenly destroyed, neurons are left susceptible to neurodegeneration, leading to permanent disability in patients. Current therapies are aimed to suppress the immune system in efforts to reduce disease progression; however, there are no current therapies that promote regeneration of the myelin sheath, a process known as remyelination. Oligodendrocytes play an essential role in the facilitation of signal transduction in the developing and adult CNS, and are a novel target for therapies that aim to promote myelin regeneration. A significant contributor to demyelination is deregulated protease activity. Proteases can impede myelin production by activating protease-activated receptors. We specifically evaluated the role of a G-protein coupled receptor known as protease-activated receptor 2 (PAR2) in myelin regeneration. In this study, we determined the impact of the genetic deletion of PAR2 on remyelination in an acute focal demyelinating injury elicited by Lysolecithin microinjection into CNS white matter. A comparison of PAR2+/+ and PAR2-/- mice revealed pro-myelinating effects with PAR2 loss-of-function, including increased numbers of Olig2+ oligodendrocyte progenitors and mature GST3+ oligodendrocytes, and higher levels of myelin basic protein (MBP) and proteolipid protein (PLP). These changes were reflected in an increased number of remyelinated axons. Together, the results suggest that PAR2 may represent a new therapeutic target for myelin sheath regeneration.

Investigating the Innervation of Taste-Receptor-like Chemosensors in the Gut By Vagal Sensory Neurons

Discipline: Life Sciences
Subdiscipline: Neurosciences

Samantha Oviedo[*]; Saima Humayun; Zacnite Garcia and Lindsey Macpherson, *University of Texas at San Antonio*

Abstract: Taste-receptor-like cells line the epithelium of the gut and display the ability to sense chemicals. Along with other chemosensors in the gut, these cells relay sensory information to local enteric neurons and to the brain to control digestion. The vagus nerve carries the majority of sensory information from the viscera to the brainstem. Different vagal neuron types have been identified in nutrient sensing (GPR65), stomach distension (GLP1R), and triggering swallow/cough (P2RY1). Here, we will investigate the population of vagal ganglion neurons expressing Calb1. Calb1 expressing neurons have been found in the larynx/trachea region indicating potential innervation with chemosensors along the digestive tract. We hypothesize that this specific population of vagal neurons will form close contacts with taste receptor expressing chemosensors within the larynx, trachea, and duodenum. In order to test this hypothesis, we will use Calb1-Cre expressing transgenic mice, crossed to the Cre-dependent tdtomato reporter line (AI9). Immunohistochemistry and confocal imaging is used to detect the tdtomato-expressing target sensory neuron fibers innervating the digestive tract as well as the chemosensory cells using specialized antibodies. We assess the connectivity between these chemosensors and vagal neuron populations by analyzing confocal images with ImageJ/Fiji software. Partially funded by NIH ESTEEMED 5R25EB027605.

Bisphenol a Differentially Impacts Neurodevelopment in D*rosophila Melanogaster* from Distinct Genetic Backgrounds

Discipline: Life Sciences
Subdiscipline: Neurosciences

Aliyah Penn*, *California State University, Sacramento* and Kimberly Mulligan, *California State University Sacramento*

Abstract: Evidence indicates that the interaction between environmental chemicals with specific genetic variants are linked to neurodevelopmental disorders (NDD). Thousands of genes have been linked to NDDs; by comparison, the role of environmental chemicals in conjunction with genetic risk factors to confer risk of NDDs has fallen behind. Bisphenol A (BPA) is an abundant chemical used in the synthesis of plastics and epoxy resins. Well known for its endocrine disrupting abilities, BPA has also recently been implicated in NDD etiology. However, the mechanism by which BPA disrupts neurodevelopment and its impacts when combined with NDD-associated genes are unclear. In this study, we investigated the neurodevelopmental toxicity of BPA within two genetic strains of *Drosophila melanogaster*—wild-type and the Fragile X syndrome (FXS) model*.* FXS flies have a loss-of-function mutation in *fragile X mental retardation 1 (Fmr1),* the ortholog of an NDD-associated gene in humans. We demonstrate that in wild-type flies BPA causes an increase in larval locomotion (both orientation events and peristaltic contractions), an increase in repetitive grooming behavior in adults, and induces axon guidance defects in adult brains. Interestingly, BPA has either the complete opposite or insignificant impacts for these same phenotypes in the FXS flies—upon BPA exposure, reorientation is reduced, peristalsis is unaffected, grooming is reduced, and axon guidance defects are reduced. This study is the first to demonstrate that BPA may display a gene-environment interaction with an NDD-associated gene.

Bioinformatics Analysis of the Severe Acute Respiratory Syndrome Coronavirus 2 Interactome in Human Fetal Brain Development

Discipline: Life Sciences
Subdiscipline: Neurosciences

Mariah Antopia*; Parul Varma and Jenny Hsieh, *University of Texas at San Antonio*

Abstract: A new global health concern, SARS-CoV-2 has infected millions of humans around the world; however, the impact of SARS-CoV-2 infection on the developing fetus is not well known. Recently, a study using single-cell RNA sequencing showed the presence of ACE2, a SARS-CoV-2 binding site, in both placental cells and fetal heart, liver, and lungs; brain expression was not determined, but has been revealed through other studies to be expressed in adult neuronal subpopulations. Furthermore, a recent proteomic analysis has revealed 332 SARS-CoV-2 human protein-protein interactions. The purpose of this study is to explore fetal brain expression of ACE2 and other interactive molecules that we hypothesize could be additional SARS-CoV-2 entry points during fetal development. Using Excel data mining techniques, we analyzed the expression of the 332 proteins across various brain regions and developmental timepoints in a publicly available fetal brain RNA sequencing dataset (Brainspan). Preliminary results reveal that 310 of these proteins were expressed across 12 developmental timepoints, and identified high expression of GNB1 across all developmental stages. GNB1 is a G protein subunit that is involved in transmembrane signaling systems, suggesting a potential route of neuroinvasion. We also found that GNB1 expression in 120DIV human cortical organoids (an *in vitro* modeling system to study the human brain), but further testing is needed to confirm these preliminary findings. Identification of these potential entry points for SARS-CoV-2 infection during fetal brain development opens the door for further exploration of potential long term impacts of this virus. Funding: NIH ESTEEMED 5R25EB027605

Investigating the Specificity of Anatomical Connections between Gustatory Neuron Populations and Taste Receptor Cell Types

Discipline: Life Sciences
Subdiscipline: Neurosciences

Meagan Shinn*; Zacnite Garcia; Shannon M. Landon; Ryan M. Wood and Lindsey J. Macpherson, *University of Texas at San Antonio*

Abstract: There are two major theories of peripheral taste information coding: labeled line and combinatorial coding. The labeled line theory postulates that specific nerve fibers relay signals from single taste modalities (sweet, biter, sour, salty, or umami). Whereas the combinatorial theory hypothesizes that individual gustatory neurons carry taste information from multiple taste receptor types. Preliminary work in our lab and recent publications by others indicate that genetically separable populations of gustatory ganglion neurons are responsible for specific taste responses, supporting a labeled-line arrangement. However, anatomical evidence for this specificity is still lacking. Here, we investigate the anatomical specificity of populations of gustatory neurons in their innervation to taste receptor cell subtypes. To do this, we use confocal microscopy to assess the colocalization of fluorescently labeled gustatory nerve fibers with the immunofluorescence of specific taste receptor proteins. We use three different transgenic mouse models to label all, or a subset of gustatory neurons with virally encoded Cre-dependent tdtomato fluorescence; Phox2b-Cre, Nrp1-Cre, and Penk-Cre. Taste receptor cell types are labeled using antibodies for TRMP5, Car4, and/or GNAT. Confocal image analysis with Fiji/Image J, is used to determine the preferential rates of innervation of Nrp-Cre and Penk-Cre fibers with bitter or sour taste receptor cells compared to the control Phox2b-Cre fibers.

Diet Vs. Diabetic Neuropathy: Exploring the Effect of a Carbohydrate-Rich Diet on the Severity of Diabetic Neuropathy

Discipline: Life Sciences
Subdiscipline: Neurosciences

Marissa Coppin*, *University of Texas at San Antonio* and Peter LoCoco, *University of Texas Health Science Center*

Abstract: According to the American Diabetes Association, 30.3 million Americans suffer from diabetes. Approximately 50% of people with Type 2 Diabetes experience Diabetic Neuropathy (DN). Patients that suffer from DN experience nerve pain, loss of sensation, and in extreme cases, loss of limbs due to severe nerve damage. Researchers have investigated the effect of omega fatty acids on obesity and DN and found that Omega-6 fatty acids exacerbate symptoms of DN while Omega-3 fatty acids diminish or have no effect on symptoms. However, the effect of refined carbohydrates on the progression of DN has not been well investigated. This identified gap led to the conduction of a quantitative survey of 56 people to evaluate the relationship between the general public's knowledge/experience with DN and their carbohydrate intake. In the survey, no direct correlations could be established due to the small sample size hindered by the COVID-19 pandemic. However, participants who had a low knowledge level and less experience with DN tended to consume more fast food and refined carbohydrates. Therefore, we propose to investigate the progression of DN on diabetic mice subjected to a carbohydrate-rich diet. We hypothesize that a carbohydrate-rich diet will heighten symptoms of DN. This *in vivo* study will provide insight towards the implementation of effective diets to minimize symptoms of DN.

Separate Effects of Logical Reasoning and Memory Load on Prefrontal Brain Activity in Aging

Discipline: Life Sciences
Subdiscipline: Neurosciences

Emily Sturm*; Madison Musich; John Duffy; Andrea Mendez; Max Henneke; Aga Burzynska and Michael Thomas, *Colorado State University*

Abstract: Research suggests that healthy aging is associated with a shift in neuronal activity in the prefrontal cortex (PFC) as observed during functional magnetic resonance imaging (fMRI). Possible explanations include compensation for declining neural resources and dedifferentiation (i.e., loss of specialization of cortical areas). Understanding the relationship between aging and location of brain activity could improve biomarkers for cognitive decline and provide insight into healthy aging. We used a novel task (modified Sternberg paradigm) to separately manipulate working memory load and rule complexity (logical load) to determine whether age moderated engagement of topographically separate cortical areas in the PFC for different load levels. We hypothesize that failure of these separate task manipulations to produce dissociable brain activation effects will support the dedifferentiation theory of changes of neuronal activity with age. From a target sample of 30, we recruited 20 healthy older adults (M=70.4 years, SD = 6.2 years, 55% = female). Data were acquired using a Siemens 3-Tesla system. Images were sensitive to the Blood-Oxygenation-Level-Dependent (BOLD) response using T2* weighting. BOLD data was analyzed using whole brain voxel-wise analysis. Preliminary results suggest that both load manipulations were associated with increased BOLD response throughout the executive control network, including the dorsolateral prefrontal cortex and inferior parietal lobule. Planned analyses will explore whether the association between task load and brain activity is moderated by age. Further testing will determine whether the task aids our understanding in changes in the pattern of neuronal activity with age reflect compensation or dedifferentiation.

Sfrp3 Inhibition Ameliorates Age-Related Neuroinflammation in a Mouse Model of Accelerated Aging.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Ana Mia Corujo Ramirez* and Mi-Hyeon Jang, *Mayo Clinic Graduate School of Biomedical Sciences*

Abstract: Aging is the most significant risk factor for neurodegenerative disorders typified by cognitive deficits such as Alzheimer's disease. Given the rapid and persistent rise of the world's elderly population, improving cognitive function is critical to maintaining a healthy and productive life and a major focus of scientific research and public health. Previously, our research has demonstrated that declining levels of the mitotic checkpoint kinase BubR1 as a result of natural brain aging contributes to age-related brain dysfunction. Therefore, determining a molecular target that can reverse this process governed by BubR1 is of great interest. Using BubR1 hypomorphic (BubR1H/H) mice as a novel mouse model of accelerated aging, we demonstrate that BubR1H/H mice exhibit increased level of astrogliosis and microglia activation in the dentate gyrus and molecular layer of the hippocampus, a brain region critical for learning and memory. It is well established that elevations in astrogliosis and microglia represent hallmarks of neuroinflammation and neurodegeneration. Importantly, our results show that genetic inhibition of sFRP3, a natural Wnt inhibitor, completely recovers astrogliosis observed in BubR1H/H accelerated aging mice. Therefore, our study identifies sFRP3 as a critical neuroprotective factor that improves neuroinflammation and neurodegeneration in brain aging. Given that neuroinflammation and neurodegeneration are pathological mechanisms that underlie age-related cognitive disability, targeting sFRP3 may represent a novel therapeutic strategy for age-related brain inflammation and associated cognitive deficits.

Genetic Labeling of Stress-Regulating Cells in the Zebrafish Hypothalamus

Discipline: Life Sciences
Subdiscipline: Neurosciences

Debora Brito de Andrade*; Priscilla Figueroa and Richard Dorsky, *University of Utah*

Abstract: When cortisol levels increase in response to stress, neurons in the hypothalamus release corticotropin-releasing hormone binding protein (*crhbp)* to the pituitary gland. *Crhbp* inhibits cortisol release, decreasing stress response. Zebrafish *lef1* mutants that exhibit anxiety-like behaviors have been shown to be missing *crhbp* expression in the posterior hypothalamus. We hypothesize that loss of *crhbp*+ neurons in these mutants leads to increased stress response. To test this, we will see whether *crhbp*+ neurons in the hypothalamus project to the pituitary gland and determine whether they are required for stress regulation. The *crhbp* upstream regulatory region was cloned by PCR, and Multisite Gateway Technology was used to create a construct driving enhanced green fluorescent protein (EGFP) expression. Zebrafish embryos were injected with the construct and observed under a fluorescence microscope to confirm EGFP expression. These founders were raised to adulthood, and EGFP expression was observed in the brains of their progeny at 3 days post-fertilization. Data gathered thus far shows that the *crhbp* construct is capable of driving expression in neurons and axonal projections in the posterior hypothalamus. *In situ* hybridization results will be analyzed in order to confirm that cells expressing EGFP are indeed *crhbp*+. Transcription factor binding sites in the *crhbp* regulatory region will be identified, to learn more about the regulation of this gene. Understanding how *crhbp*+ neurons are generated during development will provide insight into developing more targeted treatments for anxiety and other stress disorders that affect the general population.

Effects of Closed-Head Injury on Avoidance Memory in Rats

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alexdiel Figueroa*, *University of Puerto Rico, Rio Piedras* and Demetrio Sierra, *University of Puerto Rico, Medical Sciences Campus*

Abstract: The most common form of brain injury, concussion, is frequently seen in contact sports and military combat. Converging lines of evidence suggest that concussion may impair fear-related behaviors. One type of fear-related behavior, avoidance, occurs when the need to escape from difficult situations such as an aversive stimulus (i.e. footshock) is presented in the presence of a reward (i.e. sucrose pellets). The effects of concussion on avoidance remains unknowns. Concussion can be modeled in rodents with a closed head injury (CHI). Here, a guide tube is placed above the head of anesthetized rats, and a weight is dropped through the tube. In the current study, we hypothesize that CHI will impair avoidance. Following injury, CHI resulted in an increase in time to wake (Sham: 53s, n=11; CHI: 80.18s, n=11; p=0.0209), consistent with a loss of consciousness. In platform-mediated avoidance, rats were conditioned in an operant chamber to auditory tones co-terminating with a mild footshock. An acrylic platform in the opposite corner of the sucrose-delivering bar allowed rats to avoid the shocks. Animals that underwent a CHI spent more time on the platform throughout the test session, suggesting that brain injury results in excess avoidance (p=0.0012). The translational relevance of this work suggests that brain injury may contribute to mental health disorders, since excess avoidance is characteristic of patients with fear and anxiety disorders.

Anatomical and Functional Characterization of Rmtg-Projecting PFC Neurons

Discipline: Life Sciences
Subdiscipline: Neurosciences

Andres Gascon*; Christen L Amegashie; E Margaret Starr and Elizabeth J Glover, *University of Illinois at Chicago*

Abstract: The rostromedial tegmental nucleus (RMTg) and prefrontal cortex (PFC) share many functional similarities including a role in guiding behavioral responses to aversive stimuli. Early studies showed that the PFC projects to the RMTg, however, little is known about the precise anatomy and function of this projection. Long-Evans rats injected with a retrograde tracer into the RMTg exhibited cell body labeling throughout the medial and orbital PFC that spanned the rostrocaudal extent of the region. Labeling was restricted primarily to cortical layer V. Within layer V, approximately 8.59% ±

0.45 prelimbic and 7.94% ± 0.78 infralimbic PFC neurons project to the RMTg. Using a virally-mediated, intersectional approach, our data reveal extensive collateralization of RMTg-projecting PFC neurons throughout the dorsomedial striatum, hypothalamus, and nucleus accumbens. Stimulation of RMTg-projecting prelimbic inputs using *in vivo* optogenetics produced significant real-time place avoidance, the magnitude of which was similar to that produced by stimulation of lateral habenula inputs to the RMTg ($p \leq 0.01$). In addition, rats presented with a shock or tone predictive of shock exhibited a significant increase in cFos expression in PFC-RMTg circuitry ($p \leq 0.05$). Using slice electrophysiology, we found that exposure to repeated footshocks resulted in a significant decrease in the frequency of evoked firing in RMTg-projecting prelimbic neurons. These results demonstrate involvement of PFC-RMTg circuitry in aversive responding, and further reveal significant plasticity as a result of exposure to aversive stimuli. Altered PFC-RMTg function may play a role in neuropsychiatric illnesses associated with dysregulated signaling of aversive outcomes including addiction and mood disorders.

Retinal Sensitivity of Hormonally Modulated *Hyla cinerea* Using Electrophysiological Techniques

Discipline: Life Sciences
Subdiscipline: Neurosciences

Ashley Santana[*1]; Whitney Walkowski[2] and Hamilton Farris[2], *(1)University of Central Florida, (2)Louisiana State University Health Sciences Center*

Abstract: Hormones modulate the nervous system to regulate reproductive behavior and the processing of visual signals. However, little is known of how endocrine mechanisms modulate the retina, the peripheral sensory layer in the eye that is responsible for the transduction of light to electrophysiological events in the central nervous system. The goal of this study was to determine whether reproductive state is correlated with increased retinal sensitivity in vertebrates. The retinal physiological sensitivity of non-reproductive and gravid green tree frog, *Hyla cinerea*, females were measured using scotopic electroretinograms (ERGs). This nocturnal frog is used as an experimental model due to its ability to respond to wavelengths spanning the human visible light spectrum with similar ocular and cellular anatomy. The electrical response to flashes of light were collected using two different experimental protocols. The first approach examined relative spectral sensitivity by comparing ERG b-wave amplitudes for isointensity light flashes at different wavelengths. The second approach measures b-wave amplitude across a series of light intensities, enabling calculation of retinal threshold at each wavelength. Preliminary data show increased electrophysiological response size and decreased thresholds in reproductive females. Elucidation of peripheral sensory function under different endocrine states has potential clinical applications for treating degenerative retinal diseases such as retinitis pigmentosa. These data provide the first step toward such therapeutic approaches.

“What’s Your Favorite Color?”: Analysis of Color Preferences in Zebrafish

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jennifer Parral[1]; Michelle Vargas[*1]; Ruth Iorgovan[2] and Shannon Saszik[2], *(1)neiu, (2)Northeastern Illinois University*

Abstract:

Zebrafish color preference has been used to measure anxiety, with reduced anxiety related to a blue color preference (Pierog et al. ,2017). The current study examined the impact of color on anxiety related behaviors. Adult zebrafish were randomly placed in pairs. To begin testing, pairs were placed in the testing chamber and a color was introduced. Behavior was recorded for 15 seconds and then the color was changed. This process was repeated until all groups and colors (Red, Yellow, Green, Blue) were tested. The order of color was randomized for each pair. To determine the impact of color on anxiety, erratic swimming (average velocity; px/ms) and exploratory behavior (distance in 15 seconds; px) were measured. It was hypothesized that a decrease in anxiety related to color will be identified with a low average velocity and a high distance swam. Preliminary results showed that behavior was dependent on color. Exploratory behavior was highest in the green chamber ($\bar{x}$G=6326.70px $\bar{x}$R=5037.06 px; $\bar{x}$B= 5923.07 px; $\bar{x}$Y= 6258.94 px). The erratic swimming was lowest in the red chamber ($\bar{x}$G= 319.29 px/ms $\bar{x}$R= 244.57 px/ms; $\bar{x}$B= 249.43 px/ms; $\bar{x}$Y= 316.28 px/ms). However, distance and average velocity were not significantly different suggesting zebrafish did not have a color preference ($F(3, 22) = 0.385$, $p = 0.765$). Previous results stated blue was preferred, but our results are inconsistent, perhaps due to differences in testing procedures. Since test procedures affect color preference, researchers should be cautious about the interpretation of the results.

Deficits in Hippocampal Dependent Memory across Different Rodent Rodels of Early Life Stress: Systematic Review and Meta-Analysis

Discipline: Life Sciences
Subdiscipline: Neurosciences

Mariana Rocha[*]; Arie Kaffman; Michael Bloch and Daniel Wang, *Yale University*

Abstract: Exposure to early life stress (ELS) causes abnormal hippocampal development and functional deficits across diverse mammalian species including rodents and humans. Although several systematic reviews have examined the effects of ELS on hippocampal dependent deficits in rodents, no meta-analysis has yet been used to quantify effect sizes, heterogeneity and to assess publication bias and the moderating effects of sex and species (rats vs. mice) across different paradigms. To address these questions we conducted a systematic review followed by meta-analysis comparing the effects of handling, maternal separation (MS), and limited bedding and nesting (LBN) on performance in the Morris water maze (MWM), novel object recognition (NOR), and contextual fear condition (CFC). We found that in tasks that rely heavily on the dorsal hippocampus, such as MWM and NOR, LBN and MS cause similar cognitive deficits. In contrast, exposure to handling is associated with significant improved performance in the MWM and a non-significant effect in the NOR. In the CFC task, which relies more on the ventral hippocampus, all three paradigms reduced contextual freezing, an effect that was moderate in size and significant for handling [Hedges g= -0.41, p= 0.049, k= 4] and MS [Hedges g= -0.28, p= 0.025 , k= 12], but not significant for LBN [Hedges g= -0.37, p= 0.15, k= 3]. The heterogeneity between studies was significantly lower in LBN compared to handling and MS and there was no consistent effects of sex or species across the three paradigms.

Prefrontal Neuronal Signaling of Approach-Avoidance Conflict

Discipline: Life Sciences
Subdiscipline: Neurosciences

Gabriel Rojas-Bowe*; Albit Caban-Murillo; Shantee Ayala-Rosario; José Pérez-Torres; Jonathan Moran-Sierra; Adriana Vélez-Avilés; Viviana Valentin-Valentin; Arturo Rivera-Rivera; Hector Bravo-Rivera and Gregory Quirk, *University of Puerto Rico, School of Medicine*

Abstract: The ability to implement adaptive strategies during approach-avoidance conflict is an important evolutionary tool. However, the neural mechanisms that underlie adaptive approach-avoidance conflict resolution remain unknown. We developed a rodent conflict task that pits the motivation to approach reward against the motivation to avoid shock. In the task, rats learned that: 1) a 30s tone predicts a footshock at the end of the tone that could be avoided by stepping onto a nearby platform, 2) a 30s light-cue signals the availability of sucrose upon pressing a bar away from the platform. When the tone and light cues were co-presented, rats learned to delay avoidance to accommodate pressing early during the tone-light period. Pharmacological inactivation of the prelimbic (PL) cortex accelerated avoidance, suggesting that in contrast to previous work, PL delays avoidance when it is favorable to do so. Electrophysiological recordings showed populations of PL neurons that distinguished the combined tone-light stimulus from tone-only and light-only stimuli. Other PL neurons signaled pressing during the tone-light (high conflict), but not during the light-only (low conflict). Additionally, other populations distinguished pressing early in the tone-light (less risky) from pressing late in the tone-light (more risky). Furthermore, other PL neurons showed excitation prior to platform mounts. These findings suggest that PL resolved approach-avoidance conflict by signaling conflict stimuli and driving appropriately timed pressing and avoidance behaviors.

Induced Pluripotent Stem Cell Therapy to Treat Spinal Cord Injury

Discipline: Life Sciences
Subdiscipline: Neurosciences

Sara Timmons* and Gail Taylor, *University of Texas at San Antonio*

Abstract: Spinal cord injuries (SCIs) disrupt communication along the central nervous system, which results in loss of sensory and motor functions. In order to restore function in damaged spinal cord neurons, this study will assess the potential of induced pluripotent stem cells (iPSCs) as candidates for intraspinal transplantation. The employment of iPSCs has many benefits; the extraction of these cells can be performed through non-invasive procedures and its use is more ethically sound than using embryonic stem cells. Additionally, iPSCs are obtained directly from the model, which eliminates the need for immunosuppression. Furthermore, it may possess more affinity for neuron differentiation than mesenchymal stem cells in which its differentiation ability may be limited to mesodermal tissues. This study will employ a mouse model with an induced thoracic spinal cord injury; a lesion will be made in the spinal nerves in the T1-T5 region. Paraplegia, lower body paralysis, is expected to be observed. Researchers will then proceed to withdraw and utilize cells from the same mouse model to grow a population of cells *in vivo* capable of being reprogrammed into iPSCs, which will then be reprogrammed into neurons. The iPSC-derived neural tissue will then replace the damaged spinal tissue via intraspinal transplantation.Transplantation is expected to promote regeneration of neurons lost to SCI and allow the return of sensory and motor functions. Improvements, or lack thereof, in the mouse model post-procedure will be recorded. The purpose of this trial is to explore methods of stem cell regenerative therapy that will treat SCIs.

The Impact of Recurrent Alcohol Consumption on Corticostriatal Oscillations and Gene Expression

Discipline: Life Sciences
Subdiscipline: Neurosciences

Zev Jarrett*, *University of Massachusetts Amherst* and David Linsenbardt, *University of New Mexico*

Abstract: In 2018, 14.4 million American adults were diagnosed with an Alcohol Use Disorder (AUD). The development of an AUD is associated with attenuated corticostriatal oscillations. However, we know little about the biology behind these alcohol-driven oscillations, or how they relate to recurrent drinking. The goal of this study was to assess the extent to which gene expression and corticostriatal activity are altered by repeated alcohol exposure. C57BL/6J mice were provided with alcohol for 2 hours/day for 15 consecutive days using the 'drinking-in-the-dark' (DID) procedure. We recorded local field potentials from the nucleus accumbens and medial prefrontal cortex during the DID, after which we collected brain tissue for RNA sequencing. We hypothesized that the repeated alcohol consumption would lead to alterations in gene expression, as well as increases in basal corticostriatal activity. Using hierarchical clustering and other unbiased statistical methods, we identified several genes and frequency bands involved in recurring alcohol consumption. Understanding the dynamics between repeated alcohol use and corticostriatal activity/gene expression could shed light on the neural mechanisms driving AUD, and may point towards new avenues of treatment.

Effects of Glyphosate on Locomotion and Anxiety-like Behavior in Rats

Discipline: Life Sciences
Subdiscipline: Neurosciences

Gabriela Hernández-Busot*[1]; Mauricio Cáceres Chacón[2]; Melissa Rivera-Lopez[2]; Alexdiel Figueroa-Perez[3]; Paola Alvelo-Fernández[4]; Carlos Reyes-Sepúlveda[4]; Osmarie Martínez-Guzmán[2]; Hector Haddock-Martínez[5]; Raul Ramos-Sanchez[5]; David Ojeda-Martínez[5] and Demetrio Sierra-Mercado[2], *(1)Dept. of Biology, University of Puerto Rico, Rio Piedras campus, (2)Dept. of Anatomy & Neurobiology,University of Puerto Rico, Medical Science Campus, (3)Dept. of Chemistry, University of Puerto Rico, Rio Piedras campus, (4)Universidad de Puerto Rico, Bayamon Campus, (5)University of Puerto Rico Rio Piedras Campus*

Abstract: Glyphosate is one of the active ingredients of the most used herbicides. Initially glyphosate was considered safe by the Environmental Protection Agency (EPA) as it acts by inhibiting a metabolic route not present in mammals. The maximum dosage of glyphosate permitted by the EPA is 0.7g/ml. Recent studies have shown that a high dosage of glyphosate has led to increased anxiety and decreased locomotion. However, the effects of prolonged glyphosate exposure using lower dosages remains unclear. To determine the effects of lower dosage consumption, rats were provided with glyphosate-contaminated drinking water with *ad libitum* access*.* We hypothesize that rats exposed to glyphosate contaminated water will have decreased locomotion and increased anxiety-like behavior. Locomotion was assessed using the open field test three and twenty-two weeks after exposure. We observed that glyphosate did not affect the distance traveled at three (control: 20.82, GBH: 25.22; p=0.10) or twenty-two weeks (control: 23.13, GBH: 30.56; p=0.24).Additionally, speed was also unaffected when assessed in the open field test at both time points. Anxiety-like behavior was assessed in the elevated plus maze after three and seven weeks. No difference was seen in the anxiety index after three weeks (control: 0.66, GBH: 0.80; p=0.39) or seven weeks (control: 0.76, GBH: 0.80; p=0.38). In conclusion, the lower oral dosage provided did not affect locomotion after three or twenty-two weeks, or anxiety-like behavior after three or seven weeks. Future directions include prolonging time of exposure and assessing immunohistochemistry in areas of the brain involved with locomotion and anxiety-like behaviors.

Unbiased Identification of Significant Differences and Stages in Cortical Dynamics across Development in Calcium Imaging Videos

Discipline: Life Sciences
Subdiscipline: Neurosciences

Desiderio Ascencio*[1]; Sydney Weiser[1]; Brian Mullen[2] and James Ackman[1], *(1)University of California Santa Cruz, (2)University of California, Santa Cruz*

Abstract: Specialized neural activity patterns during late fetal development are critical for network establishment; disruptions of these patterns can lead to serious neurological defects, yet we know very little about their nature or their developmental repercussions. Studying these activity patterns in humans is nearly impossible due to technological constraints. Since mice are born prematurely, these specialized activity patterns happen largely after birth, and are thus more accessible to researchers. Our lab has harnessed advances in modern computing and biotechnology to record high resolution datasets of mouse neural activity across development using genetically expressed calcium indicators. We developed a custom automated data processing workflow to analyze these patterns and generate spatiotemporal summaries of captured neural dynamics. Additionally, we applied this analysis to hundreds of videos collected from developing mouse cortices, generating a database with tens of thousands of spatiotemporal neural activity metrics – too many to analyze manually. To identify key stages and transitions in network dynamics, I am developing a method that automatically identifies and quantifies the significance of inflection points across age, drug, region, or other categorical variables using Analysis of Variance (ANOVA) methods. Additionally, I built a graphical user interface to explore the separation and clustering of the neural database metrics using kernel density estimators and dimensionality reduction visualizations. Utilizing this automated interactive system, users can screen for many potential factors influencing network sensitivity and tuning. We can now easily visualize how mouse network development is affected by external and internal conditions.

Single Cell RNA Sequencing of Meningeal B Cells during Experimental Autoimmune Encephalomyelitis

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alexandra Martinez Lopez*[1]; Gregory Wu[2]; Sravanthi Bandla[2] and Angela Archambault[2], *(1)Wellesley College, (2)Washington University in St. Louis*

Abstract: Multiple Sclerosis (MS) is a chronic inflammatory disease of the central nervous system (CNS), characterized by demyelination and axonal damage, that affects over 2 million people worldwide. MS patients experience parenchymal inflammation along with the formation of Ectopic Lymphoid Tissue (ELT) in the meninges, the membrane that encapsulates the CNS. B cell aggregates resembling ELT in patients with MS are observed in an experimental autoimmune encephalomyelitis (EAE) mouse model of MS developed in our lab. The mechanisms by which these B cell clusters form and accumulate in the spinal meninges of mice during EAE remain unclear. We hypothesize that there are B cell intrinsic properties critical for the infiltration and retention of B cells in the meninges during EAE. To test this, we used single cell RNA sequencing to identify gene expression patterns that highlight functional differences between B cells within the spinal cord meninges and deep cervical lymph nodes (DCLN) of mice. Preliminary results confirmed the successful isolation of viable cells for analysis. We anticipate that our results will identify subpopulations of meningeal B cells that differ from those found in control DCLNs, suggesting that B cells acquire various transcriptional states during EAE that may be linked to migratory pathways to the spinal meninges and transcriptional regulators of cell retention. Investigating the formation of meningeal B cell clusters during EAE could provide insight to the formation of ELT and refine B cell depletion therapies for patients with MS.

Optical Guidance of Neuronal Growth Cones By Laser-Induced Forces

Discipline: Life Sciences
Subdiscipline: Neurosciences

Kahmina Ford*; Desiree Ramirez and Erin Craig, *Central Washington University*

Abstract: During neural development, a sensory-motor structure called a growth cone extends from the axon of a neuron and navigates to a neighboring nerve cell, guided by various chemical and physical signals from its cellular environment. In vitro experimentation on growth cone motility has demonstrated that optical signals provided by near-infrared (NIR) lasers are effective for guiding growth cone navigation, yet the underlying mechanism is not entirely known. Our leading hypothesis is that the attractive force induced by the NIR laser biases the diffusion of globular actin proteins (G-actin) from the cellular environment towards the center of the beam, aimed at the growth cone's leading-edge membrane. The accumulation of G-actin allows for more actin monomers available to polymerize at the leading edge, thus increasing the rate of polymerization and resulting in net protrusion of the growth cone in the direction of the laser spot. We have developed a model that uses the programming platform, MATLAB, to run computer-simulated experiments to investigate the effects of laser-induced G-actin distributions on leading-edge polymerization rates and to provide testable predictions for neuronal outgrowth trajectories in vitro. Our simulations demonstrate time-dependent G-actin pooling toward the center of a laser beam. Our simulated growth cone changes trajectory in response to an asymmetric G-actin distribution, turning toward the site of the NIR laser. By developing a computational tool for predicting laser-induced growth cone turning, we have addressed an essential first step for applying NIR-based treatment to neurodegenerative diseases.

Computational Model for Neuronal Growth Cone Guidance Using Optical Cues

Discipline: Life Sciences
Subdiscipline: Neurosciences

Desiree Ramirez*; Kahmina Ford and Erin Craig, *Central Washington University*

Abstract: A growth cone is a structure at the tip of nerve axons that guides axonal outgrowth to synaptic targets by responding to extrinsic guidance cues during neural development. Several experimental studies have shown that near infrared (NIR) lasers can change the direction of growth cone motility and axonal outgrowth, which could potentially be used for neural repair once the mechanism for optical guidance of growth cone motility is better understood. Here, we develop a computational model of the growth cone turning mechanism in response to a NIR laser, based on the hypothesis that the laser induces asymmetric growth of an intracellular network of filaments called f-actin. To test our hypothesis, we developed a computational framework in MATLAB to simulate growth cone motility in response to an optical signal with a Gaussian distribution. Our simulations predict that the placement of a laser beam with a Gaussian distribution near a growth cone can change the direction and shape of the growth cone. The framework we established for predicting growth cone motility for different laser placement strategies can be used as a tool for planning experimental tests. Detailed understanding of NIR laser guidance of growth cones could contribute to the development of minimally invasive techniques for neural repair.

Quantifying Approach and Avoidance Behaviors in Mice Using Eztrack Behavioral Analysis Software

Discipline: Life Sciences
Subdiscipline: Neurosciences

Brianna Parrington*, *University of California, Los Angeles* and William Giardino, *Stanford University*

Abstract: There is an urgent need to develop new therapies that target the neural circuits driving psychiatric symptoms like anxiety, substance abuse, and sleep disruption. Previous studies from our lab implicated a complex brain region called the bed nuclei of stria terminalis (BNST) in generating stress and reward, particularly BNST neurons containing the neuropeptides corticotropin-releasing factor (CRF) and cholecystokinin (CCK). Despite recent advances, the necessity of CRF-BNST and CCK-BNST neurons in mediating stress and reward remains unclear. To address this, we focused on characterizing behavioral processes that require distinct subpopulations of BNST neurons. To quantify mouse behavior subjected to BNST manipulations, we utilized behavioral tracking software for rapid video analysis. Using a Cre-dependent virus expressing Caspase3 for cell type-specific ablation of discrete BNST neuronal populations, mice were tested for behavioral approach/avoidance of salient stimuli under control conditions, predator odor, and opposite-sex social stimuli using ezTrack tracking software. We expect that ablation of CRF-BNST neurons will alter avoidance behavior in response to predator odor and ablation of CCK-BNST neurons will modify approach behavior in response to opposite-sex social stimuli in mice. Our preliminary results show that CRF-BNST neurons may be required for stress and CCK-BNST neurons may be required for reward in mice. Employing ezTrack has allowed us to quantify how ablation of distinct BNST neuronal populations influenced approach/avoidance behavior in response to different stimuli. In the future, we will utilize automated behavioral tracking software to further investigate the role of specific BNST neurons in mediating stress and reward.

Increased Irritability and Repetitive Behaviors in Ab-Precursor Protein (β-APP) Transgenic Monkey Models of Alzheimer's Disease

Discipline: Life Sciences
Subdiscipline: Neurosciences

Rebecca Rusnak*, *Emory University* and Jessica Raper, *Yerkes National Primate Research Center*

Abstract: More than five million Americans are afflicted by Alzheimer's Disease (AD). Although the notable clinical symptom of AD is cognitive decline, behavioral disturbances like repetitive and stereotypic phenomena have been reported and can be equally distressing. The β-amyloid peptide (Aβ) has been widely implicated in AD pathology, making Aβ and its precursor (β-APP) of research interest. Overexpression of human β-APP induces β-amyloid plaque formation and cerebral amyloid angiopathy in transgenic rodents, but the full phenotype of AD has not been demonstrated in any nonhuman species. Nonhuman primates provide a unique opportunity to develop an animal model of AD with greater translational potential. The current study utilized a transgenic β-APP monkey model to examine potential evidence of early, non-cognitive symptoms of AD. We prepared a β-APP gene construct with Swedish/Indiana mutations regulated by the human polyubiquitin promoter. Three transgenic APP rhesus macaques were produced by lentiviral transfer of the transgene into oocytes, followed by in vitro fertilization and embryo transfer. Two monkeys expressed mutant *b-APP* in tested somatic cells, whereas one was a transgene-mosaic. Behavioral reactivity to an acute stressor was examined in the transgenic β-APP monkeys and five wild-type controls during early adulthood. β-APP monkeys, unlike controls, lacked the species-typical freezing response when faced with the mild threat. β-APP monkeys also exhibited increased repetitive/stereotypic behaviors and augmented aggression in the absence of stimuli. Overall, results reveal that β-APP transgenic monkeys exhibit early behavioral disturbances similar to AD patients, making them useful to understanding the pathogenesis of non-cognitive AD symptoms.

Prevalence of Mosquito-Borne Pathogens in Urban Areas of Southern Oklahoma

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Brandon Henriquez* and Bruce Noden, *Oklahoma State University*

Abstract: Urban mosquitoes have become a problem across the globe, feeding on animals and humans and transmitting an array of bacteria, protozoa, and viruses. The Asian Tiger mosquito, *Aedes albopictus*, and the Common House mosquito, *Culex pipiens,* are two of the most important mosquito species. *Aedes albopictus* is competent for at least 22 arboviruses (including dengue and chikungunya), avian malaria species, and *Dirofilaria immitis* (canine heartworm) in North America. *Culex pipiens* is a major vector for *D. immitis,* as well as many arboviruses (West Nile virus, St. Louis Encephalitis, Western Equine Encephalitis) as well as avian malaria. The involvement of *A. albopictus* and *C. pipiens* in pathogen transmission in urban areas in southern Oklahoma is understudied. In 2017, 6,628 mosquitoes were collected and identified to species from six urban clusters in southern Oklahoma. The objective of the current study was to determine the prevalence of medical and veterinary pathogens in the *A. albopictus* (n=4,791) and *C. pipiens* (n=1,045) collected. The DNA extracted from the mosquitoes was tested by polymerase chain reaction (PCR) using various primer sets focused on *D. immitis* and avian malaria. Of 830 pools screened to date, *D. immitis* was detected in 6 pools while avian malaria was not detected. Further testing will focus on whether any pools contain *Rickettsia* sp. DNA. Results from this study will provide information regarding the transmission of potential pathogens in the southern Great Plains and the potential involvement of different host species.

Sink or Swim: Predator Avoidance By Cultured and Wild Chesapeake Logperch (*Percina bimaculata*)

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Candace Narvaez*; Sara Mueller and Jay Stauffer, *Pennsylvania State University*

Abstract: Invasive species have become a growing concern in Pennsylvania. Several studies have shown that certain chemosensory behavioral cues may help fish avoid predation. This study seeks to understand the visual and chemosensory behavioral cues behind predator avoidance in wild-caught and cultured Chesapeake Logperch (*Percina bimaculata*), and endangered fish in Pennsylvania. Also, this study seeks to investigate if predator detection and avoidance behaviors are learned or innate in Chesapeake Logperch. Seventeen wild-caught and 24 cultured Chesapeake Logperch were video recorded during predator avoidance trials conducted in early 2020. Fish behaviors were scored based on the amount of time spent in each quadrant in the tank as well as type of behavior exhibited during observation. The results of this study will be used to better predict the survival of Chesapeake Logperch upon interaction with a predator when released for conservation recovery efforts.

An Accessible Method for Dynamical Behavior Analysis of Large Gene Regulatory Networks

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Sandy Kim* and Eric Deeds, *University of California, Los Angeles*

Abstract: The temporal and spatial patterns of gene expression are fundamentally integral in all organisms. These patterns are governed by a set of genes and their interactions are known as a gene regulatory network (GRN) that underlie and influence many critical processes in the cell such as development, differentiation, and responses to environmental changes. Thus, dysregulation of GRNs is extremely detrimental and often leads cells to disease states or even senescence. The ubiquity and necessary role of GRNs across all organisms make them of great interest to study. However, due to their often large and highly complex nature, little is currently known about the dynamic properties of many GRNs. Although advances in high-throughput sequencing methods and their applications to temporal studies have produced time course data for gene expression, there remain many challenges in analyzing such high-dimensional data. Using principal component analysis, a dimensionality reduction technique, along with other mathematical methods, we developed an easily-accessible method to analyze the dynamics of high-dimensional time-course gene-expression data to infer the behavior and robustness of GRNs. We demonstrate its ability to uncover the dynamics underlying a wide variety of gene expression data by applying our tool to the analysis of simulations of very large GRNs.

The Effects of Eating a High Fat or a Ketogenic Diet on Sensitivity of Female Rats to Methamphetamine

Discipline: Life Sciences
Subdiscipline: Pharmacology

Madeline Elsey*; Nina Beltran and Katherine Serafine, *The University of Texas at El Paso*

Abstract: Ketogenic diets (which are high in fat and low in carbohydrates) have been used for the treatment of epilepsy and weight loss. In contrast, traditional high fat diets (which are high in carbohydrates) can lead to obesity and weight gain, suggesting these two diets might produce opposing effects. Eating a high fat chow enhances the sensitivity of rats to the behavioral effects of drugs of abuse (i.e., methamphetamine); however, it is not known if ketogenic chow impacts drug sensitivity. To test the hypothesis that diet would impact sensitivity of rats to methamphetamine-induced locomotion, rats eating standard chow (17% kcal from fat, 58% kcal from carbohydrate, 25% kcal from protein), high fat chow (60% kcal from fat, 21% kcal from carbohydrate, 18% kcal from protein), or ketogenic chow (90.5% kcal from fat, 0.3% kcal from carbohydrate, 9.2% kcal from protein) were tested once weekly with cumulative doses of methamphetamine (0.1-3.2 mg/kg; i.p.). Dose-response curves were analyzed using two-way repeated measures ANOVAs. After 4 weeks, rats eating high fat chow were more sensitive to the locomotor-stimulating effects of methamphetamine at smaller doses (0.32-1.0 mg/kg) than rats eating standard chow. Rats eating ketogenic chow were also more sensitive than rats eating standard chow to the locomotor-stimulating effects of methamphetamine, but only at the largest cumulative dose (3.2 mg/kg). These results suggest that traditional high fat diets and ketogenic diets do not always produce identical effects. Future research will investigate the impact of these diets on sensitivity of rats to other drugs of abuse.

Co-Delivery of paclitaxel, Doxorubicin, and 5-Fluorouracil Using Hybrid Peptide Drug Carriers for Synergistic Combination Chemotherapy

Discipline: Life Sciences
Subdiscipline: Pharmacology

Andrew Alvarez* and Katarzyna Slowinska, *California State University, Long Beach*

Abstract: The usage of combination chemotherapy in treating cancers have shown increased efficacy compared to single-agent chemotherapy due to potential synergistic clinical effects. Unfortunately, the administration of multiple unmodified chemotherapeutics limits the treatment effectiveness due to the different pharmacokinetics of each drug used, such as blood solubility and cell uptake rate. We have designed a hybrid collagen/cell-penetrating peptide carrier designed to bypass these limitations and hypothesize that the carrier will be able to simultaneously deliver multiple agents to the cancer cells in a controlled manner to induce or maximize synergistic antitumor effects. The drugs to be carried will include paclitaxel (PTX), doxorubicin (DOX), and 5-fluorouracil (5FU) as these drugs can be bioconjugated to the peptide. To test its effectiveness, the carrier will be evaluated on MCF-7 breast cancer cells, a model breast cancer cell line, with drug efficacies expressed as half-maximal inhibitory concentrations (IC_{50}). The IC_{50} of PTX, DOX, and 5FU will be determined individually

and compared with the efficacies of their corresponding peptide-drug version (e.g. PTX versus PTX-peptide) to assess the cell-penetrating and drug-releasing capability of the peptide carrier. The IC_{50} of peptide-PTX-DOX-5FU will be compared to the IC_{50} of PTX, DOX, and 5FU administered in combination to evaluate the carrier's potential synergistic effects. Confocal fluorescence microscopy will be used throughout the experiments as verification of the peptide's intracellular/subcellular localization. We anticipate that the peptide carrier will be able to mediate effective cell uptake of multiple drugs for enhanced antitumor effects.

Effect of Endogenous Hydrogen Sulfide and Nitric Oxide Gasotransmitters on Cataract Formation in Intact Bovine Lenses, *Ex Vivo*.

Discipline: Life Sciences
Subdiscipline: Pharmacology

Dariush Yalzadeh[*]; Neetu Singh; Segewkal Heruye and Catherine Opere, *Creighton University*

Abstract: Cataract, a major cause of blindness globally, is a multifactorial ocular disease characterized by degradation of the optical quality of crystalline lens. The gasotransmitter, hydrogen sulfide (H_2S), which is endogenously formed by cystathionine β-synthase (CBS) and cystathionine γ-lyase (CSE), mitigates cataract formation in cultured bovine lenses ex vivo when applied exogenously. Like H_2S, nitric oxide (NO), which is biosynthesized by the NO synthase (NOS) enzymes, plays a significant role in the cardiovascular and nervous systems. Ingestion of the nitroglycerin, a NO-producing drug increases the risk of cataract formation in cardiovascular patients. However, the role of endogenous H_2S and NO in cataract formation has not been completely elucidated. We hypothesize that endogenous H_2S and NO can regulate cataract formation in cultured bovine lenses, ex vivo.

To investigate the effect of endogenous production of H_2S and NO on cataract formation, cultured bovine lenses, were exposed to CSE, CBS, and NOS inhibitors. Cataract formation was qualitatively and quantitatively assessed at 3, 6, 24, 48 and 72 h-time points by photographic captures and measurement of transmittance using a plate reader (Synergy H1 hybrid). After 72h, the dual CSE and CBS inhibitor, aminooxy acetic acid (2mM) reduced transmittance by 58.21±1.77% ($P<0.001$, n=5), compared to DMEM (t=72 h). On the contrary, after 48h, the NOS inhibitor, L-NAME (0.01 and 3 mM) elicited an increase in transmittance by 40.49±1.74% ($P<0.0001$, n=8) and 23.66±1.97% ($P<0.05$, n=5) respectively, compared to DMEM (t=48 h). In conclusion, both endogenous H_2S and NO regulate cataract formation in cultured bovine lenses, ex vivo.

Toxoplasma Gondii Cell Structure and Division Modulated By Unique Protein Phosphatase, Ppkl

Discipline: Life Sciences
Subdiscipline: Pharmacology

Nora Gilliam[*1]; William Blakely[2] and Gustavo Arrizabalaga[2], *(1)Indiana University Purdue University Indianapolis, (2)Indiana University School of Medicine*

Abstract: The parasite *Toxoplasma gondii* can be pathogenic in immunocompromised individuals and those infected congenitally. During infection, *Toxoplasma* undergoes repeating cycles of invasion into host cells. This cycle is tightly regulated by signaling pathways and reversible phosphorylation events driven by kinases and phosphatases. Our lab has recently focused on the unique Protein Phosphatase, PPKL, which is similar to plant phosphatases that regulate hormonal signaling. As humans do not possess this type of phosphatase, it is a potential drug target. Our goals are to determine the localization and function of PPKL. To determine its localization, we used CRISPR-Cas9 to tag the endogenous protein HA-PPKL and conducted Immunofluorescent Assays. We found that PPKL is in the cytoplasm and it associates with the nascent cytoskeleton of daughter cells during division. To determine the function of PPKL, we generated a parasite strain in which PPKL's promoter was replaced by one that can be turned off by addition of tetracycline. This strain replicates normally in the absence of tetracycline, but addition of tetracycline results in parasite death. Through microscopic investigation of parasites in the presence of tetracycline, we determined that they are dying because of a disruption in the cytoskeleton of daughter cells during division. These results lead us to a model in which PPKL is at the center of a signaling pathway that regulates parasite division. Our current focus is to identify the substrates and signaling partners of PPKL in order to ultimately elucidate the mechanisms that regulate cell division in this important human pathogen.

Antibiotic Resistant Gene *blaCARB*-2 is in a Multidrug Resistance Region in an Environmental *Escherichia coli*

Discipline: Life Sciences
Subdiscipline: Pharmacology

Stephanie Harchenko[*1]; Andrei Tatarenkov[2] and Luis Mota-Bravo[1], *(1)University of California, Irvine, (2)School of Biological Sciences, University of California, Irvine*

Abstract: Antibiotic resistance bacteria are increasing globally, leaving humans with no options to treat bacterial infections. The drug class penams, or penicillins, accounts for about 20 most commonly used antibiotics. CARB-beta-lactamase encoded by the *blaCARB* gene confers resistance to penams. The objective of this study was to identify and characterize the antibiotic resistant regions of a plasmid belonging to *Escherichia coli* SW2826 and focus on the *blaCARB-2* gene that confers resistance to penams. This isolate was collected in Doheny Beach Creek California and was identified through MALDI-TOF,

sequenced through Illumina and Oxford Nanopore, and annotated using PATRIC and Geneious. The antibiotic resistance profile was obtained with Disk Diffusion Tests. The antibiotic resistance region in the plasmid encodes seven antibiotic resistance genes which account for resistance to 22 tested antibiotics. These antibiotics belong to seven antibiotic classes: aminoglycosides, beta-lactams, macrolides, phenicols, sulfonamides, tetracyclines, and trimethoprims. Comparative analysis using Genbank sequences showed that an identical region was found in Acinetobacter, which suggests the occurrence of horizontal gene transfer. This full region that includes the *blaCARB-2* and *dfrA16* genes is shared only among eight isolates which implies they were mobilized to the other genetic regions. Plasmids harboring this region belong to different incompatibility groups indicating transposition events. The plasmid from SW2826 shows that the *blaCARB* gene has spread among bacteria species and plasmid types via mobile genetic elements. The case of the *blaCARB* gene helps to understand the spread of antibiotic resistance genes among diverse bacteria and illustrates the role of natural habitats.

Sex Differences in Ozone-Induced Lung Inflammation and Injury in an Allergic Asthma Mouse Model

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Deborah Montes*[1]; Jose Bermudez[1]; Nathalie Fuentes[2]; Marvin Nicoleau[3]; Lidys Rivera[2]; Patricia Silveyra[1] and Patricia Silveyra[4], *(1)The University of North Carolina at Chapel Hill, School of Nursing, (2)Department of Pediatrics, Penn State College of Medicine, (3)Pennsylvania State University, College of Medicine, (4)PennState Medical Center*

Abstract: Asthma is a chronic lung disease that leads to airway constriction and inflammation, affecting more than 300 million people worldwide. Common triggers for asthma include allergens and/or airborne irritants, like air pollutants. Studies indicate that adult women have higher asthma exacerbation rates than men. However, the specific underlying causes of these sex disparities are not yet well characterized. Here, we sought to examine the effects of air pollution exposure in an asthma mouse model, hypothesizing that increased levels of inflammation and damage would be differentially observed in females than males.

To induce an asthma phenotype, we challenged adult male and female C57BL/6J mice with a house dust mite (HDM) solution from *Dermatophagoides pteronyssinus* and *Dermatophagoides farinae*. The protocol consisted of five consecutive intranasal challenges with 25µg of HDM or control (PBS) followed by two days off, repeated for five weeks. Mice were then exposed to 2 ppm ozone or filtered air. We measured protein levels in bronchoalveolar lavage (BAL) samples to assess the relative degree of lung inflammation and injury. Significant differences were assessed by 2-way ANOVA.

As hypothesized, female mice showed significantly higher inflammation and injury via increased protein load in BAL after HDM treatment and ozone exposure. Males showed no significant response with HDM treatment, but showed increased protein levels after ozone exposure.

Exposure to HDM and ozone induces differential inflammatory responses in the male and female lung. Our results support conclusions from previous studies on sex-specific differences in asthma phenotypes.

Can Metabolic Flexibility be Shown through Dynamic Metabolic Adjustments during Exercise?

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Jorge Rodriguez* and Michael Harris, *California State University, Long Beach*

Abstract: Metabolic flexibility is an enigmatic concept, involving responses of carbohydrate (CHO) and fatty acid (FA) metabolism to changing energy demands. Poor metabolic flexibility contributes to severe and debilitating diseases. We propose that metabolic responses to sustained low to moderate intensity exercise (SLMIE), may provide a useful index of metabolic flexibility. We test the hypothesis that metabolic adjustments to SLMIE, as well as measurements of body composition, insulin sensitivity, A1C, and blood glucose, may be quantifiable indicators of metabolic flexibility. Oxygen consumption and CO2 production in healthy male and female subjects were measured before and during a period of SLMIE (50% VO max) using a cycle ergometer. The pattern of change in Respiratory Exchange Ratio (RER) illustrated changes in proportional CHO and FA metabolism. Body composition, assessed by dual energy X-ray absorptiometry (DXA), as well as blood measurements of insulin sensitivity, glycated hemoglobin, and blood glucose were used to estimate metabolic flexibility. Patterns of RER illustrated increasing CHO metabolism at the onset of exercise, and subsequent adjustments increasing FA metabolism within 10 to 25 minutes. Subjects with longer metabolic adjustment latencies had body compositions suggesting lower metabolic flexibility. Blood assessments of metabolic flexibility are ongoing. These preliminary results suggest that metabolic adjustment latencies can be resolved, and may indicate, and correlate to characteristics associated with metabolic flexibility.

Metabolism and Fuel Selection in Holometabolous Insects: An Investigation Using Quantitative Magnetic Resonance Body Composition Analysis and High Resolution Metabolic Phenotyping

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Jiun Tseng*, *University of Massachusetts Amherst* and Lawrence Schwartz, *University of Massachuetts Amherst*

Abstract: The holometabolous insects are among the most successful eukaryotes on the planet, in large part because they have distinct body morphs for feeding (larva) and reproduction (adult). In some species the adults do not feed at all, meaning that the larva must consume all of the nutrients required to drive growth, development and reproduction. Using several complementary methods including Quantitative Magnetic Resonance body composition analysis (QMR), high resolution metabolic phenotyping, and Soxhlet body composition analysis, we have determined the water content, lean body mass, fat content and VCO2 throughout pupal-adult development in two representative Lepidoptera (the tobacco hawkmoth *Manduca sexta* and the silkmoth *Antheraea polyphemus*) and in Diptera (the flesh fly *Sarcophaga bullata*). We observed that in each species, there was an exponential decrease in body fat content that was mirrored by an exponential increase in VCO2 as pupal-adult development progressed. Fat utilization was arrested in both Lepidoptera species during diapause, but then increased exponentially when development resumed, meaning that fat metabolism was correlated with developmental stage rather than chronological age. These data support the hypothesis that fat is the primary fuel driving metabolism. As well, they demonstrate that QMR technology can be applied to invertebrates to non-invasively monitor metabolic changes over time.

Development of a Urinary Biomarker Assay for Measuring Acute Oxidative Stress

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Micaela Ruiz*; Kendan Jones-Isaac and Ed Kelly, *University of Washington*

Abstract: Advances in medicine have significantly increased life expectancy for much of the population. However, aging-associated diseases such as cancer, heart disease, and hypertension amongst others continue to significantly impact the aging population. Biological aging is defined by the gradual accumulation of cellular damage and development of physiological abnormalities from repeated acute insults or chronic disease states. A major driving force in biological aging is due to generation of reactive oxygen species (ROS), natural byproducts of cellular metabolism, possessing an unpaired electron that is highly reactive with essential biomolecules. ROS generation is increased by factors like lifestyle or exposure to toxic concentrations of drugs or environmental toxins. Accessible biomarkers can serve as early indicators of cellular stress, allowing for early intervention. One marker of oxidative stress (OS) is oxidative modification of nucleic acids, in particular the modification of guanine in RNA and DNA to 8-oxo-Gsn and 8-oxod-Gsn respectively. We hypothesize that 8-oxo-Gsn is a superior biomarker to 8-oxod-Gsn for assessing transient and acute incidences of elevated OS due to RNA having a higher turnover rate than DNA. Utilizing a recently published HPLC-MS/MS method, we plan to assess the production of 8-oxo-Gsn and 8-oxod-Gsn in human proximal tubule epithelial cell (PTECs) 2D culture and in 3D microphysiological systems (MPS) in response to induction of OS under experimental conditions. This study will provide insight into use of 8-oxo-Gsn as a urinary biomarker for acute OS in acute kidney injury patients as well as in non-clinical animal safety studies of new drug candidates.

In Vitro Mechanics of Skeletal Muscles of Abdominal Wall and Diaphragm, and Effects of Aging in Mouse.

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Zaina Boriek*[1]; Nora Rodriguez[2]; Aubri Ford[2]; Violet Kimble[2]; Michael Lopez[2]; Shari Wynd[3]; Aladin Boriek[2] and Michael Liebschner[2], *(1)The University of Houston, (2)Baylor College of Medicine, (3)Texas Chiropractic College*

Abstract: Our lab has established that the diaphragm muscle is anisotropic. We tested the hypothesis that in contrast to diaphragm (DIA), the passive length-tension relationships of abdominal wall (AB) are independent of the direction of stretch. In addition, we tested the hypothesis that diaphragm anisotropy is affected by aging. Using an in-vitro biaxial loading apparatus filled with oxygenated Krebs-Ringer solution, a section of the left lateral side of abdominal wall was passively stretched and passively shortened along the fibers (AF) and transverse to fibers (TF) of the external oblique muscle of the abdominal wall. For AB muscles we used three 129SV mice (weight: 19.90 ± 1.82 g; age: 90 ± 8.89 d) and for the DIA we used three 129SV mice (weight: 25.57±6.78 gms; age: 46±20.81 days). We computed the extension ratio, l, at a tension of 0.1 Newton/cm (Diaphragm; AF: l= 1.68±0.08; TF: l= 1.16 ±0.02; Abdominal wall; AF: l = 1.29 ± 0.08 g/cm; TF: l= 1.32 ± 0.13 g/cm). Older diaphragms exhibited a decreased extensibility as demonstrated by a leftward shift in the passive length-tension curves of diaphragms from 2- and 1-yr-old mice relative to 2-mo-old mice. Furthermore, the anisotropy of the diaphragm muscle was reduced in 1- and 2-yr-old mice compared to diaphragm of 2 months old mouse. Overall, upon stretch, abdominal wall exhibited muscle isotropy, whereas muscle anisotropy of the diaphragm was reduced by aging.

Kinematics and Volume Displacement of Lower Rib Cage Is Modulated By Level of Muscle Activation of Diaphragm Muscle in Supine Dogs

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Aubri Ford*[1]; Aladin Boriek[2]; Violet Kimble[3] and Nora Rodriguez[2], *(1)Texas Southern University, (2)Baylor College of Medicine, (3)Drew University*

Abstract: We hypothesized that level of muscle activation of the diaphragm modulates its mechanical interaction with the lower rib cage, particularly at low lung volume. To test this hypothesis we evaluated the effects of unilateral and bilateral activation of phrenic nerve roots on volume displacement and surface area of the lower rib cage. Titanium screws were attached to the lower three ribs. In addition, radio-opaque markers were attached to the peritoneal surface of three neighboring muscle bundles in mid-costal diaphragm in six beagle dogs (7-8.6 kg). Spinal roots of the phrenic nerves (C5 and C6) were identified and isolated on either or both sides of the neck in supine posture. Insulated hook electrodes were then placed under the nerve roots, stimulating them at frequency of 50 Hz. We recorded biplane images before and after stimulation at lung volumes spanning the vital capacity. Marker locations were tracked, and three-dimensional software modeling techniques were used to compute normalized volume displacement relative to surface area of lower rib cage. Extreme muscle shortening of right hemidiaphragm (RHD) caused about 20% lengthening of the passive hemidiaphragm relative to FRC. In contrast, during bilateral maximal stimulation, diaphragm muscle shortened to about 40% of its FRC length. At low lung volume, normalized volume displacement of lower rib cage during unilateral maximal stimulation of RHD was significantly smaller than that during bilateral stimulation ($P<0.01$). Our data suggest that at low lung volume, kinematics and volume displacement of lower rib cage are modulated by level of diaphragm muscle activation.

Hydrogen Sulfide Emission As a Marker of Microvascular Disease in Humans

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Sophia Salbato*[1]; Benjamin Matheson[2] and Nancy Kanagy[2], *(1)University of New Mexico, (2)University of New Mexico Health Sciences Center*

Abstract: Microvascular disease is more common in individuals with diabetes. Undiagnosed, microvascular disease causes irreversible tissue damage and may lead to amputation. Early diagnosis is essential to minimize detrimental outcomes, but current detection methods are insufficient. Production of the gasotransmitter hydrogen sulfide (H_2S) decreases when vascular endothelial cells lose function. Since H_2S is readily diffusible through biological membranes including skin, H_2S emission from skin can potentially function as a biomarker to assess the health of small blood vessels (microvasculature). We developed the transdermal arterial gasotransmitter sensor (TAGS) to measure transdermal H_2S. If TAGS readings correlate with biomarkers of microvascular disease, TAGS could serve as a clinical diagnostic devise for early detection of this condition. This study tested the hypothesis that low TAGS readings will correlate with biomarkers of microvascular disease. The research team measured 12 microvascular disease markers including: body mass index (BMI), high-density lipoproteins (LDL), and hemoglobin A1c (HgbA1c). Biomarker measurements and TAGS readings were made in 15 relatively healthy human participants. Simple linear regression analyses revealed that 2 of the 12 biomarkers significantly correlated with TAGS readings. Triglycerides ($R^2=0.2969$, $p=0.0357$) and blood creatinine ($R^2=0.3991$, $p=0.0205$) both negatively correlated with TAGS. In addition, several other biomarkers trended in the predicted directions. In conclusion, TAGS appears to detect an increased risk of microvascular disease. Increasing sample size to include more individuals with abnormal biomarker levels will help determine whether the TAGS system can detect early stages of microvascular disease.

Attenuation of Sulfur Mustard-Induced Oxidative Stress By Anti-Tnfα Antibody Treatment in Rat Lung

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Chenghui Jiang* and Rama Malaviya, *Rutgers University - New Brunswick*

Abstract: Exposure to sulfur mustard (SM), a blistering chemical warfare agent, is associated with acute oxidative stress in the lung. Tumor necrosis factor (TNF)α, a pro-inflammatory cytokine, plays an important role in the pathogenic response to SM inhalation. In this study, we examined the effect of anti-TNFα antibody treatment on SM-induced oxidative stress in rat lung. Spontaneously breathing male Wistar rats were anesthetized, intratracheally intubated and exposed to 0.4 mg/kg SM by vapor inhalation. After 15 minutes of SM exposure, a subset of these rats was treated with anti-TNFα antibody (15 mg/kg, *i.v.*, 1x). Animals were euthanized 3 days after exposure and lung tissue was fixed and excised. Expression of oxidative stress markers including heme oxygenase (HO)-1 and Ym-1 was analyzed using immunohistochemistry and staining quantified. SM exposure resulted in significant increases in the numbers of HO-1^+ and Ym-1^+ alveolar macrophages as compared to air exposed controls. Treatment of rats with anti-TNFα antibody reduced the numbers of HO-1^+ and Ym-1^+ alveolar macrophages. These findings suggest that blocking TNFα is an effective approach to control vesicant-induced lung injury.

Evaluation of Aeration and Growing Arrangements for Lettuce (*Lactuca sativa*) Grown in Aquaponics Systems

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Maegan Marie Delfin* and Mari Marutani, *University of Guam*

Abstract: Aquaponics is a highly sustainable alternative method for growing crops which combines the benefits of aquaculture and hydroponics. When compared to traditional farming, aquaponics reduces water usage and improves nutrient retention efficiency. With an aquaponics system comes a need for aeration to provide adequate oxygen to plant

roots. By examining the best aeration placement and plant arrangement in an aquaponics system, crop production can be optimized. This study evaluates aeration systems and plant arrangements for lettuce (*Lactuca sativa*) production in an aquaponics system. Aeration treatments included: 1) eight airstones connected to a mounted PVC pipe, 2) eight airstones connected to a submerged PVC pipe, and 3) sixteen airstones connected to a submerged PVC pipe. Within each aeration treatment, three plant arrangements were evaluated: 1) closed raft (18 plants, 10 plugged holes), 2) full raft (28 plants), and 3) open raft (18 plants, 10 holes). All aeration treatments showed a range of 7.8 - 8.5mg/L dissolved oxygen and pH of 7.0 - 7.4. Further study is being conducted to determine the effect of aeration on plant growth and to further investigate flow rate effects. The full raft arrangement showed the lowest leaf biomass possibly due to a higher plant density. Our goal for this project is to redesign aquaponics systems to help maximize crop production and reduce aeration costs.

Early Devonian Glomeromycotan Spores in the Battery Point Formation (Quebec, Canada)

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Madison Lalica* and Nievita Watts, *Humboldt State University*

Abstract: The Early Devonian (Emsian) plant fossil assemblages of the Battery Point Formation (Gaspé, Quebec, Canada) include both compression fossils and permineralized plants. Some of the permineralized fossils have been shown, previously, to host fungal material. This consists of spores found in the cortex or inside the cells of plant axes. The spores are large, with two distinct wall layers, and evidence of hyphal attachment, similar to extant glomeromycotan spores. Our recent investigations of permineralized plants from the Battery Point Formation have uncovered abundant material similar to these previously described spores, as well as other associated structures, such as hyphae and nutrient storing vesicles, that allow us to speculate on their relationships with the host plants. In some instances of excellent preservation, we observe that the presence of the spores alters the host plant tissue. The spores, preserved within trimerophyte axes, cover a broad size range and exhibit diverse morphology, for example showing varying levels of occlusion that are used in taxonomic identification. In terms of size, the spores fall in two distinct classes: small spores, c. 20-80 μm, are smaller than any previously reported; the larger spore category covers a broad size range (90-160 μm). Up until now the classic Rhynie chert of Scotland has provided an abundance of information on Early Devonian plant-fungal interactions. The new Battery Point Formation material, although not as well preserved as that of the Rhynie chert, re-emphasize the importance of permineralized fossils for uncovering plant-fungal interactions deep in the fossil record.

Differential Responses of Nuclear-and Chloroplast-Encoded Genes to Yellow Light in *Chlamydomonas Reinhardtii*

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Ronald Horne*; Adriana Gonzalez; Laura Arce and Amybeth Cohen, *California State University, Fullerton*

Abstract: In the unicellular green alga *Chlamydomonas reinhardtii* the photosynthetic D1 protein is translationally regulated by a set of nuclear-encoded RNA binding (RB) proteins (RB38, RB47, and RB60). The RB proteins bind to a stem loop structure in the 5'-untranslated region of the chloroplast-encoded *psb*A mRNA to activate the translation of D1, which is the primary electron acceptor in photosystem II. While white, red and blue light regulate the transcription of the *rb38*, *rb60* and *psbO* (encodes the Oxygen-Evolving Enhancer protein 1) genes (Alizadeh and Cohen, 2010), the effects of yellow light are unknown. Because the animal-like cryptochrome (aCRY), which absorbs red, blue and yellow light, regulates the expression of several biosynthetic and metabolic genes in *C. reinhardtii* (Beel et al, 2012), the expression of the *rb* and *psb* genes in response to yellow light was explored. *C. reinhardtii* cells were cultured to a density of $5x10^6$ cells/mL before exposure to yellow light for 0 to 120 minutes. Total RNA was isolated and reverse transcribed into cDNA. RT-PCR analyses showed that yellow light induces *rb47*, *rb60* and *psbO* maximally after 90 minutes of exposure, suggesting that aCRY may be involved in regulating these genes. While *rb38* is induced by a number of light qualities, it is not induced by yellow light. As seen with exposure to white, red, and blue light, *psbA* is constitutively expressed. The role of aCRY in regulating the *rb* and *psb* genes will be further tested using aCRY knock-out and rescue strains.

Morphological Analysis and Ecological Niche Modeling of Dwarf Mistletoes in the *Arceuthobium Campylopodum-Occidentale* Species Complex

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Madison Panzino*; Nicholas Torres; Joann Lam; Alisa Hernandez; Jada Smith; Trina Miller; William J. Hoese and Joshua P. Der, *California State University, Fullerton*

Abstract: Dwarf mistletoes (*Arceuthobium* spp.) are highly reduced obligate hemiparasites that attack conifers. The *Arceuthobium campylopodum-occidentale* species complex is distributed throughout Western North America and is notoriously difficult to differentiate; consequently, taxonomists disagree about the number of taxa that should be recognized. We hypothesized that the *Arceuthobium campylopodum-occidentale* complex is composed of separate species, and used morphological analysis and niche modeling to examine its taxonomic diversity. We predicted morphology would

differ across taxa and taxa would occupy distinct niches. We also examined the importance of host distribution and climate in predicting mistletoe distributions. The host niche hypothesis predicts that host distribution mediates parasite distribution, while the parasite niche hypothesis predicts that the parasite's own physiological requirements determine parasite distribution. We compared morphological characters from herbarium specimens of *Arceuthobium abietinum, A. campylopodum, A. cyanocarpum, A. microcarpum,* and *A. occidentale.* Our niche models used occurrence and bioclimatic data for each mistletoe taxon and their hosts. *A. cyanocarpum* is morphologically distinguished from the other taxa by its reduced size, and several taxa had distinct niches. These results suggest that some members of this complex represent distinct species. Our data support the parasite-niche hypothesis, and while hosts are important in predicting mistletoe niches, mistletoe and host niches differ because mistletoes parasitize multiple host species in a subset of their range. *Arceuthobium* is an ecologically important genus, providing habitat and food for animals. By gaining a better understanding of biodiversity in this group, we obtain insight into the eco-evolutionary dynamics of dwarf mistletoes and their hosts.

Regulation of Innate Immunity in Maize By Peptide Hormones

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Miguel Ruiz*; Elly Poretsky; Keini Dressano; Philipp Weckwerth and Alisa Huffaker, *University of California, San Diego*

Abstract: Like animals, plants mount immune responses to protect themselves when attacked by pathogens. A better understanding of how plants recognize attackers and turn on their protective responses will facilitate breeding and development of crop plants that are more resistant to pests and disease, thus enabling long-term food stability. Plant Elicitor Peptides (Peps) are peptide hormones that act as conserved regulators of plant innate immunity. Despite their importance, little is known about how these hormones function in crop plants such as maize. Using genetics, protein biochemistry, transcriptome analyses, and targeted metabolomics, we define here the function of individual maize Peps and their cognate receptors. Activities of these hormones were examined by assessing changes in defense-associated phytohormones, specialized metabolites and global gene expression patterns, in combination with heterologous expression assays and analyses of CRISPR/Cas9-generated knockout plants. Beyond simply delineating individual peptide hormone activities, these experiments led to a number of new insights into Pep signaling mechanisms. In all, seven new maize (Zm) Peps were identified and the peptides were found to have specific activities defined by relative magnitude of response output rather than by uniqueness. Peptide structure-function studies and ligand-receptor modeling revealed structural features critical to ZmPep function and led to identification of a potential antagonist peptide able to competitively inhibit activity of other ZmPeps, a regulatory mechanism not previously observed for this family. Together, our results help define activity of a critical immunoregulatory hormone family in maize and pave the way for better understanding maize resistance to pathogens and pests.

Effect of Chloride Salt Solutions on the Unconfined Compressive Strength of Heat-Treated Clay Pellets Made for the Abatement of Uranium Contaminated Water

Discipline: Materials Research
Subdiscipline: Materials Research

Joshua Herrera* and Antonio S. Lara, *New Mexico State University*

Abstract: Uranium contamination in drinking water is an ongoing crisis for citizens of the Navajo Nation. This problem can be mitigated with locally produced clay pellets known to abate uranium, but parameters that effect the robustness of these pellets must be understood before they are utilized. It is known that chloride salt solutions affect the plasticity and liquid limit of clays, but there is little study on how these solutions alter the robustness of a clay, especially following heat-treatment. This is surprising given how cations affect clay platelet coordination, such as with potassium in illite clays. To better understand this effect, chloride salt solutions were mixed into two clays, a sodium-bentonite clay and a local illite-smectite clay, at specific weight ratios during the pellet fabrication process. The chloride salt solutions used were LiCl, NaCl, and KCl with each at a concentration of 0.8M. The robustness of each set of pellets was quantified by the maximum compressive force (MCF) measured during unconfined compression testing. The addition of NaCl had little to no effect on the pellet robustness. The bentonite pellets maintained a MCF of 700±100 ftlb (n=15) while the illite-smectite pellets slightly decreased in MCF from 2300±200 ftlb (n=15) to 2000±300 ftlb (n=15). The addition of LiCl and KCl, however, has preliminarily shown to increase pellet robustness. The bentonite pellets' MCF increased to 900±100 ftlb (n=5) when using LiCl and 1300±300 ftlb (n=5) when using KCl. This finding suggests that externally added cations can have a significant effect on a pellet's robustness.

Electrospun Electroactive Coated Nanocomposites for Photocatalysis

Discipline: Materials Research
Subdiscipline: Materials Research

Veronica Marin Ponce*; Jennifer Irvin; Mariana Ocampo and Kelli Burke, *Texas State University*

Abstract: Photocatalysis can be used to convert harmful organic contaminants into water and carbon dioxide. Current photocatalytic methods require the use of artificial ultraviolet lamps within expensive infrastructures. Developing areas with a need for clean water are unable to afford such systems. Novel electroactive photocatalytic nanocomposites would

result in affordable and sustainable water purification methods. Electroactive polymers can lower the activation energy required for photocatalytic nanoparticles, allowing solar light to be used. Poly(3,4-ethylenedioxythiophene) (PEDOT) is a widely used electroactive polymer due to its stability and low bandgap (1.6eV). Two PEDOT-containing nanocomposites were investigated to compare their efficiencies as visible light photocatalysts. Methyl orange (MO) dye, at 50ppm, was used as a model organic contaminant. Polyacrylonitrile (PAN) and PAN with titanium dioxide (TiO_2) nanoparticles were electrospun to form nanofiber mats. PEDOT and a PEDOT functionalized with solubilizing dodecyl groups ($PEDOTC_{12}$) were synthesized and used. The PAN and PAN/TiO_2 blends were coated with PEDOT and $PEDOTC_{12}$ via oxidative polymerization. The PAN and PAN/TiO_2 electroactive coated nanofibers were studied photocatalytically using a solar simulator lamp (1 sun) for one hour. Aliquots were taken of MO solutions at regular intervals with and without irradiation. Changes in MO concentration were obtained by analyzing MO absorbance values via UV-Vis spectrophotometry. Results show that PAN/TiO_2/PEDOT and PAN/TiO_2/$PEDOTC_{12}$ nanofibers under irradiation reduce the concentration of MO by 56% and 97%, respectively. These results confirm our hypothesis that the combination of a highly conjugated electroactive polymer and TiO_2 will impart increased stability and boost photocatalytic performance.

An NMR Transport Study of Highly Diffusing Electrolytes

Discipline: Materials Research
Subdiscipline: Materials Research

Brandon Pereira*[1]; David Clarkson[1] and Steve Greenbaum[2], *(1)Hunter College of City University of New York, (2)Hunter College of City University of New York, Dept of Physics*

Abstract: The lithium-ion battery development in the 1980s enabled the functionality of many modern-day technologies, including laptops, cell-phones, and electric tools. However, limitations inherent to the materials used as electrodes and electrolytes have challenged efforts to improve the lithium-ion battery's performance. A principal concern is safety, which is crucial for large-format batteries in electric cars; current liquid electrolyte are flammable. A unique solid polymer electrolyte for the lithium battery has been designed, boasting promising transport properties, energy storage capacity, and enhanced safety features, such as non-flammability. It was developed by Ionic Materials, Inc., a company that our laboratory collaborates with. It contains the electrolyte salts LiTFSI (lithium bis-trifluoro methyl sulfonyl imide) and LiFSI (lithium bis-fluoro methyl sulfonyl imide), and a proprietary solid polymer backbone. We used Pulse Field Gradient Nuclear Magnetic Resonance to measure the self-diffusion coefficient of Li-ions and the salt counterions using Li-7 (Lithium 7) and F-19 (Fluorine 19) probe nuclei, respectively. We used the Stejskal-Tanner equation to determine self-diffusion coefficients of the nuclei at different temperatures for three samples: Rev 2, 3, and 5. Based on the experimental data, the ions in the electrolytes are extremely mobile even at 0 °C. At 0 °C, Li-ions in Rev 5 diffused at 2.2 * 10^-11 cm^2/s while FSI ions in Rev 5 diffused at 2.9 * 10^-11 cm^2/s, both unprecedented in a non-liquid electrolyte, especially at such a low temperature. As such, these materials offer great possibilities for further applications in lithium-ion batteries, particularly for safe and affordable electric cars.

How Long Does Plastic Last in the Environment: A Literature Review and Experimental Case Study

Discipline: Materials Research
Subdiscipline: Materials Research

Briana Prado*, *University of California, Santa Cruz* and Collin Ward, *Woods Hole Oceanographic Institute*

Abstract: Lifetimes of complete and partial photochemical oxidation are estimated to occur on centennial and decadal time scales, respectively. These lifetimes are orders of magnitude faster than biological respiration of polyethylene terephthalates and thus challenge the prevailing assumption that polyethylene terephthalates persist in the environment for millennia. Additives may disproportionately alter the relative susceptibility to complete and partial photochemical oxidation of polyethylene and accelerated breakdown by shifting light absorbance and reactivity to longer wavelengths such as Ultraviolet light. Collectively, sunlight exposure appears to be a governing control of the environmental persistence of polystyrene, and thus, photochemical loss terms need to be included in mass balance studies on the environmental fate of polystyrene. The experimental framework presented herein should be applied to a diverse array of polymers and formulations to establish how general these results are for other plastics in the environment.

Design of a Biomaterial Scaffold for the Delivery of Short Chain Fatty Acids (SCFAs)

Discipline: Materials Research
Subdiscipline: Materials Research

Dora Ogbonna* and Nisarg Shah, *University of California, San Diego*

Abstract: Graft versus Host Disease (GvHD) is an inflammatory disease that is a common side-effect of allogeneic bone marrow transplant. Adaptive immune cells of the donor attack the organ tissues of the host in major organs like the GI tract, Liver. Current treatments leave long lasting damages on the body creating a need for a less damaging treatment. Donor regulatory T cells (Tregs) are key mediators in peripheral tolerance and have been shown to inhibit lethal GvHD in mice by slowing the proliferation of donor T cells while maintaining graft tumor versus tumor activity. Certain small molecules can induce Treg differentiation and their application as a therapy may promote the induction of Tregs and the mitigation of GVHD. We hypothesized that the local sustained delivery of small molecule immunomodulators (SMI) of T cell activation to the affected tissue will enrich Tregs. To test this hypothesis, we designed a biomaterial scaffold to encapsulate and release the SMIs.The biomaterial was made from degradable Alginate and was modified to encapsulate the SMIs. A release assay was performed to record the amount of SMIs released over a period of 30 days. An ELISA was used to quantify the amount of SMIs released over time.. These results derived will guide the optimization of the biomaterial-based SMI carrier as an immunomodulatory therapy. We expect this project to inform the development of treatments for addressing immunological regulation in GvHD and other tissue-specific autoimmune diseases.

Porous Electrospun Fiber Mats for the Recovery of Polyphenolic Compounds in Water

Discipline: Materials Research
Subdiscipline: Materials Research

José Ramírez-Colón*; Eduardo Nicolau; Xaimara Santiago; Simara Laboy; Pedro Méndez; Agnes Ríos and Elix Hernández, *University of Puerto Rico, Rio Piedras*

Abstract: Polyphenolic compounds occur naturally in plants, as part of their defense mechanisms and in marine organisms, as adhesives. The chemical features and functionalities that these compounds exhibit, have made them biomolecules of great interest in food and biomedical industries. This study presents a method to recover polyphenolic compounds from water environments, as a sustainable model, to reuse them for future development of adhesives for water purification processes and biomedical applications. Electrospinning was used to develop a porous mat with high surface area permeable structures based on Cellulose Acetate (CA), granting hydrophilicity and biocompatibility to the produced fibers, and allowing the effective recovery of the targeted polyphenols: Catechol (CAT) and Gallic Acid (GA). The further addition of polyethylene oxide-b-4 vinyl pyridine (PEO-*b*-P4VP) and trimethoxy(2-phenylethyl)silane (TMPES) onto the films improved its selectivity towards polyphenolic adducts via available sites for hydrogen bonding and provided stability to avoid minimal damage of mechanical strength of the films in water. The presence of PEO-*b*-P4VP and TMPES onto the support membranes was confirmed by SEM, EDS and FTIR analysis. Finally, the mats' adsorption capacity was measured using UV-Vis spectroscopy after subjecting them to different concentrations of the targeted polyphenols, within different time intervals. The results showed a maximum absorption of 18 mg of GA and 3 mg of CAT absorbed per gram of composite film at 50ppm, after reaching 4h of exposure. Based on these results, an optimal biomaterial is presented, demonstrating suitability for the recovery of polyphenolic compounds from aquatic environments.

Zinc Sulfide Nanoparticles-Induced Photodegradation of Azo Compounds

Discipline: Materials Research
Subdiscipline: Materials Research

Gabriel Torres-Mejias* and Sonia Bailon-Ruiz, *University of Puerto Rico*

Abstract: Good quality water is essential for proper human health, ecosystem conservation, and socioeconomic development. Nevertheless, with population growth and industrial progression guaranteeing there are sufficient clean water supplies for every person is becoming increasingly challenging. At Present, millions of gallons of industrial wastewater are discharged worldwide without any prior treatment. Although a major part of the problem is indeed the massive waste production, current treatment mechanisms do not meet the required standards of efficiency nor cost-effectiveness. Fortunately, the emergence of novel nanoparticles-induced procedures such as photon-driven Reactive Oxygen Species (ROS) generation has granted an effective yet affordable solution to the water pollution crisis. Based on these statements, we developed the following objectives: 1) Synthesize and characterize Zn-based semiconductor nanoparticles, 2) Conduct photodegradation of azo-dyes such as azorubine and amaranth at different pH, and 3) Determine the degree of reusability of the photocatalytic properties of the nanoparticles. Nanoparticles evidenced to be spherical and of approximately 5 nm in width also was demonstrated that maximum emission occurred at a wavelength of 444 nm and maximum absorption at 302 nm. Finally, the photocatalytic capacities of the nanoparticles showed to be enhanced at higher concentrations.

Nanotoxicity in Aquatic Systems

Discipline: Materials Research
Subdiscipline: Materials Research

Genesis Suriel-Jaquez* and Sonia Bailon-Ruiz, *University of Puerto Rico*

Abstract: Nanoparticles that are semiconductor materials such as cadmium and selenium, have many applications according to the size of the nanoparticle. The size-dependent emission makes these nanomaterials important in light-emitting diodes, photovoltaic devices, solar cells, lasers, and biomedical labels. Selenium and cadmium nanoparticles are used often and constantly reach the environment; consequently, the interest of the toxicity of these nanoparticles has grown in the scientific community. Based on the previously mentioned, the present project has three objectives: 1) synthesis of selenium and cadmium nanoparticles; 2) optical characterization of this nanomaterial; 3) evaluation of the toxicity of CdSe nanoparticles in aquatic organisms. With the purpose of studying the effect of the nanoparticle size in the toxicity of aquatic organisms, two sizes of nanoparticles were fabricated through change of the Cd/Se/TGA (thioglycolic acid) molar ratio. The synthesis of CdSe at Cd/Se/TGA molar ratio of 1/0.05/3.6 showed an emission peak centered at 637 nm; while Cd/Se/TGA molar ratio of 1/0.1/3.6 showed a fluorescence peak centered at 644 nm. The recombination processes of the electron-hole pairs in the CdSe lattice are represented through the emission peaks. Correspondingly, the results showed that the growth of nanoparticles is encouraged by increasing the concentration of selenium, achieving a red-shift. Future works are centered on assessing the effect of particle size in larval stages of aquatic organisms. An inverse relationship of toxicity and particle size is expected.

Bottom-up Synthesis and Raman Spectroscopy of Atomically Precise Graphene Nanoribbons for Nanoelectronic Devices

Discipline: Materials Research
Subdiscipline: Materials Research

Wyatt Jebef[*1]; Zafer Mutlu[2] and Jeffery Bokor[2], *(1)Santa Barbara City College, (2)University of California, Berkeley*

Abstract: Recent advancements in the bottom-up synthesis of graphene nanoribbons (GNRs) have provided ultimate control over GNR width and edge topologies through the rational design and self-assembly of small-molecule precursors on substrates. Since bottom-up synthesized GNRs exhibit homogeneous ultra-narrow ribbon width, atomically smooth edges, and a uniform bandgap, they possess excellent electron transport characteristics and are therefore ideal for use as the channel material in post-silicon complementary metal-oxide-semiconductor (CMOS) transistors. The promising electronic properties and nano-scale size of GNR-based CMOS transistors can lead to the ultimate scaling of high performance digital electronics. However, in spite of all their potential, significant challenges remain for the processing and characterization of GNRs due to their extremely small dimensions. In this work, we address one of the most pressing challenges: large-scale ex-situ characterization of GNRs on both gold and insulator substrates. Seven atom wide armchair GNRs (7-AGNRs) are grown on Au/mica substrates using a throughput ultra-high vacuum (UHV) system and transferred onto SiO2/Si substrates via a wet-transfer method to enable field-effect transistor (FET) fabrication. The ex-situ characterization of the GNRs is performed by scanning tunneling microscopy (STM) and Raman spectroscopy using 532 nm wavelength laser excitation. By varying experimental parameters, such as growth conditions of the GNRs, substrate transfer, and chemical doping of the GNR FETs, we have identified correlations between Raman activity and the material quality and electrical properties of the GNRs - attributes critical to the development of GNR-based nanoelectronics and next-generation devices.

Development of a Novel Additive Manufacturing Method for Fabricating Complex Multi-Material Ceramics

Discipline: Materials Research
Subdiscipline: Materials Research

Samuel Figueroa[*1]; Joshua Pelz[1]; Nicholas Ku[2]; Lionel Vargas-Gonzalez[2] and Marc Meyers[1], *(1)University of California San Diego, (2)US Army Research Laboratory*

Abstract: Ceramics are a class of materials that have gained attention due to remarkable mechanical properties such as high hardness, wear resistance, temperature resistance, and low densities, making them optimal materials for structural applications. However, production of complex structured ceramics that can enhance mechanical properties is almost an impossible task due to limitations of current fabrication technologies. Thus, the development of additive manufacturing (AM) methods are of great interest for advanced ceramic materials development due to the ability to fabricate materials with engineered structures and multi-material compositions for improved mechanical properties.

In this study, we present the design and use of a novel AM system to fabricate multi-material ceramics. Our AM system utilizes a commercially available 3D printer and modified it to print with both multi-material and auger mixing capabilities using B4C and SiC ceramic slurries. The goals of this study are to optimize the processing parameters of this AM method to increase the quality of control of structure and composition variety. 3D modeling softwares are used for fabricating complex structures and analysis of composition change within printed samples is done via scanning electron microscopy and optical imaging. We anticipate that changing design parameters in the machine such as nozzle size, auger pitch, and varying the pressure within the ceramic slurries will allow tailoring of structural and compositional characteristics of gradients within our sample. In the future, we will characterize the mechanical properties of printed ceramic samples to evaluate what compositional changes and structures lead to augmentation of mechanical properties.

Investigating the Structure and Phase Properties of Spider Silk

Discipline: Materials Research
Subdiscipline: Materials Research

Brittany Puzio[*]; Dillan Stengel and Gregory Holland, *San Diego State University*

Abstract: Spider silk is exceptionally strong, lightweight, and biocompatible making it an ideal biomaterial for countless applications in defense, industrial, and medical fields. Dragline silk, the strongest silk spiders make, is assembled primarily from two large (300-350 Kda) intrinsically disordered proteins (IDPs) called spidroins that are synthesized and stored within the major ampullate (Ma) glands dubbed MaSp1 and MaSp2. These proteins are highly repetitive and consist of alternating poly(Ala)n (n = 4-9) motifs interspersed by Gly-Gly-X regions (X = Gln, Pro, Tyr, Ser or Arg), where Pro is found only in MaSp2. Using computational molecular dynamics (MD) simulations, we have identified that Tyr and Pro residues are solvent exposed in solution. We believe these residues are critical in the fiber assembly process and contribute to the high

toughness observed. Our goal is to probe the structure of these alternating regions to understand their role in silk formation and structure-function relationship. Utilizing synthesized silk-like peptides with sequences taken from MaSp1 and MaSp2, we are using solution nuclear magnetic resonance (NMR) spectroscopy to determine their overall structure. We believe there are inter- or intramolecular interactions involving the aromatic ring of tyrosine and proline that are essential to protein structure and stability. Additionally, we are applying differential scanning calorimetry (DSC) to investigate the phase characteristics of these peptides to understand how each motif imparts solubility and stability. Together, this work will inform on key interactions that guide the organization and solubility of spider silk proteins and should be related to intrinsically-disordered proteins in general.

Tri Hybrid Ultra Light Dual Matrix Composites for Bio-Applications

Discipline: Materials Research
Subdiscipline: Materials Research

Christopher Oyuela* and Khaled Morsi, *San Diego State University*

Abstract: The current research is focused on advancing microstructure tunability by designing micro-scale powders for use in novel Tri-Hybrid Ultra-Light Composites for orthopedic implants with superior wear resistance and a modulus that matches that of bone. Previous work from our lab has shown success in dispersing titanium di-boride (TiB_2) particles inside micro-scaled titanium powders to produce composite powders of Ti-TiB_2. These same powders were then mixed and sintered with pure titanium powder to produce Ti-TiB_w dual matrix composites (through a high temperature in-situ reaction that converts TiB_2 to TiB_w). The idea is to produce a titanium composite where the TiB_w reinforcements are not homogeneously distributed but rather occupy regions of the microstructure that are separated by pure Ti. This microstructure creates superior tailorability of the properties and allows significantly improved properties than that of conventional composite, even at the same volume fraction of TiB_w. However, we have previously found that these TiB_w whiskers tend to grow outside the region and go inside the supposedly pure titanium regions. Hence this project expects that by a novel approach one can produce dual-matrix composites with whiskers totally bound within the microscopic regions. This would be accomplished by milling Ti-TiB_2 powders followed by converting the TiB_2 to TiB_w through high-temperature annealing then remilling to entrap the grown whiskers back into the Ti-TiB_w particles followed by mixing with titanium powder and sintering. An additional step will be to add to the Ti-TiB_w/titanium powder mixtures to foaming precursor (Ti-TiH_2) powders to produce tri-hybrid (partially foamed) composites.

Quantum Efficiency of HL-3 Quantum Dots

Discipline: Materials Research
Subdiscipline: Materials Research

Jordan Green*, *Pomona College* and Robert Cobene, *corning Incorporated*

Abstract: Quantum dots are nanoparticles that absorb light and fluoresce at a certain wavelength. The utilization of quantum dot semiconductor particles has quickly become fundamental to a variety of fields in recent years, with their technologies being applied in televisions, solar cells, and in biological screenings. An issue with quantum dots is the efficiency at which they radiate the energy that they absorb. This project seeks to calculate the Quantum efficiency of these Quantum dots at different wavelengths of light.

The experimental setup uses non- cadmium quantum dot films layered on top of a glass slide that is illuminated by a calibrated light source. The reflection is collected by an integrating sphere and then measured by a spectrometer, giving values for the intensity of the light at a given wavelength. With this information it is possible to extract a function for the values of light transmitted and fluorescent by the Quantum dots, and further calculate their Photonic efficiency.

Synthesis of Salicylic Acid-Based Poly(anhydride-esters) Using Two Methods; Melt-Condensation Polymerization and Solution Polymerization

Discipline: Materials Research
Subdiscipline: Materials Research

Diana Lopez* and Kathryn Uhrich, *University of California, Riverside*

Abstract: Polymers are macromolecules consisting of repeating subunits. Biodegradable polymers like salicylic acid-based poly(anhydride-esters) (SAPAE) releases its subunits; salicylic acid (SA) and adipic acid upon upon degradation. SA is known to have antibacterial, anti-inflammatory, anti-pyretic, and anti-proliferative properties, and both SA and adipic acid are biocompatible. Thus, SAPAE polymers have potential in medical applications. Two methods were used to synthesize SAPAE polymers, melt-condensation polymerization and solution polymerization. The goal was to successfully reproduce these two methods and obtain SAPAE polymers in high yield and high molecular weight. High molecular weight allows for longer degradation times. Previous studies show that melt-condensation polymerization is reproducible and gives a higher molecular weight product compared to solution polymerization. Both methods use the same salicylate-based diacid (SAA) as the starting material and produce the same SAPAE product. On a scale of ~7 g of salicylic acid, the overall percent yield for solution polymerization method was 27% with an average molecular weight of 2400 g/mol, measured by gel-permeation chromatography (GPC). The percent yield for the melt-condensation method was 52% and the average molecular weight

was ~3200 g/mol, measured by GPC. Comparing these results, melt-condensation polymerization gives higher yields and higher molecular weight polymers making it a more effective method. But an even higher molecular weight is desired to use the polymer in medical applications.

Performance Evaluation of Silver-Based Nanomaterials Enhanced with Fullerenes As Cathodes Forflexible Zinc-Air Batteries

Discipline: Materials Research
Subdiscipline: Materials Research

Danae Chipoco-Haro* and Juan Carlos Fabian Rodriguez-Reyes, *Universidad de Ingeniería y Tecnología - UTEC*

Abstract: Metal-air batteries are characterized by a high energy density with relatively simple and safe chemistry, which makes them suitable for many applications, especially those requiring flexibility. These energy storage devices consist of an electrolyte, a metal electrode and an air electrode, which enhances the oxygen evolution and oxygen reduction reactions (OER and ORR, respectively). The air electrode is lighter than most metal electrodes present in batteries; therefore, these batteries have a high energy density. However, the most critical problem this technology faces involves the air electrode design, especially because of the requirement of a bifunctional catalyst for OER and ORR.

Here, the enhancement of the OER and ORR reactions of a carbon nanotube (CNT) electrode decorated using silver nanparticles and polyhydroxy fullerenes (PHF) is evaluated. Cyclic voltammetry and charge-discharge tests demonstrated that silver nanoparticles from 60 nm to 70 nm were successfully impregnated over the CNT electrodes and their stability was confirmed. The PHF was also successfully impregnated, but the electrode was not as stable as the only silver nanoparticles electrode. However, the higher current achieved by the latter confirmed the hypothesis, since the presence of PHF enhanced the catalytic activity of silver nanoparticles. This study contributes to the worldwide efforts of the scientific community to develop flexible, small and light batteries and may be a starting point in the use of PHF in components of electrodes.

Predicting ssNMR Shifts through DFT Simulations on Nasicon-Na3+xV2-Xmgx(PO4)3 Cathode for Na-Ion Batteries

Discipline: Materials Research
Subdiscipline: Materials Research

Aryan Zaveri* and Raphaële Clément, *University of California, Santa Barbara*

Abstract: $Na_3V_2(PO_4)_3$ (NVP) has been considered a promising candidate as a cathode for sodium - ion battery (SIB) applications, owing to high structural stability and high Na-ion mobility. In this study, we investigate the structural effects of Mg doping into the NVP framework and a series of $Na_{3+y}V_{2-y}Mg_y(PO_4)_3$ (y = 0, 0.25, 0.5, 0.75, 1.0) compounds via solid-state nuclear magnetic resonance (ssNMR) techniques in combination with first principles calculations. Notably, ssNMR spectra collected on battery electrode materials consist of broad and overlapping signals, due to strong interactions between the nucleus under study and nearby open-shell transition metal ions, and are particularly difficult to interpret. First principles DFT calculations are needed to assist the assignment of individual resonances. This is done using the all-electron gaussian basis set CRYSTAL17 code, which enables us to compute the unpaired electron spin density at the position of the nucleus of interest with high accuracy. In particular, by using the spin-flipping technique (Middlemiss *et al*) it is possible to break down the observed chemical shift into individual contributions from nearby V species and obtain further information on the arrangement of V/Mg in the cathode structure, with important consequences on Na+ ion dynamics and electrochemical properties. Using hybrid Hartree-Fock/Density Functional Theory methods, 23Na ssNMR shifts were found within 75-400 ppm corresponding to each crystallographic environment surrounding Na atoms in the alpha and beta polymorphs of $Na_3V_2(PO_4)_3$. Understanding the different mechanisms of Na insertion and extraction is important for improving the efficiency, understanding, and reliability of future SIBs.

Cerium Oxide Nanoparticle's: Photocatalysis and Toxicity Effects.

Discipline: Materials Research
Subdiscipline: Other Materials Research

Natalie M. Lopés Velasco* and Sonia Bailon-Ruiz, *University of Puerto Rico*

Abstract: Cerium Oxide Nanoparticles are important functional materials because of their interesting applications. These are used as catalytic converters for internal combustion engines, polishing lenses, optical instruments, pigments, and photocatalytic processes. Preliminary studies have reported that CeO_2 has the capacity to destroy organic dyes by the generation of reactive oxygen species (ROS) in aquatic environments. However, there is a concern about the potential adsorption of CeO_2 in aquatic organisms and toxicity in these living systems. Scarce studies about the nanotoxicity of CeO_2 in the aquatic organism have been reported. The objectives of this work were; 1) Characterize Cerium Oxide Nanoparticles; 2) Evaluate the toxicity of CeO_2 in marine organisms; 3) Study the photocatalytic degradation of organic dyes. This Nanoparticles evidenced a high absorption peak in the ultraviolet range, which suggests the charge-transfer transition from O2- (2p) to Ce4+ (4f) orbitals. The toxicity was evaluated in marine crustaceans with different CeO_2 size nanoparticles and at different concentrations from the 0ppm to 1000ppm range. The results indicated that the smallest nanoparticle had a negative interaction in marine organisms with the increase of concentration and exposure time. At 24 hours of exposure, it was observed an increase in mortality with CeO_2 concentrations higher than 100ppm. However, when the exposure time was increased by 48 hours, nanoparticles were toxic at concentrations higher than 10ppm. This nanoparticle could be damaging the cellular structures because of the oxidative stress in the cell. The catalytic activity of CeO_2 is been evaluated in aqueous solutions with different organic dyes.

Correspondence between Standard Young Tableaux and Webs for the Hecke Algebra

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Samuel Heard* and Jonathan Kujawa, *The University of Oklahoma*

Abstract: Classically, representations of the symmetric group are represented using Standard Young Tableaux. Work by Russell, Tymozcko, Rhoades, and others gives an alternate construction using web diagrams. We generalize this approach to the Hecke Algebra. We examine the directed graph for representations of the Hecke Algebra and use this combinatorial object to examine nice properties of the transition matrix between the bases given by Standard Young Tableaux and web diagrams.

Grouping Origamis: More Than Just Paper Folding

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Edray Goins, *Pomona College*; Sarai Gonzalez, *Eastern University*; Elisa Rodriguez, *Ursinus College* and William Sablan*, *University of Guam*

Abstract: An origami is defined as a morphism $\phi: S \to E$ where S is a closed surface and E is an elliptic curve which has one branch point,O_E. Considered geometrically, an origami can be created from a group $(G,*)$ generated by two elements a and b in the following way: if G is generated by a and b, label $|G|$ squares uniquely by the elements of G, glue a square h on the right of square g if $h=g*a$, and glue a square h to the top of square g if $h=g*b$. Let V be the set of vertices of an origami and e_P as the number of squares which are incident to a vertex P. When the edges of the origami are glued together, we obtain a Riemann surface S that has genus g and the origami $\phi: S \to E$ has degree $|G|=\sum_{P\in V}e_{P}=|V|+(2g-2).$ Furthermore, the group G that generates the origami is the monodromy group $\phi,$ and we obtain an equivalent geometric representation of the Fundamental Group $\pi_1(E-O_E)$.

On this poster, we focus our attention on this geometric interpretation of origamis. We first create various origamis from groups generated by two elements and consider their respective Riemann surfaces. Secondly, given an arbitrary origami, we consider the monodromy group G which generates it.

Finding Monodromy Groups for Fuchsian Groups

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Ra-Zakee Muhammad* and Edray Goins, *Pomona College*

Abstract: The triangle groups $\Delta(m, n, k) \subseteq P\,SL2(R)$ have been discovered to be Fuchsian groups, and additionally, each Fuchsian group Γ is contained in a triangle group for some integers m, n, and k. In 2006, Jürgen Wolfart provided a way to compute the monodromy group of a branched cover $\varphi : \Gamma\backslash H^2 \to \Delta(m, n, k)\backslash H^2$.

Prompted by a 1963 result by Leon Greenberg, we are given that every finite group G is the monodromy group of some branched cover. This project seeks to illustrate this using Wolfart's ideas by constructing a Fuchsian group Γ such that the branched cover $\varphi : \Gamma\backslash H^2 \to \Delta(m,n,k)\backslash H^2$ has monodromy group $G \simeq Mon(\varphi)$.

A Catalogue of Monodromy Groups for Fuchsian Groups Abstract

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Javier Ivan Santiago*, *University of Puerto Rico, Rio Piedras Campus* and Edray Goins, *Pomona College*

Abstract: It is known that the triangle groups $\Delta(m,n,k) \subseteq PSL2(R)$ are Fuchsian groups, and that each Fuchsian group Γ is contained in a triangle group for some integers m, n, and k. In 2006, Jurgen Wolfart provided a way to compute the monodromy group of a branched cover $\varphi : \Gamma\backslash H \to \Delta(m, n, k)\backslash H$.

Motivated by a 1963 result by Leon Greenberg, we know that every finite group G appears as the monodromy group of some branched cover. This project seeks to make this explicit using Wolfart's ideas by constructing a Fuchsian group Γ such that the branched cover φ : Γ\H^2 → Δ(m, n, k)\H^2 has monodromy group $G \simeq Mon(\varphi)$.

Computation of Monodromy Groups for Toroidal Belyi Maps

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Rebecca Lopez*, *Marist College*; Edray Goins, *Pomona College*; Chidera Okenwa, *University of California, Berkley* and Adrienne Sands, *University of Minnesota*

Abstract: A \Belyi map $\beta: \mathbb P^1(\mathbb C) \to \mathbb P^1(\mathbb C)$ is a rational function with at most three critical values: $\{ 0, \, 1, \, \infty \}$. We focus on Torodial \Belyi pairs. A Dessin d'Enfant is a planar bipartite graph obtained by considering the preimage of a path on the interval between two of these critical values, usually taken to be the line segment from 0 to 1. Such graphs can be drawn on the sphere by composing with stereographic projection: $\beta^{-1} \bigl([0,1] \bigr) \subseteq \mathbb P^1(\mathbb C) \simeq S^2(\mathbb R)$. Replacing $\mathbb P^1$ with an elliptic curve E, there is a similar definition of a \Belyi map $\beta: E(\mathbb C) \to \mathbb P^1(\mathbb C)$. The corresponding Dessin d'Enfant can be drawn on the torus by composing with an elliptic logarithm: $\beta^{-1} \bigl([0,1] \bigr) \subseteq E(\mathbb C) \simeq \mathbb T^2(\mathbb R)$.

For the purpose of our research, we utilize \texttt{Mathematica} to write code which takes an elliptic curve E and a \Belyi map β to return information about the monodromy group and it's structure. We use a method which solves a system of first-order differential equations allowing our research to focus on several examples of \Belyi maps which appear in the L-Series and Modular Forms Database (LMFDB).

Categorizing Visualizations for Cartographic Groups

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Nicholas Arosemena*, *Morehouse College* and Edray Goins, *Pomona College*

Abstract: A Belyi map is a morphism of degree, N, defined on a compact, connected Riemann surface which is branched at some subset of the points 0,1, and infinity. Its monodromy group is a transitive subgroup of the symmetric group S_n; it is contained in a certain triangle group generated by the permutations sigma_0, sigma_1, sigma_2 in S_n satisfying the relations (sigma_0)^m = (sigma_1)^n = (sigma_2)^k = (sigma_0) (sigma_1) (sigma_2) = (1). The associated Dessin d'Enfant is that bipartite graph whose "black'' vertices are representative of the points in the Domain which man to 0, and the "white'' vertices are the points in the Domain which map to 1, and the edges are all the points in the domain which map to some number between 0 and 1. The monodromy group may be viewed as the cartographic group of this bipartite graph.

In this project, we work in the opposite direction. Say that we are given a triple sigma_0, sigma_1, sigma_2 of permutations belonging to S_n such that (i) (sigma_0) (sigma_1) (sigma_2) = (1) and (ii) G = {(sigma_0), (sigma_1), (sigma_2)} is a transitive subgroup of S_n. There exists a unique bipartite graph which can be drawn on a compact, connected Riemann surface in such a way that its cartographic group is G. This project focused on drawing such Dessin d'Enfants when the Riemann surface has genus 1 or greater by focusing on examples which appear in the L-Series and Modular Forms Database (LMFDB).

A Catalogue of Monodromy Groups for Fuchsian Groups

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Eyob Tsegaye*[1]; Edray Goins[2]; Javier Ivan Santiago[3] and Ra-Zakee Muhammad[2], *(1)Stanford University, (2)Pomona College, (3)University of Puerto Rico, Rio Piedras Campus*

Abstract: It is well-known that the triangle groups $\Delta(m,n,k) \subseteq PSL_2(R)$ are Fuchsian groups, and that each Fuchsian group Γ is contained in a triangle group for some integers m,n, and k. In 2006, Jürgen Wolfart provided a way to compute the monodromy group of a branched cover $\varphi: \Gamma\backslash H^2 \to \Delta(m,n,k)\backslash H^2$.

Following a theorem by Leon Greenberg, we know that every finite group G can be expressed as the monodromy group of some branched cover. In this project, we aim to make this result explicit using Wolfart's ideas by constructing a Fuchsian group Γ such that the branched cover $\varphi: \Gamma\backslash H^2 \to \Delta(m,n,k)\backslash H^2$ has monodromy group $G' \cong Mon(\varphi)$.

Monodomy Groups and Automorphism Groups of Classical Modular Curves

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Vanessa Sun*, *Macaulay Honors College at Hunter College, City University of New York*; Edray Goins, *Pomona College*; Fabian Ramirez, *Sonoma State University* and Samuel Heard, *The University of Oklahoma*

Abstract: It is well known that all Riemann surfaces $X = \Gamma(H^2)$ of genus at least two are quotients of the upper-half plane (H^2) by a discrete subgroup Γ of $PSL_2(R)$. For example, when Γ is a classical congruence subgroup such as $\Gamma_0(N)$, $\Gamma_1(N)$, or $\Gamma(N)$, then the Riemann surfaces, namely $X_0(N)$, $X_1(N)$, and $X(N)$ are well-known. By projecting to the "j-line" X(1) isomorphic to $P^1(C)$, we have Belyi maps $\beta: X \to P^1(C)$, that is, morphisms which are branched above 0, 1, ∞.

In this project, we consider the monodromy groups Mon(β) and automorphism groups Aut(β) of such Belyi maps.

Tight Forests and the Chromatic Polynomial

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Miliano Mikol[*] and Joshua Hallam, *Loyola Marymount University*

Abstract: Let G be a graph without three-cycles. A spanning forest F of G is said to be tight if, for each tree in F, all paths beginning with the smallest vertex of the tree avoid the patterns 231, 312, and 321. The generating function for tight forests of G is equal to the chromatic polynomial of G up to a sign change iff the total order on the vertices of G is a quasi-perfect order. This project strives to determine which graphs have such characteristics by first exploring the following concept: gluing two or more of such graphs to create a new quasi-perfect order graph. We proved that gluing along a single vertex produces our desired result if the vertex is the smallest of at least one graph for every connected pair of graphs. Additionally, we proved that if, for every pair of connected graphs, there are no three cycles and the two smallest vertices of at least one graph are adjacent, then gluing on that edge produces our desired result. Future research will consider other gluing cases.

Music Generation with Markov Chains

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Sarah Redden[*] and Tracy Redden, *College of the Sequoias*

Abstract: A Markov Chain is a mathematical system that experiences transitions from one state to another according to certain probabilistic rules. A main quality of a Markov Chain is that no matter how the process arrived at its present state, the possible future states are fixed. Given a specific song, I was able to track the chord progression, create a matrix describing the probability a note will occur, and use those probabilities to create multiple versions of a new song. We use Markov chains to take into consideration the prevalence one chord occurs after another which gives limitations to this random process. More specifically, we use a discrete time Markov chain which means that the probability of moving to the next state (or chord) depends only on the present state and not any of the previous ones. I was able to mathematically model this by starting with a series of chords in a song, count the transitions, create a matrix with the values, then determine the probabilities by normalizing the matrix. The output is a transition matrix used to determine the probability of each note occurring after so many iterations, which is a Markov model. Since this model is still a random process, even though it has many weighed values and limitations, I was able to use python to model this theory more accurately and display every possible output. In the end, I was able to go through and play some of the songs I generated, which sound like real songs.

Investigating the Oversimplification of Mathematical Hormone Models in Medicine through Comparison to Polycystic Ovarian Syndrome

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Vanessa Montano[*] and Brandy Wiegers, *Central Washington University*

Abstract: There are mathematical models used today that were developed many decades ago. These are models that are still being used to create treatment plans and understand biological systems. For example, the Lacker model is a model of follicle growth and release for female ovulation. The limitations of this model can be investigated by looking at how it needs to be adapted for the population of women who live with Polycystic Ovarian Syndrome (PCOS). We will be examining these systems as a means of investigating the mathematical oversimplification of medical models. To do this we will begin by creating computational code of the basic model and then use adaptations such as those provided by Chavez-Ross et al to modify that computational code. Once both models are verified by comparison and review to past published work we will then look at ways to improve on the accuracy of the model by first doing improved parameterization of the model parameters and making other changes with further experimentation. Once we have finalized those revisions to the models we will present the findings to an informed audience and seek feedback for further improvement of the results. Final work will be presented and published with the goal of opening an avenue for better personalized health care through improved, less biased mathematical modeling

Using Computational Modeling and Three-Dimensional Reconstruction to Predict Pulmonary Function in Cystic Fibrosis Lungs

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Amanda N. Lee[*1]; Ashley V. Schwartz[1]; Rebecca J. Theilmann[2] and Uduak Z. George[1], *(1)San Diego State University, (2)University of California, San Diego*

Abstract: Cystic fibrosis (CF) is an autosomal recessive genetic disorder that leads to mucus accumulation in the lungs, respiratory infections, and early mortality. A commonly used metric to assess pulmonary function is forced expiratory volume in one second, or FEV1. Lower than normal FEV1 readings are an indicator of restricted breathing and poor pulmonary function. Though poor pulmonary function is a major factor in CF, it remains unknown how mucus distribution in the lung is related to FEV1. We have developed a framework to better understand FEV1 by accessing CF severity as a function of mucus distribution in the lungs as indicated by three-dimensional reconstructions of lungs from images acquired by research MRI scans for CF subjects and healthy controls. An image processing algorithm was developed and implemented in MATLAB for this study to automatically quantify the spatial distribution of mucus in the lungs of CF and healthy controls from these images. Additionally, we found a functional relationship between FEV1 and mucus distribution by fitting a quadratic function to the quantified mucus and FEV1 data via least-squares regression analysis. Our model demonstrates that FEV1 is well-predicted in lung regions that are hallmarks of CF. This study is the first of its kind to assess pulmonary function in differing severities of CF subjects and healthy controls as a function of mucus distribution and allows for a better understanding of the effects of CF severity on patients' everyday lives.

Using Mathematical Modeling to Predict the Effect of Vaccination on Measles Outbreaks

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Fabian Ramirez* and Dr. Omayra Ortega, *Sonoma State University*

Abstract: Measles is a highly infectious disease, with a basic reproduction number between 12 - 18, that quickly spreads throughout a population once introduced. However, the lifelong immunity developed by those who recover from measles as well as the development of modern vaccinations suggest that modern measles outbreaks will inevitably reach a disease-free equilibria. In mathematical epidemiology, a model's equilibrium point represent the point at which no disease is present in the population. The purpose of this project is to find and test the stability of the disease-free equilibria of the SIRV model for measles presented by Jansen et al, "Branching Processes: Variation, Growth, and Extinction of Populations." The result of this project demonstrates that measles does indeed have a disease free equilibrium, but in order to be stable we need the vaccination rate to be roughly 10 times that of the overall death rate in the population. This result suggests that vaccination is an effective way to curtail the spread of measles and prevent future out breaks.

Fractal Dimension As a Dimensionality Tool

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Rebecca Bernal* and Hansapani Rodrigo, *University of Texas Rio Grande Valley*

Abstract: A fractal dimension helps to measure the complexity of an object by providing a statistical index of complexity as a ratio, describing on how detailed measurements can increase or decrease as we change a scale. The idea of fractal dimension can be utilized to solve dimension reduction problems associated with big data.

In this work, we demonstrate how fractal dimension can be used as a dimensionality reduction tool using a combination of two scalable algorithms; the box method approach and the fractal dimensionality reduction algorithm. The box method approach allows us to break our data set and compute the fractal dimension. The fractal dimensionality reduction algorithm allows us to compute the fractal dimension of our Gene Expression data set using the backward elimination. To illustrate the concept, we use the Sierpinski triangle as a practice and then applied this dimensionality reduction method to solve high dimensionality problems related to gene expression data.

The Effect of Delayed Setting on the Chemical Plume of Sinking Marine Snow

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Bailey Bass*[1]; Jennifer Prairie[1] and Nicholas Battista[2], *(1)University of San Diego, (2)The College of New Jersey*

Abstract: Aggregates formed from phytoplankton in the surface ocean, often referred to as marine snow, play an important role in transferring carbon from surface waters to the deep ocean. Marine snow is a key food source for copepods, a common type of zooplankton. Copepods can use chemical sensing to detect marine snow, which leave plumes of organic solutes as they sink through the water. However, marine snow does not always sink at a constant rate; previous studies have shown that these particles can slow down at sharp density gradients through a process called delayed settling. This change in settling velocity may change the chemical plume left by sinking marine snow, thus affecting the potential for copepods to find and eat these particles.

In this study, we mathematically modeled the concentration of organic solutes originating from a sinking aggregate to determine how the shape of its chemical plume is affected by delayed settling. Our model uses the advection-diffusion equation in spherical coordinates, applying boundary conditions for when the radius is equal to the that of the aggregate and when the radius is very large. We then solved the equation numerically using the finite difference method in MATLAB. Here, we present our results showing how the chemical plume changes over time and compare our findings to previous work done with a steady-state model. Our findings can help explain how delayed settling may impact a copepod's ability to locate marine snow, and ultimately the marine carbon cycle.

Time-Dependent Scattering By a Sound-Hard Sphere

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Tomas Virgen* and Arnold Kim, *University of California, Merced*

Abstract: Time-dependent scattering in three dimensions is a difficult mathematical problem to solve analytically and numerically. This problem has applications in many different fields including satellite imaging, acoustics, and the physics of colloids. We specifically consider the acoustics problem for scattering off a moving sound-hard sphere. This sound-hard boundary condition corresponds to a no-slip condition in which the surrounding fluid has no velocity on the boundary of the sphere. We seek to develop a new method of solving this problem based on the method of fundamental solutions. For this method, we approximate the scattered field as a linear combination of exact solutions of the wave equation, each of which is the response by a discrete source. The coefficients of each term in the scattered field are then determined as to satisfy the sound-hard boundary condition. This method leads to an effective and efficient computational method of solving this problem.

Investigating Blood Pressure Losses at Junctions in Patient-Specific Simulations

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Elena Martinez*, *Loyola Marymount University* and Martin Pfaller, *Stanford University*

Abstract: Knowledge of cardiovascular pathologies largely relies on an understanding of the fluid dynamics of the circulatory system. However, fluid dynamics can be difficult, expensive, and sometimes impossible to study using traditional experimental techniques. Although reduced-order modelling offers a robust approach to predicting blood flow, existing models do not account for energy loss at bifurcations. When assessing the accuracy of reduced-order models, this energy loss can cause significant discrepancies. In order to find a more suitable method for analyzing cardiovascular flow, we seek to construct a reduced-order model that accounts for pressure drops at bifurcations. We conducted a literature search on junction models for blood pressure loss and built these mathematical formulas using Python. Using OSMSC's Cardiovascular and Pulmonary Model Repository, we will cross-reference the junction models with blood pressure measures at points before and after the bifurcations. We will select the junction model that produces a blood pressure loss closest to that produced by the repository data. This junction model will be implemented to our existing 0D and 1D reduced-order models. A high fidelity model that looks at different anatomies such as aorta, aneurysm, and pulmonary anatomies will serve as ground truth. Our goal is that when compared to the high-fidelity model, these new enhanced 0D and 1D reduced-order models will compute blood flow with greater accuracy than before.

Quantifying the Impact of Chronic Lead Toxicity on the American Bald Eagle Population in the Great Lakes Region.

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Christine Brasic*[1]; Latimer Harris-Ward[2]; Gregoire Moreau[3]; Carlos Bustamante[4]; Jordy Cevallos[4]; Fabio Milner[4]; Leon Arriola[5]; Baltazar Espinoza[4]; Baojun Song[6]; Jose Flores[7] and Marlio Paredes[8], *(1)University of Wisconsin-Whitewater, (2)University of the Pacific, (3)CUNY Medgar Evers College, (4)Arizona State University, (5)University of Wisconsin Whitewater, (6)Montclair State University, (7)University of South Dakota, (8)Universidad del Valle*

Abstract: An American icon, the bald eagle, was placed on the endangered species list in 1967 after its population hit critically low levels due to the reproductive effects of DDT. After DDT was banned in 1972, another environmental contaminant continued to affect their recovery, lead. Ingestion of lead-based ammunition was shown to be the eagles' top cause of death, resulting in 1991 ban of its use for waterfowl hunting. Nearly thirty years later, cases of lead-toxicity in the bald eagle population continues into the present. Noting the 1991 ban excluded other hunting game, the main source of lead is now linked to the fall and winter big game hunting seasons. This coincides with the eagles' scavenging season, resulting in an annual addition of lead to the eagles' diet. Due to their acidic stomach environment, the eagle is especially susceptible to lead-toxicity. Lead-toxicity causes severe clinical symptoms (including death), but also more subtle, chronic symptoms. A bald eagle may suffer from chronic toxicity for many years of its life, resulting in continual physiological damage and affected biological mechanisms, including reduced fertility and metabolism. Its ecological role as both a scavenger and apex predator make the eagle a valuable resource in the assessment of the Great Lakes ecosystem's health. In order to quantify the impact of lead-contaminated food sources on the bald eagle's population of the Great Lakes, we formulated a system of ordinary differential equations to show the progression through the stages of lead-toxicity and its role in the eagle's population dynamics.

A *K*-Means Hypergraph-Based Image Segmentation Algorithm

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Juan Valencia*[1]; Darcy Brunk[1]; Jessica De Silva[1] and Talita Perciano[2], *(1)California State University, Stanislaus, (2)Lawrence Berkeley National Lab*

Abstract: In medical imaging, X-ray micro-tomography is commonly used to construct images of the structure of an organism such as the bones, tissues, and composite materials. One way of processing images is using image segmentation,

which partitions an image into multiple components.The Parallel Markov Random Field (PMRF) algorithm is a graph-based image segmentation algorithm that is able to parallelize the optimization scheme to efficiently process large images. Within the PMRF structure, we implement a hypergraph representation for the image to take into account higher-order relations between the pixels of the image. The hyperedges are formed via a clustering algorithm, specifically k-means, to construct the initial hyperedges. These hyperedges are then augmented to respect the way the graph is partitioned in the PMRF model for parallelization. Then a higher-order energy term is added to take into account the hyperedge relations. Results of this algorithm have shown improved precision from the PMRF algorithm, but as expected, an increase in computational time.

Image Segmentation Via Hypergraphs Using Mean-Shift

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Darcy Brunk*[1]; Juan Valencia[1]; Jessica De Silva[1] and Talita Perciano[2], *(1)California State University, Stanislaus, (2)Lawrence Berkeley National Laboratory*

Abstract: Image processing techniques have continued to advance as experimental facilities generate more complex data sets. The Advanced Light Source at Lawrence Berkeley National Laboratory houses a micro-tomography instrument which uses X-rays to visualize cross-sections of the object and recreate it as a virtual 3D model. This technique is often used in medical imaging due to its ability to see inside an object without destroying it. Segmentation is an image processing technique used to create a simplified representation of the image so that it is more meaningful and easier to analyze. We develop a hypergraph-based image segmentation algorithm that can be parallelized to handle large volumes of data. This algorithm is built off the Parallel Markov Random Field (PMRF) graph-based image segmentation algorithm. We build a hypergraph model of the image using the Mean-Shift clustering algorithm. The hyperedges are then augmented to respect the graph partition used in the PMRF model to allow for parallel computations. When optimizing the associated energy function, we incorporate a higher-order term which calculates the from the hypergraph model. When applied to micro-CT images from the Berkeley Segmentation Data Set, this algorithm is shown to have improved accuracy when compared to previously tested algorithms. In the future, we aim to improve the scalability of this algorithm.

Racism in Red Carding?

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Tiana Chargin* and Susan Mathews Hardy, *Kennesaw State University*

Abstract: As a mixed ethnic first-generation university student, I am passionate about closing the gap in racial inequality and discrimination. Current research has investigated the disparity in pay scale, jobs, college admissions, and even education for people of color. I decided to study disparate treatment in sports after reading an article that analyzed whether the proportion of red cards given to a soccer player was more prevalent for darker-skin-toned players. The original dataset, which consisted of player/referee dyads, was collected on 2053 players. To facilitate these analyses, I compiled it into what I call the player dataset. Each dyad was averaged over all the referees that the player encountered within their career. I then tested whether you can predict if a player will receive a yellow card or red card during a soccer game by the player's color of skin, height, position or country. My research shows that skin tone does indeed predict the average proportion of red cards. Other relationships between the six variables will be investigated with two-sample and K-sample nonparametric and parametric methods including permutation tests, regression, and post-test procedures to detect which subgroups within skin tone, position, etc. are given the most yellow and red cards. Graphics, such as stratified bar charts, stratified histograms, and scatterplots, will be used to tell the story of my results. Ending discrimination and racial inequality is a necessity. Change begins with awareness of the disparate treatment. Disparities documented by statistical research advance diversity more than mere opinion.

Interterventions on Chlamydia and Trichomoniasis Epidemiological Models Based on a Donovanosis Eradication Plan

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Frances Aponte*; Aixamar Aponte and Mayteé Cruz, *University of Puerto Rico at Cayey*

Abstract: Sexually transmitted diseases (STDs) are an epidemic driven by human behavior. Such is the case of Chlamydia and Trichomoniasis within the Puerto Rican heterosexual population between 15-35 years old and general female population, respectively. We aimed to apply an isolation-type quarantine intervention to Chlamydia and Trichomoniasis to study the possibility of eradication or containment of these epidemics. The goal is to assess if the measurements that the Australian Government took to eradicate the Donovanosis epidemic and control HIV cases could be applied to these STDs. We will study the epidemic development by calculating the basic reproductive number (R_0) of the mathematical models of Chlamydia and Trichomoniasis with and without intervention. Then, assess if these interventions in fact can eradicate or only lessen the epidemic. Our preliminary results show that, in effect, the R_0 of Chlamydia and Trichomoniasis decreases significantly, but quarantine was not enough to eradicate the diseases. The reason was partially due to the asymptomatic

individuals that are not yet diagnosed and continue spreading the infections. For Chlamydia, the R_0 decreases 57.28% for women and 52.73% for men, and for Trichomoniasis, the R_0 decreases a 14.04% for women if this intervention is implemented. However, we want to combine additional interventions to figure a plan to eradicate these STDs epidemics in Puerto Rico.

Characterizing the Function of a Multi-Enzyme Complex

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Vinnie Widjaja*; Nabeela Ariqat; Zaeda Blotner; Christopher Jakobson and Daniel Jarosz, *Stanford University*

Abstract: The spatial organization of metabolism is common across all domains of life. Subcellular compartmentalization of reactions is common in biology, allowing cells to control the kinetics of metabolic pathways, and enzyme colocalization may enhance metabolic flux. We are interested in investigating the multi-enzyme complex called the purinosome, which organizes the enzymes of the conserved *de novo* purine biosynthesis pathway. Though the enzymes of the pathway are well-studied, it remains unclear how the organization of these proteins influences metabolism and cellular phenotype. We use a coupled reaction-diffusion model to probe the system in three different organisms (*Saccharomyces cerevisiae, Escheria coli, and Homo sapiens*) and impose relevant physiological conditions. After deriving the kinetic and diffusive parameters for the six enzymes catalyzing the ten step pathway, we predict enzyme and metabolite concentrations, essential to estimating flux and understanding the effect of the purinosome. Characterizing the function of multienzyme complexes, such as the purinosome, is vital to deciphering the effects of higher-order organization of metabolic proteins. Our study will reveal how cells reorganize their contents to adapt in response to environmental stimuli.

Using Theory and Computation to Understand How Organization Influences the Function of a Multi-Enzyme Complex

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Nabeela Ariqat*; Vinnie Widjaja; Zaeda Blotner; Christopher Jakobson and Daniel Jarosz, *Stanford University*

Abstract: Subcellular compartmentalization of biomolecules is common across all domains of life; organizing a system provides a strategy for improving and controlling kinetics in metabolic pathways. To assess whether organizing a metabolic pathway via compartmentalization enhances metabolic flux, we will use a computational model to examine functions and behaviors across a large range of parameters. Our goal is to apply a reaction-diffusion model to an enzymatic system, the purinosome, in *Homo sapiens, Saccharomyces cerevisiae,* and *Escherichia coli*. The purinosome is a multi-enzyme complex composed of 6 enzymes from the de novo purine biosynthetic pathway. It forms under conditions of starvation or depletion of adenine, a key metabolite for genome duplication and growth. Although the enzymes of the pathway are well known, the effects of the purinosome on metabolic flux remain unclear. To understand the function of the purinosome, we estimated concentrations of key metabolites inside and outside the purinosome and established kinetic parameters for the 6 enzymes. Based on these concentrations and fluxes, we can analyze how the purinosome affects metabolic function, providing a framework for experimental observations and helping us formulate experimental designs. Understanding the formation and function of the purinosome will provide insight into how reorganization helps cells adapt to the diverse insults they face from the environment.

Hopscotching Jellyfish: Mix and Matching Contraction Kinematics

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Tierney Baldwin* and Nicholas Battista, *The College of New Jersey*

Abstract: Jellyfish (Medusozoa) have been deemed the most energy-efficient animals in the world. They are soft body marine organisms composed of gelatinous bell, tentacles containing nematocists for prey capture, and either 4 or 8 oral arms. Their simple morphology and nervous systems make them attractive to robotocists, but we do not understand the limits of jellyfish jet propulsion and maneuverability. Traditionally scientists assume a uniform contraction profile when modeling jellyfish locomotion computationally. In this study we used computational fluid dynamics to model jellyfish swimming behavior and shuffled different contraction profiles corresponding to different frequencies and contraction phase kinematics to see how it impacts swimming performance. Complex vortex interactions and wake topologies suggest enhancements in swimming speeds or energetic cost of transport are possible.

Analyzing the Control Measures for the Homeless Population and Quantifying Their Impact on the COVID-19 Epidemic in New York City

Discipline: Mathematics
Subdiscipline: Mathematical Biology

George Avecillas*, *Haverford College* and Fabio Milner, *Arizona State University*

Abstract: An outbreak of Coronavirus Disease 2019 (COVID-19) emerged in Wuhan, China in late December. Within four months, the World Health Organization (WHO) characterized the disease as a pandemic. As of July 10, 2020, the United

States has reported more confirmed cases than any other country, and the count continues to increase. The state of New York has been the hardest hit with 404,000 confirmed cases, 223,000 of which are attributed to New York City (NYC) alone. Given that homelessness in NYC has reached its highest level since the Great Depression and many of the precautionary measures for preventing COVID-19 are not an option for the homeless, a major concern is the contribution of this group to the prolongation of the epidemic. In order to analyze the role of the homeless population in NYC's COVID-19 dynamics, we use a SEIR-like two-group epidemic model, for the homeless and housed populations under preferential mixing. Parameter values and initial states, whenever possible, were defined using publicly available data about COVID-19 and homelessness in NYC. Our findings indicate that a significant number of secondary infections in the population of NYC are due to transmission of COVID-19 via the homeless. This is most directly attributable to the higher effective reproductive number for the homeless population. We use these results to study the efficacy of various control measures.

A Valveless Pumping Technique Based on Insect Hearts and Geometric Asymmetry

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Zain Moin* and Nicholas Battista, *The College of New Jersey*

Abstract: Valveless pumps are found extensively throughout nature. At the earliest stages of life in vertebrates, the heart is nothing more than a mere valveless tube capable of pumping embryonic blood throughout its closed, developing circulatory system. Many invertebrates, like arthropods, also have valveless, tubular hearts. In comparison with the long slender heart tube of vertebrates, insect hearts (dorsal vessel) have a successive chamber-like morphology. A peristaltic-like contraction is suspected to drive the flow of hemolymph in these hearts and the heart is suspected to have a significant role in mixing the hemolymph. In this work, we developed a fluid-structure interaction model for a biomimetic pump based on the morphology of an insect heart, using an open-source implementation of the immersed boundary method. Preliminary scaling studies showed the pump was more effective when pumping at higher intermediate Reynolds Numbers (Re>100). The geometric and kinematic variations explored highlighted significant differences in volumetric flow rates and fluid mixing properties of the pumping system.

A Mathematical Model on the Influence of Diet on Colorectal Cancer

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Dana Winterringer* and Deena Schmidt, *University of Nevada, Reno*

Abstract: It is well known that diet influences health, and can play an important role in certain diseases, such as colorectal cancer. The association between colorectal cancer and diet has been studied widely, sometimes with conflicting results. In this study, we develop and analyze a stochastic model of tumor progression to explore how different dietary factors may influence the risk of developing colorectal cancer. In particular, we use a five state, continuous-time Markov chain model in which each state transition represents progression towards cancer via the inactivation of a particular tumor suppressor gene (TSG). A key step in the model is the inactivation of TSG p53; the final TSG that must be inactivated before a malignant tumor appears, and the most frequently mutated gene in human cancers. It is widely accepted that p53 can be manipulated via diet adjustment or lifestyle changes. Experiments in mice suggest that a low carbohydrate diet reduces mutant type p53 expression, and that glucose restriction depletes mutant type p53 through autophagy. In humans, high red meat intake and a diet with a high glycemic index are commonly associated with an increased risk of colorectal cancer, specifically due to increasing the incidence of mutant type p53. We incorporate these two risk factors in our model to investigate the extent to which different diets can alter rates of p53 inactivation, and hence increase or reduce the risk of colorectal cancer.

Mathematical Model of Myxobacteria Migration in Starving Conditions

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Geron Williams; Joseph Hibdon and Geron William*, *Northeastern Illinois University*

Abstract: Mathematical Model of Myxobacteria Migration in Starving Conditions
Geron Williams, Joesph Hibdon[1]
Department of Mathematics, Northeastern Illinois University
Myxobacteria are non-photosynthetic soil bacteria, which respond to light frequencies forming dynamic multicellular groups referred to as swarms and fruiting bodies as a result of starvation. Myxobacrteria are unique do to societal communication between cells within swarms. Recently, biologists have discovered in the lab that under constant light/dark conditions rings of fruiting bodies are formed. Data also shows that under continuous oscillatory light cycles bacteria cells migrate more and display more sporadic ring formation and periodicity between rings. The near symmetrical ring formations have also been suggested to be results of an internal circadian clock. In our research we have developed an agent based model (ABM) and

equation-based model (EBM) to describe the dynamics of the formation of fruiting bodies. The ABM consists of a NetLogo program developed to simulate the transformation of the bacteria under exposure to varied light conditions The EBM uses differential equations to model the growth, amount of fruiting bodies, and area covered under various light conditions. Our work will be used to further exploration and understanding under specific parameters does fruition of myxobateria occur. Which can be used to categorize similar soil based bacteria.

Dynamics of Converging Polynomials

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Devin Becker* and Joanna Furno, *DePaul University*

Abstract: In this analysis, we explore the complex dynamics of a family of polynomials defined in the extended complex plane by $P(z) = az^m(1+z/d)^d$, where m and d are nonnegative integers, and a is a complex number. We first use the computer program FractalStream to analyze the behavior of this family graphically, with a particular interest in the structures that appear in the Fatou and Julia sets for different parameter values. We find that the behavior of the family is extremely sensitive to our inputs for m, d and a. Apart from known patterns dependent on the parameter values we confirmed graphically, we prove the symmetry of the parameter space about the real axis, some preliminary results on escape radii (i.e. finding expressions for values that are in the Fatou component containing infinity) and the overall limiting behavior of the family.

Creating Dessin D'enfants for Toroidal Belyi Pairs.

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Deion Elzie*, *California State Polytechnic University, Pomona* and Edray Goins, *Pomona College*

Abstract: A Belyi map β: P^1(C) to \P^1(C) is a rational function with at most three critical values; we assume these values to be { 0, 1, infinity}. A Dessin d'Enfant is a bipartite graph obtained by considering the preimage of a path between two of these critical values, usually taken to be the line segment from 0 to 1. Such graphs can be drawn on the sphere by composing with stereographic projection. Similarly, for an elliptic curve E, there is a definition of a Belyi map β: E(C) \to P^1(C). The corresponding Dessin d'Enfant can be drawn on the torus by composing with an elliptic logarithm: β^{-1}[0,1] ⊆ E(C) ≅ T^2(R).

In this project, we use mathematica to write code which takes an elliptic curve E and a Belyi map β to return the Dessin d'Enfant of this map -- both in two and three dimensions. Following a 2013 paper by Cremona and Thongjunthug, we make the elliptic logarithm E(C) ≅ C /λ explicit using a modification of the arithmetic-geometric mean, then compose with a canonical one-to-one correspondences C /λ ≅ T^2(R). Using this, we focus on several examples of Belyi maps which appear in the L-Series and Modular Forms Database (LMFDB).

From 2-Generated Groups to Origamis: Where Geometry Meets Algebra

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Edray Goins, *Pomona College*; Elisa Rodriguez*, *Ursinus College*; Sarai Gonzalez, *Eastern University* and William Sablan, *University of Guam*

Abstract: An origami is a morphism $\phi: S \to E$ to an elliptic curve E which is branched at one point O_E. However, there is a different geometric construction which involves 2-generated groups: if G is generated by two elements a and b, we label $|G|$ squares with the elements of G, and connect square h with square g on the right (top, respectively) if $h = g \, a$ ($h = g \, b$, respectively). If we denote B as the collection of vertices and e_P as the number of edges adjacent at each vertex P, the resulting Riemann surface S of genus g will have an origami $\phi: S \to E$ of degree $N = \sum_{P \in B} e_P = |B| + (2 \, g - 2)$. Moreover, G is the monodromy group of ϕ, so we have an explicit geometric representation of the Fundamental Group $\pi_1(E - O_E)$.

In this project, we consider this geometric construction of origamis in some detail by considering a database of 2-generated groups, we draw various origami. Conversely, we consider how to generate monodromy groups from randomly constructed origami.

Starting from Square One: How Groups and Origamis Are Related

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Sarai Gonzalez*, *Eastern University*; Elisa Rodriguez, *Ursinus College*; William Sablan, *University of Guam*; Edray Goins, *Pomona College* and Sofia Martinez, *Purdue University*

Abstract: Consider a morphism $\phi: S \to E$ which maps a closed surface S to an elliptic curve E which is branched at the singular point O_E. This morphism is an origami constructed geometrically by 2-generated groups where the elements in G are generated by a and b in G. In this geometric interpretation, there will be $|G|$ squares each labeled with a distinct element of G all of which are connected accordingly by composing them with the generators. In constructing the origami, a square h will be glued to the right of square g if $h=g \, a$, and similarly a square h will be glued to the top of square g if $h=g \, b$. Denote the collection of vertices as B and the numbers of edges adjacent to each vertex P be e_P, then the Riemann surface S will have genus g where the degree of its origami $\phi: S \to E$ is $N = \sum_{P \in B} e_P = |B| + (2 \, g - 2)$. Furthermore, the monodromy group of ϕ is G being a geometric representation of the Fundamental Group $\pi_1(E - O_E)$.

In this research, we focus on the geometric construction of origami in detail. Initially, we construct various origami by considering different examples of 2-generated groups. Contrarily, we begin with an arbitrary origami and determine its corresponding monodromy group.

Dessin D'enfants from Cartographic Groups

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Edray Goins, *Pomona College*; Nicholas Arosemena, *Morehouse College*; Yaren Euceda, *University of Minnesota, Twin Cities* and Ashly Powell*, *University of the Virgin Islands*

Abstract: A Belyi map is a morphism $\varphi:S \rightarrow P^1(C)$ of degree N defined on a Riemann surface S which is branched above $\{0,1,\infty\}$. Its monodromy group is a transitive subgroup of the symmetric group S_N; it is contained in a triangle group $\Delta(x,y,z) = \langle \sigma_0, \sigma_1, \sigma_\infty \rangle$ generated by permutations $\sigma_0, \sigma_1, \sigma_\infty \in S_N$ satisfying the relations $\sigma_0 x=\sigma_1 y=\sigma_\infty z=\sigma_0 \circ \sigma_1 \circ \sigma_\infty=1$. The Dessind'Enfant $\Delta\varphi=(B \cup W, E)$, associated with the monodromy group, is the bipartite graph whose "black" vertices are $B = \varphi^{-1}(0)$, "white" vertices are $W=\varphi^{-1}(1)$, and edges $E=\varphi^{-1}([0,1])$. The monodromy group may be viewed as the cartographic group of the bipartite graph.Our objective for this project is to work in the reversed direction. Lets say that we are given a transitive permutation triple $\sigma_0, \sigma_1, \sigma_\infty \in S_N$, which satisfy (i)$\sigma_0=\sigma_1=\sigma_\infty=\sigma_0 \circ \sigma_1 \circ \sigma_\infty=1$ and (ii)$G= \langle \sigma 0, \sigma 1, \sigma \infty \rangle$ and is a subgroup of S_N. Then there exists a special bipartite graph $\Delta \boxed{\hookrightarrow} \rightarrow S$ that can be drawn on a Riemann surface in a way that its cartographic group is G. Essentially for this project we focused on drawing Dessin d'Enfants when the Riemann surface has genus greater or equal to 1 ($g \geq 1$) by using the examples that appears in the L-Series and Modular Forms Database (LMFDB).

Visualizing Toroidal Belyi Pairs

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Edray Goins[1]; Mikaela Nishida*[1]; Deion Elzie[2] and Cameron Thomas[3], *(1)Pomona College, (2)California State Polytechnic University, Pomona, (3)Morehouse College*

Abstract: A Belyi map is a rational function that maps from the Riemann surface to the Riemann sphere with at most three critical values; we may assume these values are {0, 1, infinity}. A Dessin d'Enfant is a planar bipartite graph obtained by considering the preimage of a path between two of these critical values, which is taken to be the line segment from 0 to 1. Such graphs can be drawn on the sphere by composing with stereographic projection. There is a similar definition of a Belyi map when we replace the complex projective line with an elliptic curve. The corresponding Dessin d'Enfant can be drawn on the torus by composing with the elliptic logarithm.

In this project, we use Mathematica to write code which takes an elliptic curve and a Belyi map as inputs and returns Dessin d'Enfant of this map - both in two and three dimensions – as outputs. We make the elliptic logarithm that creates the isomorphism between the elliptic curve and the complex numbers modulo a period lattice of that elliptic curve explicit using a modification of the arithmetic-geometric mean from a 2013 paper by Cremona and Thongjunthug, then compose with a canonical one-to-one correspondences of the complex numbers modulo the period lattice and the torus. Using this, we focus on several examples of Belyi maps which appear in the L-Series and Modular Forms Database (LMFDB).

Analysis of a Length-Structured Density Dependent Model for Fish

Discipline: Mathematics
Subdiscipline: Mathematics (general)

Geigh Zollicoffer*, *University of Nebraska-Lincoln* and Richard Rebarber, *University of Nebraska -- Lincoln*

Abstract: Invasive or superabundant populations can often become dominated by small members. This is usually undesirable, so common management goals for such species are to lower the biomass, skew the long-term population away from dominance by small fish, or both. In order to attempt to better analyze this problem, we propose and analyze a discrete-time length-structured matrix model for fish populations

in which the probability that a fish grows into the next length class is a nonlinear function of the total biomass of the population. We present mathematical results classifying the dynamics that this density-dependent model predicts. This presentation will illustrate these results with numerical simulations for an invasive white perch population and show how the mathematical results can be used to predict the convergence, persistence and/or boundedness of the population as well as an equilibrium structure that is dominated by small fish. We illustrate the results with management recommendations for an invasive white perch population.

Standardizing a Process of Forensic Digital Imaging By Creating an Algorithm for Comparing Image Transformations

Discipline: Mathematics
Subdiscipline: Other Mathematics

Liliana Delgado* and Jennifer Newman, *Iowa State University*

Abstract: There is a lack of scientifically sound methods of comparisons in the forensics fields. This problem expands to the area of digital image comparison. The goal of this research is to find a way to standardize a procedure that image comparison experts use to validate comparisons. In order to do this, an algorithm will be developed in MatLab to compare objects in an image. This will be a very simple object, such as a square. An objective procedure will be used to take an image of this shape and compare it with transforms of this shape. Then a data set will be created with different types of affine transforms of this shape. The intention is to develop a procedure that will result in a distinct match on the shape before and after the transformation. Quantifiable steps will ensure the procedure is consistent, also reducing the error that might arise. Features must be defined, such as the number of features that are needed to determine a match. This procedure that is developed can be used to help standardize the process of image comparison as well as increase consistency among image comparison examiners, and reduce error.

Sparse and Low Rank Regularization for Robust Deep Nets

Discipline: Mathematics
Subdiscipline: Other Mathematics

Everardo Olivares-Vargas*[1]; Constantin Puiu[2]; Louis Maestrati[3] and Jared Tanner[2], *(1)University of Texas Rio Grande Valley, (2)University of Oxford, (3)University of Lille*

Abstract: Deep neural networks achieve state-of-the-art performance in a variety of domains including image classification, machine translation, and text-to-speech. However, dense supervised networks are easily prone to overfit and lack generalization when inputs show slight perturbations. In this project we show how sparse and low-rank representations of neural networks can be more robust to noise and interference caused by an adversarial image attack. We evaluate four state-of-the-art techniques of sparsification and projection to low rank manifolds, for a Resnet-18 trained on a subset of ImageNet. We then assess the regularized networks using the Fast Gradient Sign Method (FGSM), an adversarial attack whose goal is to ensure misclassification. Using our methodology, we are able to show that regularized networks demonstrate significantly improved robustness and stability compared to dense networks, while maintaining competitive accuracy.

HIV and the Black Community in America: A Statistical Analysis By: Alexander Carter 2020

Discipline: Mathematics
Subdiscipline: Statistics

Alexander Carter* and Dr. Omayra Ortega, *Sonoma State University*

Abstract: HIV disproportionately affects the Black community in America. This study answers questions surrounding how significant HIV impacts the Black community as compared to other ethnicities. First we investigate how the different socioeconomic classes and how an individual becomes infected with HIV relate to one another. Shortly after the research began anomalies in the data were found. It was found that Black Americans consistently represented much higher proportions than other ethnicities of those diagnosed with HIV in 2018. Because HIV is so heavily criminalized in America, and because Black Americans are disproportionately incarcerated, there was a need to dig deeper to find out if these proportional differences of HIV were significant. Information from the 2018 census and 2018 data from the Center for Disease Control and Prevention (CDC) were used to draw conclusions about how HIV impacts the 7 different ethnicities identified in the CDC's report. It was found that in a great majority of subcategories, involving age, gender, transmission type, and region of residency; a statistically significant number of Black Americans were disproportionately diagnosed with HIV in 2018, more than any other ethnicity. Black Americans make up 13% of the national population but 43% of all new HIV cases in 2018. This report does not attempt to answer why HIV is disproportionately present in Black communities, but suggestions are made to answer this question.

Bayesian Phylogenetic Inference of Stochastic Block Model on Random Graphs

Discipline: Mathematics
Subdiscipline: Statistics

Yanqiu Guo* and Wenjian Liu, *Queensborough Community College*

Abstract: Determining the reconstruction threshold of a broadcast models on random graphs, as an interdisciplinary subject, has attracted more and more attention from probabilists, data scientist, statistical physicists, biologists, etc. This project analyzes a classification problem on a deep network, by considering a broadcasting process on an infinite communication tree, where information is transmitted from the root of the tree to all the vertices with certain probability of error. The tree reconstruction problem is to determine whether symbols at the *n*-th level of the tree contain non-vanishing information about the root, as *n* goes to infinity. Its connection to the clustering problem in the setting of the stochastic block model, which has wide applications in machine learning and data mining, has been well established. Inspired by the recently proposed "*q_1+q_2*" SBM, our major task is to extend the classical works on the Ising model and the Potts model, by studying a general symmetric model which incorporates the characteristics of both Ising and Potts through different in-community and out-community transition probabilities, and rigorously establishing the exact conditions for the non-tightness of the reconstruction bound. Furthermore, the mentee will concentrate on the phase transition of the reconstructability of this SBM by establishing the distributional recursion and moment recursion by analyzing the recursive relation between nth and (*n+1*)th generation's structure of the tree. The last work of the mentee is to apply numerical analysis and MATLAB to compute rigorously a combination of basic arithmetic operations and simulate the signal propagation on random graphs.

Catching Trout

Discipline: Mathematics
Subdiscipline: Statistics

Natalie Maurice, *Carleton College*; Danielle Sebring, *California State University, Fullerton*; Jaquelyn Valenzuela[*], *University of California, Santa Barbara* and Ron Yurko, *Carnegie Mellon University*

Abstract: Front offices and scouts across professional sports leagues are constantly looking to identify players that outperform their contracts, providing their teams with the best value and competitive edge. In this study, we create a model using data from Major League Baseball’s 2017 and 2018 seasons to distinguish high performing offensive players from their peers. One way to examine their offensive performance is to compare players to all-star players. Mike Trout, an 8-time MLB all-star, is arguably the best offensive player. Using statistical shrinkage methods and logistic regression on player performance data collected from Box Scores and Statcast tracking systems, we uncover which skills (e.g. home runs, stolen bases, walks, hits, exit velocity, and launch angle) distinguished Mike Trout from his peers. The variables identified were used to create a classification model. This model successfully identifies players who had Trout-like monthly performances on various offensive measurements across the two seasons. Thus, the model is an effective way to identify high performing players from their peers and introduce a new way to evaluate offensive performance.

Forecasting Amazon Stock Price Using the Best ARIMA Model

Discipline: Mathematics
Subdiscipline: Statistics

Mariam Alaverdian[*], *Los Angeles City College* and Valarie Poynor, *California State University Fullerton*

Abstract: Time series forecasting is an active area of research that has attracted attention in a variety of applications. One such area of application is the stock market, which plays a crucial role in the economic health of countries around the world. The stock market is comprised of a number of companies in which individuals and corporations may invest. One such company is Amazon.com, Inc. an American-based company that has grown into a multinational entity, peaking the interest of economists and stock investors. The autoregressive integrated moving average (ARIMA) model is a commonly utilized time series model. Due to its powerful forecasting potential yet simple and interpretable model structure, the ARIMA model is an attractive model for stock market predictions. In our research, we considered the problem of selecting the best ARIMA model for the prediction of the Amazon stock. We implemented our analysis using the statistical language R. We selected Amazon.com, Inc.’s daily closing price from July 1st, 2014 to July 1st, 2019 to construct the ARIMA model. Our research carried on the forecast for 5 weeks to forecast the closing price of Amazon.com, Inc. stock that occurred and compared it with the actual value, which tested the accuracy and viability of the model in the short term.

Using standard model selection criteria, we evaluated the forecasting performance of various candidate ARIMA models with a view to determining the best ARIMA model for predicting the Amazon.com, Inc stock price.

From Data to Interactive Visualizations: A Tool for Modeling and Forecasting Longevity across U.S. Sub-Populations

Discipline: Mathematics
Subdiscipline: Statistics

Rosalia Hernandez[*] and Michael Ludkovski, *University of California, Santa Barbara*

Abstract: Longevity analysis provides valuable public health facts that improve quality of life and influence public policy. Analytical dashboards provide graphical displays of data that allows users to identify and share valuable trends and insights on the spot.

This project's objective is to create an interactive and easy-to-use dashboard that statistically models and forecasts mortality trends among racial groups in the United States. These groups are categorized by Hispanic ethnicity, gender, and cause-of-death. Cause-of-death options include all-cause, cardiovascular disease, cancer, stroke, and external causes. Predictions of mortality data would offset the 2 to 3 year lag of compiling such data, allowing us to see what is likely happening right now, to forecast future mortality scenarios, and to illustrate de-noised past trends.

We use Gaussian process regression on detailed mortality data from the Centers for Disease Control Wide-ranging Online Data for Epidemiologic Research. This modeling approach provides simultaneous modeling of metrics used by actuaries for mortality studies: mortality rates and improvement factors. We use Shiny, a free publicly accessible module package in R, to develop our longevity forecasting tool. Shiny provides flexibility in developing interactivity in data visualizations and a platform to deploy them for public access. The longevity forecasting tool interactively engages users to explore and gain a clearer picture of the mortality experiences across different U.S. sub-populations. With this app, we can examine longevity inequalities, diverging, or converging mortality experiences, identify cohort effects, compare mortality improvements among specific populations, and quantify associated uncertainties.

Privacy Profiling and Accessibility: The Ethics of DNA Databases

Discipline: Other
Subdiscipline: Humanities

Sierra Forler* and Samantha Noll, *Washington State University SACNAS*

Abstract: With increasing accessibility to at-home DNA testing kits, the ability to find out your ancestral heritage is easier than ever. But at what cost to you and your family's privacy? Unsolved criminal investigation (Cold cases) are now able to be solved by using 3rd and 4th cousin DNA samples from individuals who have legally consented to upload their information to a database, which police also have access to. This study will be examining a case from Melbourne Florida, where the local police have partnered with a privately owned laboratory to begin building a crime DNA database for the police department of Melbourne. An officer came across a car with five juvenile boys between the ages of 15-16 in 2016. He confronted the boys about multiple car break-ins in the area at the time. After further questioning, he then demanded that one of them provide a DNA sample, which one of the 15-year-olds did. The major issues raised with this case study is the lack of communication and transparency from the interaction between the officer and the boys. Along with the boys are minors who consented to give a DNA sample without parents present. That is why this literature review aims to apply Beauchamp and Childress's principles of biomedical ethics to examine the issues of privacy, profiling, and accessibility to local law enforcement. This literature review is to provide knowledge about current ethical considerations and practices in working with DNA databases to inform policymakers and the general public.

A Qualitative Rhetorical Analysis of COVID-19 Messaging on U.S. Campuses

Discipline: Other
Subdiscipline: Humanities

Jesus Sanchez Orozco* and Sam Robinson, *California State University, Monterey Bay*

Abstract: The world first heard of the novel coronavirus in late 2019. Within months the pandemic had spread around the world impacting millions. Health officials recommended a stop to large gatherings and implemented social distancing. Universities across the United States were faced with an unprecedented challenge of clearing campuses and transitioning to remote instruction. This required quick and clear communication with multiple stakeholders.

This research project examines University messaging collected during the spring terms in which campuses were closing. Our research explores the rhetoric used by colleges and universities while communicating the changes and decisions made due to the COVID-19 pandemic. Using a qualitative rhetorical analysis of approximately 300 messages this study provides insights into the effectiveness of COVID-19 messages, while the pandemic is still active and campuses have much more messaging to do.

Our initial findings show a clear distinction between community colleges and four-year institutions, the message pathos based on the gender of the administrator sending the message, and the number of external resources offered by some institutions. Analyzing and comparing demographic information for the campuses and communities helps us to determine if the communication style matches the audience's needs. Thus far, our data show an issue related to inclusivity and a lack of language access, and little consideration for those who don't have reliable Internet access. We hope to strengthen the rhetoric used by higher education for future crisis communications to be more accessible, diverse, equitable, and inclusive.

Higher Education Is Not Immune to Messaging Mishaps: A Rhetorical Analysis of COVID-19 Messaging on U.S. Campuses

Discipline: Other
Subdiscipline: Humanities

Amelia Parker* and Sam Robinson, *California State University, Monterey Bay*

Abstract: The global pandemic of COVID-19 introduced a multitude of challenges for the nation, including the need to rapidly shift for virtual instruction at university and college campuses. The response from higher education, as well as the *capacity* to respond to an issue of this magnitude, reflects upon the universities' preparedness, ability to pivot in times of crisis, and preexisting care for their students. As such, campus administrators had to communicate quickly with an array of audiences, while keeping in mind the daily changes and decisions being made needed to also be as informative, concise, and widespread as possible. Thus, communication became extremely essential to the implementation of protocol and handling of the crisis.

We have collected COVID-19 related messaging from universities across the U.S., including from two of the largest public university systems in the world: the CSU and UC. We are developing criteria for assessing these messages and their effectiveness through rhetorical analysis in order to examine factors such as accessibility, quality, the inclusion of resources, reading level, diction, and appropriateness for the target audience. Initial findings indicate a difference in messaging between public and private institutions and between the gender of the administrator. We have also noted that despite having a high number of Spanish-speaking constituents in California, universities only messaged in English. By studying the factors in which different campuses handle their emergency communication, we can better understand the resources and care that is essential for a university, regardless of the emergency.

Influence of Synoptic Conditions on Ozone Episodes in the El Paso Juarez Airshed

Discipline: Other
Subdiscipline: Other Professional Fields

Nohemi Beltran*[1]; Nakul Karle[1]; Suhail Mahmud[1]; Daniel Melendez[2] and Rosa Fitzgerald[1], *(1)The University of Texas at El Paso, (2)NOAA National Weather Service*

Abstract: Both the synoptic and mesoscale conditions impact the ground-level ozone formation and accumulation. In order to understand their influence on ozone episodes, a systematic analysis of the synoptic and mesoscale patterns was performed for all the high ozone episodes that were recorded for a period of 7 years, from 2013-19 in the El Paso Juarez Airshed. A total of 57 high ozone days were identified during the study period and were systematically categorized into prevailing synoptic-scale patterns. Mesoscale wind trajectories were analyzed via the Hybrid Single Particle Lagrangian Integrated Trajectory Model (HYSPLIT) for each of the selected episode days. A high pressure ridge at the 500 mb height was observed during all the high ozone days. The high ozone episodes in the region were associated with the presence of a nearby high-pressure system which produced light southeasterly winds. Hence, a large frequency of southeasterly wind patterns were observed on the windroses analysis performed for the region. The stagnant surface wind patterns also played a significant role during these events. The results from this research will improve the understanding of the synoptic and mesoscale meteorology contributing towards high ozone episodes.

Using Exoplanet Formation Theory to Shape NASA's Target Selection for Future Atmospheric Study

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Junellie Gonzalez Quiles*[1]; Sarah Ballard[2] and Elisa Quintana[1], *(1)NASA Goddard Space Flight Center, (2)University of Florida*

Abstract: NASA's Kepler mission has found that M dwarfs can host an abundance of exoplanets. These often seem to be small planets with less than twice the size of the Earth, which are of the most interest due to its potential for harboring life. TESS, the Transiting Exoplanet Survey Satellite, is on the hunt for these types of planets orbiting nearby stars. While TESS will find the planets, it cannot study their atmospheres in search of biological signatures alone. Instead, the James Webb Space Telescope (JWST) will characterize the atmospheres of the most promising planets from TESS. Using simulated TESS data for planets around small stars, we aim to understand the planetary systems around these stars, as well as prioritize those planets that have the most promising atmospheres for atmospheric follow up with JWST. Planet formation theory predicts a relationship between the orbital spacing between planets in a system, and the bulk density of the planets. Using this relationship and a realistic synthetic TESS sample, we apply this theory to predict what the densities of those planets will be. Obtaining these densities is crucial to predicting the thickness of their atmospheres, from which we can make a recommendation as to which planets are of interest to observe with JWST. Most importantly, we recommend the amount of time it would require to observe their atmospheres with JWST, so that the exoplanet community can prioritize this precious resource.

Modeling the Three-Body Sun-Earth-Moon System's Differential Equation and Solving It through Computational Methods to Simulate Its Kinematic Properties

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Alden Andrei Fernandez*, *University of Hawaii at Manoa* and Herve Collin, *Kapiolani Community College*

Abstract: For a two-body system, Kepler's first law of planetary motion states that orbiting masses travel in an elliptical path, with the object being orbited positioned at one of the ellipse's foci. For a three-body system, the motion of celestial bodies are no longer elliptical and are also strongly susceptible to initial conditions. The purpose of this project is to model, solve through computation the three-body system Sun-Earth-Moon, and simulate its kinematics properties.

First, the second-order differential equations containing the dynamical properties of the Sun, Earth, Moon were derived using Newton's second law. The second-order equations were then converted to a set of first-order differential equations describing the kinematics properties of the three-body system. The solution of these equations were calculated using OCTAVE with specific initial conditions. The Sun was modeled to be at the center of our reference frame, and known values of position and velocities of the Earth and Moon were used in the algorithm.

Using a planar circular restricted condition, simulations were obtained to visualize the motion of the Earth and the Moon around an assumed fixed Sun. A range of initial conditions are currently sought to increase the stability of the orbits for an acceptable period of time. A set of ranges for these conditions will be obtained to simulate "stable" kinematics properties of the Earth and Moon systems before chaotic behavior starts to exhibit itself.

Equilibrium Constants of Supernova Explosions

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Marcos Garcia*, *University of Texas at El Paso* and Prof. Jorge Munoz, *The University of Texas at El Paso*

Abstract: A supernova explosion occurs when the mass of a star is so large that gravity brings its constituent electrons, protons, and neutrons very close and provides enough energy for them to ignite a nuclear reaction that combines one electron with one proton and produces a neutron and an electron neutrino. Although the production of neutrinos lasts only for about 10 seconds, the energy produced in this time is larger than the energy that the sun will produce in its lifetime. The expansion of the neutrinos into space is what causes the explosion. We developed a simple classical model of the neutron and proton as symmetric tops in which two of their quarks have the same mass (up quark in the case of the proton and down quark in the case of the neutron) and the third one is different (down quark in the case of the proton and up quark in the case of the neutron) and derived an expression for the equilibrium constant of the reaction in terms of the partition function. The temperature dependence of the equilibrium constant depends on the moments of inertia of the neutron and proton because the partition function depends on the separation between energy states, so we calculated the moments of inertia. We also investigated the case in which the mass of the quarks is distributed throughout the neutron or proton. We show the temperature dependence of the equilibrium constants for the different mass configurations.

Quantifying Star Formation Rate Uncertainties in Compact Starburst Galaxies

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Sofía Edgar*; Natasha Jones; Chidubem Umeh; Christian Bradna; Rebecca Minsley and Aleksandar Diamond-Stanic, *Bates College*

Abstract: The universe forms stars inexplicably inefficiently. There are several possible causes of this phenomenon, including the quenching of star formation by active galactic nuclei and stellar feedback, which can expel gas into the intergalactic medium. Compact starburst galaxies may provide insight into the limits of stellar feedback. These galaxies exhibit the fastest gas outflows and the highest star formation rate (SFR) surface densities of any known star-forming galaxies. We are interested in the connection between stellar feedback and the recent star formation histories of these galaxies. Measuring the recent SFR of galaxies at visible and ultraviolet wavelengths is hindered by the presence of dust, which obscures the light of newly formed stars. However, we can measure the dust luminosity at infrared wavelengths to estimate SFR without directly observing the stars themselves. This requires modeling of the infrared spectral energy distributions, and we use published spectral templates to extrapolate the total infrared luminosity from the existing measurements at mid-infrared wavelengths. While this technique works well for many galaxies, we find that a subset of the galaxies displays infrared colors that do not match a standard set of infrared templates, and we explore the implications of this result for the physical processes heating the dust. We quantify the uncertainty this introduces on estimates of the recent star formation histories of these galaxies and the evidence that stellar feedback has truncated star formation.

SMEAR(Statistical Modeler of Extended Astrophysical Radio Sources) As a Potential Improvement to Epoch of Reionization Foreground Models

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Kelcey Davis*[1]; Ruby Byrne[2]; Bryna Hazelton[2]; Miguel Morales[2] and Kate Rubin[1], *(1)San Diego State University, (2)University of Washington*

Abstract: The twenty-one centimeter emission has the potential to trace the ionization of neutral Hydrogen in the early universe and map its structure. Detection of the signal will require a model of the radio bright foreground. The foreground, which is mostly radio galaxies, is 4-5 orders of magnitude brighter than the signal and will therefore play a crucial role in its detection. Previously, most radio sources have been modeled as bright points to be subtracted from the data and used in calibration. Our approach combines observations of various radio-bright objects over multiple nights to build more accurate models of the radio sky. Data was taken at the MWA (Murchison Widefield Array) and is expected to improve analysis at both the MWA and HERA (Hydrogen Epoch of Reionization Array) telescopes. We do this by using a software package called FHD (Fast Holographic Deconvolution), which models objects with complicated internal structures as many points. We combine these point sources over multiple observations by treating individual points as Gaussian surfaces. We believe that using our new models for calibration of the observations could reduce contamination of the reionization signal from foreground emission. Code used to generate these models will be published in the form of a public Github repository, SMEAR (Statistical Modeler of Astrophysical Radio Sources).

Determining Dynamical Stellar Masses with Niri Data

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Kim Miskovetz*[1]; Keivan Stassun[2]; Trent Dupuy[3] and Jessica Schonhut-Stasik[2], *(1)University of Hawai`i at Hilo, (2)Vanderbilt University, (3)Institute for Astronomy, University of Edinburgh*

Abstract: Mass is one of the most fundamental parameters to measure in stellar astronomy, and the most common methods of doing so often rely on binary orbit monitoring. A more recent method of determining stellar masses uses imaging, astrometry, and radial velocities to directly measure the acceleration that is caused by the gravitational influence of mass. Using this method, acceleration can be obtained from only two samples, given that they are taken some years apart. Dynamical masses can then be calculated as a result. From the *Hipparcos* catalogue, we selected approximately 700 stars with image data gathered with Gemini Observatory's Near InfraRed Imager (NIRI). All data is available on the Gemini Observatory Archive (GOA). Of those 700 stars, we focused on 32 with known or suspected exoplanets, as a means of selecting systems where at least one additional massive body is known. We reduced NIRI image data of these stars using the recently released pipeline DRAGONS (Data Reduction for Astronomy from Gemini Observatory North and South) and for wide double stars we compare our findings to astrometry from *Gaia* in order to validate our methods. These results tell us the spectral types, absolute magnitudes, and angular separations of the stars. We have begun orbital analysis and will later determine the dynamical masses of binary stars from the *Hipparcos-2* catalogue. The masses we find will aid in characterizing these planet-hosting systems.

Search for Extragalactic Tev-Emitting Sources

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Kara Whitaker*, *San Diego State University* and Miguel Mostafa, *Pennsylvania State University*

Abstract: Although charged cosmic rays have been observed up to energies exceeding 10^{20} eV, their origin and acceleration mechanisms remain unknown. The study of gamma rays is an excellent opportunity to study cosmic rays because photons have no electric charge, and therefore come straight to us from their original sources. Having detected galactic sources beyond 100 TeV, the High Altitude Water Cherenkov (HAWC) Observatory is currently the gamma-ray detector with the highest energy reach. Beyond our own galaxy, photons suffer attenuation in the extragalactic background light. Thus, by observing multi-TeV emission from extragalactic sources we would be identifying the most powerful accelerators in the universe. We start our study from a predefined list of relatively nearby extragalactic radio-emitting X-ray sources and search for very-high-energy emissions using data from the HAWC Observatory. If no significant excess is found, we use the HAWC data to determine upper limits at TeV energies for each extragalactic candidate allowing for constraints on the physical parameters of the sources (e.g., energy cutoff, spectral index, etc.). We also identify possible interesting candidates for further studies.

Effects of New Veto Methods on the Pycbc Search for Compact Binary Coalescences

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Brina Martinez*, *University of Texas Rio Grande Valley* and Derek Davis, *California Institute of Technology*

Abstract: The PyCBC search pipeline has been used since the first gravitational wave detection made by Advanced LIGO. To identify gravitational waves from compact binary coalescences PyCBC uses methods of data quality vetoes to flag and remove triggers in LIGO data that are believed to have terrestrial origin. To confidently detect gravitational waves, we need to mitigate noisy data, which in return improves the sensitivity of searches. Current veto methods risk accidentally removing signals and must be finely tuned to prevent a decrease in the search sensitivity. In this investigation, we test different veto methods based on the current set of data quality flags and other detector characterization tools to analyze how simulated signals are recovered by the PyCBC pipeline and the overall change in the sensitivity of the pipeline. We anticipate our results to show an improved removal of many glitches while increasing the significance of signals and the overall number of detectable signals. The results of this investigation can be implemented in the PyCBC search pipeline in future observation runs held by LIGO as a data quality tool to improve the search for gravitational waves from compact binary coalescences.

Ligo's Mystery Black Hole Mergers and Common Envelope Evolution

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Matthew Zárate*[1]; Rosa Wallace Everson[2] and Enrico Ramirez-Ruiz[2], *(1)University of California, Berkeley, (2)University of California, Santa Cruz*

Abstract: This work explores common envelope (CE) evolution of high mass binary star systems as a pathway to the formation of LIGO-type binary black holes (BBHs). CE occurs in a binary star system when one star enters its giant-branch

phase and engulfs its partner. The giant star creates an envelope of gas with a particular density gradient, through which its partner then spirals in toward the giant's core.

A CE event may produce one of three possible outcomes for the binary: the partner and giant's core will merge, remain a wide binary, or become a close binary such as LIGO BBHs.

According to the traditional energy formalism, there is potential in high mass systems for excess energy produced by the inspiraling partner to eject the envelope at a separation too wide for the resulting BBH to merge.

Through analysis of 1D stellar evolution simulations from MESA (Modules for Experiments in Stellar Astrophysics), we predict the physical outcomes of various binary systems undergoing CE evolution.

Applying physically motivated adjustments to the traditional energy formalism, we produce new insights relating to conditions necessary for the existence of LIGO BBHs and their resulting populations. This work aims to solve the excess energy problem of BBHs that would result in too large of a separation to merge in the age of the universe.

We explore the viability of a general description for CE as a pathway for BBH mergers detected within recent years, clarifying the significant considerations within CE when creating specific LIGO BBHs.

Studying Galaxy Outflows with Spatially Resolved Spectroscopy

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Edgar Sarceno*; William Jaekle; Rebecca Minsley and Aleksandar Diamond-Stanic, *Bates College*

Abstract: Observing how matter flows into and out of galaxies is critical for understanding how galaxies evolve with cosmic time. In particular, the negative feedback process associated with gas outflows driven by star formation has been proposed to explain why star formation in galaxies is so inefficient. We seek to test this hypothesis by identifying which galaxies display signatures of galaxy outflows. Spatially resolved spectroscopy allows us to map the movement of gas between the interstellar medium within galaxies and the circumgalactic medium surrounding galaxies. We use data from the Mapping Nearby Galaxies at Apache Point Observatory (MaNGA) survey, which is producing spectral maps of 10,000 galaxies as part of the Sloan Digital Sky Survey. We identify a class of galaxies harboring signatures of stellar driven outflows based on kinematic properties of their emission lines, which trace ionized gas. This is based on velocity asymmetries and the velocity dispersion of gas above and below the galaxy disk. We find that galaxies with higher surface densities of star formation are more likely to have outflow signatures. In particular, we find statistically significant differences between the galaxies with outflow signatures and those without when looking at total star formation, the surface density of star formation, and the ratio of star formation to stellar mass. In conclusion, our findings support physical models in which higher levels of star formation yield stronger, more pronounced outflowing winds.

Tidal Stripping of Two-Component Systems

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Peter Santana*, *University of Puerto Rico, Mayaguez* and Nicole Drakos, *University of California, Santa Cruz*

Abstract: In minor mergers, smaller dark matter halos fall into larger host halos and lose mass through tidal stripping, while the remaining bound material may exist as substructure within the host halo. The ability to accurately predict the evolution of tidally stripped halos is important for understanding galaxy formation and testing the properties of dark matter. The aim of this project is to see how two-component systems are tidally stripped in energy space. One approach to studying dark matter halos is through the use of isolated N-body simulations, one example being that tidal stripping is often simulated using an isolated satellite in a static background potential. We are using GADGET-2 to simulate the evolution of the density profile and mass loss of a two-component sys- tem, and studying the process in energy space. This will ultimately lead to a better understanding of the mechanisms involved, and allow us to develop a physical model of the stripping of multiple component systems.

Exoplanet Imaging: Studying Clouds on Other Worlds with Polarimetry

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Filiberto Padilla*, *Butte Community College* and Rebecca Jensen-Clem, *University of California, Santa Cruz*

Abstract: Among the thousands of exoplanets that have been detected, only a select few dozen have been directly imaged. Because direct imaging allows us to take a spectrum of a planet's atmosphere, it allows us to obtain new information crucial to our understanding of a planet, such as the composition of the clouds that often envelop the planet. Clouds can also polarize exoplanets' thermal emission. A newly-developing instrument for exoplanet imaging named the Santa Cruz Array of Lenslets for Exoplanet Spectroscopy (SCALES) will possibly provide us with signal-to-noise ratios high enough for us to be able to detect the predicted 1% linear polarization signal due to clouds. In this poster, we present signal-to-noise ratios of known directly-imaged exoplanets when observed by SCALES. There are constraints to which already discovered exoplanets must abide by to be observable by SCALES. If the exoplanet fits within these conditions, then we will utilize evolutionary models to determine the planet's probable luminosity based on its age and mass. This project's results yield

the potential to pave the way to new findings and discoveries that could very well alter our conclusions we've made about the universe and it's variety of astronomical bodies.

Measuring the Covariance between Galaxy Cluster Properties Using Cosmological Hydrosimulations.

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Adam LaFontaine*[1]; Alexie Leauthaud (Prof UCSC, PhD)[2]; Joe DeRose (postdoc UCSC+Berkeley, PhD)[2]; Johannes Lange (postdoc UCSC+Stanford, PhD)[2] and Christopher Bradshaw (Grad student UCSC)[2], *(1)University of California, Berkeley, (2)University of California, Santa Cruz*

Abstract: One of the most important problems in astrophysics is understanding the makeup, or cosmology, of our universe. We know that ~95% of the universe consists of dark matter and energy, but have little knowledge about the exact cause of these phenomena. The spatial distribution of galaxy clusters, the largest structures in our universe, can answer these cosmological questions and in the next decade a number of large surveys (LSST, eROSITA, Simmons Observatory) will observe many clusters. In order to combine these multiwavelength surveys, we need to understand the covariance between their observables (e.g. Stellar mass, X-ray luminosity).

We propose to measure these covariances in the IllustrisTNG hydrosimulation. The TNG simulation accurately reproduces these observables and has a large enough volume (300 Mpc3) to provide statistically significant results. Using a simulation is useful as we have full information about the clusters, but we plan to later perform a similar analysis in observations. Initially we will focus on reproducing the results from Farahi+2018 in the BAHAMAS simulation and LOCUSS observations. We will then focus on measuring the covariance between newly developed properties designed for next generation surveys, the cen+N mass (Bradshaw+2019) and M★,100 mass (Huang+2018).

We have already verified the negative correlation between central galaxy mass and cluster richness, and plan to begin working on the X-ray features. Completing this work will both improve our understanding of the physics of galaxy clusters, and better allow us to use clusters to infer cosmology.

Improving the Precision of Exoplanet Atmospheric Detections through Pixel-Level Decorrelation (PLD)

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Kevin Ortiz Ceballos*, *University of Puerto Rico - Río Piedras* and Néstor Espinoza, *Space Telescope Science Institute*

Abstract: The study of planets around stars other than our Sun is an exciting endeavor that has been substantially limited by the long distances to these planets. Some decades ago, only basic properties such as the time they take to orbit their stars could be determined. Current astronomical telescopes at the forefront of our technological capabilities are now able to observe the atmospheres of these planets through spectrophotometry, detecting the elements that make up these distant worlds. These detections are, however, difficult, and laden with instrumental systematics that contaminate these weak signals. Thus, the challenge of removing these systematics to achieve higher precision in these detections must be solved to obtain improved results.

This presentation will report our efforts to employ the technique of Pixel-Level Decorrelation (PLD) to observations of exoplanets performed with the Hubble Space Telescope. In PLD, the data itself is used to remove the systematics, without using external models or parameters. PLD has been tested for photometry but not yet for spectrophotometry. We specifically report the first results of our attempts to use PLD with both the STIS and WFC3 detectors of the Hubble Space Telescope. Our ultimate goal is to exploit the precision of exoplanet atmospheric detections for current and future telescopes such as Hubble and the James Webb Space Telescope. If successful, this technique could become the standard future exoplanet observations.

An Asteroseismic Age for a Solar Type Star in a Wide Binary with an M Dwarf

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Erica Sawczynec*[1]; Jennifer van Saders[2]; Daniel Huber[2]; Jason Curtis[3] and Nicholas Saunders[2], *(1)University of Hawaii at Manoa, (2)Institute for Astronomy, University of Hawaii at Manoa, (3)Department of Astrophysics, American Museum of Natural History*

Abstract: M dwarfs are popular targets for modern surveys as they are the most numerous and longest-lived stars in the universe. Their close habitable zones make them ideal candidates for finding exoplanets using typical planet-finding methods. Being able to estimate the ages of M dwarfs is crucial; young M dwarfs produce high energy flares which may affect the atmospheres of and the probability of finding bio-signatures on surrounding planets. However, estimating the ages of M dwarfs is challenging, and conventional techniques often fail. Some age-dating techniques, such as period-age relations, could be widely used, but require further calibration. The system HIP 43232, comprised of an M dwarf in a wide binary pair with a late F type star, can provide a benchmark for such calibration as ages of solar-like stars can be estimated using asteroseismology. Asteroseismology is the study the oscillations in stars using the visible pulsations to determine stellar properties such as age, radius, and mass. Here we present the stellar parameters of the late F type star in HIP 43232 derived using asteroseismology utilizing data from the K2 survey. Additionally, we present the stellar parameters and rotation period of the M dwarf and their implications for testing M dwarf spin down.

Imaging Simulated Exoplanets with the James Webb Space Telescope

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Jea Adams*, *Amherst College* and Jason Wang, *California Institute of Technology*

Abstract: Over the past decade, society has had the incredible opportunity to peer into thousands of newly discovered worlds known as exoplanets - planets outside our own Solar System. The launch of the James Webb Space Telescope (JWST) in 2021 will revolutionize astronomy by providing the first characterizations of exoplanets at 3-13 microns, the infrared range where these objects are their brightest. This is of particular interest to the field of direct imaging, a technique that aims to capture images of exoplanets often hidden behind immensely bright starlight at visible wavelengths. pyKLIP is a python library that has substantially advanced imaging by allowing its users to empirically model and remove excess starlight from imaged extrasolar systems, but it isn't presently capable of handling incoming James Webb data. In preparation from the launch of this telescope, we aim to develop and refine pyKLIP data analysis tools in order to create a functional data reduction pipeline. Using simulated data of an extrasolar system observed by JWST's Near-Infrared Camera (NIRCAM), we have 1) established pyKLIP's ability to isolate and subtract the stellar light from an image to reveal exoplanets, 2) computed NIRCAM's sensitivity to exoplanets at various separations from the star, and 3) upgraded pyKLIP to more accurately determine the brightnesses and positions of exoplanets. Our analyses have been publicly released as Python/Jupyter notebook tutorials to facilitate a goal of swiftly disseminating early JWST results to the community, allowing astronomers to optimize observing programs during the telescope's limited lifetime.

Biases in Orbit-Fitting of Directly-Imaged Exoplanets

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Rodrigo Ferrer Chavez*[1]; Jason Wang[2] and Sarah Blunt[2], *(1)Autonomous University of Yucatan, (2)California Institute of Technology*

Abstract: Over 4000 exoplanets have been discovered as of 2020. With such a large and varied set of known exoplanets, there is a greater interest in understanding their properties and histories. One of the ways this can be achieved is by studying the orbit of the planet and its elements, like the eccentricity and the inclination of the orbital plane. However, exoplanets detected via the direct-imaging technique are often only observed for a very small fraction of their period, making it challenging to reliably estimate their orbits. The aim of this project is to investigate biases in the estimation of orbital parameters of directly-imaged exoplanets, particularly their eccentricities, and to define general guidelines to perform better estimations. For this, we constructed various orbits, and generated mock data for each spanning a representative portion of its orbital period. We ran orbit-fitting algorithms with those data sets to obtain orbit estimates, and compared those with the values of the original orbit. We found that the inclination of the orbital plane is the parameter that most affects our estimations of eccentricity, with orbits that appear near edge-on producing highly biased eccentricity distributions. We also found that for near face-on orbits, the mode is in general a better estimator of eccentricity than the median. Our results will be beneficial to the exoplanet-imaging community, since we propose practical recommendations, guidelines and warnings relevant to orbit-fitting.

Over-Massive Brown Dwarfs

Discipline: Physics & Astronomy
Subdiscipline: Other Physics & Astronomy

DORSA Majidi*, *University of California Los Angeles* and John Forbes, *Flatiron Institute*

Abstract: Brown dwarfs are stellar objects with masses too low to fuse hydrogen in their cores. The dividing line between low-mass hydrogen burning stars and brown dwarfs, called the hydrogen burning limit, is about 0.07 solar masses. Under special circumstances, for instance collisions or binary interactions, it is possible for a brown dwarf to gain mass. If a brown dwarf gains enough mass to bring it above the hydrogen burning limit, does it become a low mass star, i.e. does fusion ignite in its core? The answer depends on whether the core is heated in the course of this process. A collision will likely ignite a new star, but if mass is added sufficiently slowly to a sufficiently old brown dwarf, then according to recent results a new, as-yet-unobserved, variety of "over-massive" brown dwarf may be formed. While over-massive brown dwarfs are allowed to exist according to the laws of physics, the rate at which mass can be added to a brown dwarf before it ignites as a star is highly uncertain. This critical rate determines which astrophysical circumstances may produce over-massive brown dwarfs, and hence how common they are in the Galaxy. We are employing the MESA stellar evolution code's binary evolution model to learn the fate of brown dwarfs gaining mass under different scenarios. We are currently studying the most promising scenario which is mass transfer via accretion from an AGB wind. So far, we have been able to create an over-massive brown dwarf under realistic conditions.

BOD Carbon: A Tunable Morphology

Discipline: Physics & Astronomy
Subdiscipline: Physics

Aaron Austin* and David McIlroy, *Oklahoma State University, Stillwater*

Abstract: Our group has successfully synthesized a new mesoscopic material via Chemical Vapor Deposition (CVD) technique in an attempt to dope boron on a form of Pseudo-Graphite known as GUITAR. By adding a boron precursor into the solution we discovered new mesoscopic structures that have formed with varying tubular morphologies. We call these novel structures BOD (Boron Orthocarborane Doped) Carbon and intend to explore their growth characteristics and possible applications. Some of these applications include hydrogen storage and improved battery technologies. Chemical vapor deposition is the technique used to grow this material. Through this method we flow nitrogen into a flask that is heated on a hotplate. The vapor is then carried through a tube furnace at 900 °C where the structures are then grown for various times. We have found that by manipulating time of the reaction and amount of boron in our mixture as well as cooling rate we can create different morphologies. Due to the nature of the material growth we hypothesize that it is possible to tune the structures to vary in their application. For instance, an important aspect of improving Li-Ion batteries is surface area of the electrode material. Naturally, BOD Carbon has a high surface area due to the tubular structure increasing the storage capacity and performance of Li-Ion batteries. In the future, we plan to further tune the structure and growth of this material in order to better understand the influence of outside elements in the reaction.

Cavity Time-Dependent Nuclear Dynamics Via Exact Factorization

Discipline: Physics & Astronomy
Subdiscipline: Physics

Phillip Martinez*, *Hunter College of the City University of New York* and Neepa Maitra, *Physics Department Rutgers University-Newark*

Abstract: The study of cavity light-matter interactions, are essential to many areas in science such as chemical physics, engineering, and even the detection of gravitational waves. Theoretical quantum mechanics provides the platform into which fundamental limits in our reasoning of such systems are reached and they illuminate phenomena that platforms in application must include if we are to reach those limits in life. Previous methods used for studying molecular systems have been shown to be difficult in application. With Exact Factorization, a complete picture of the dynamics in such systems are obtained since this provides the Exact Time-Dependent Potential Energy Surface which yields the full information of the system previously lost in the Born-Oppenheimer approximation and subsequent methods. With our approach, we solve Shroëdinger's Equation using a Hamiltonian that fully accounts for the system which we are able to factorize into a product of sub-systems, one nuclear and one electron-photon, without losing any information of the their couplings. We are able to recover time-dependent mechanisms describing nuclear motion, photon-coupled electron-transfer, and suppression. These equations are solved via software for a model of cavity induced suppression or enhancement of proton-coupled electron transfer and we generate and plot data describing the dynamics and we show that a TDPES is needed to recover mechanisms of said dynamics. We therefore assert that models built on E.F. will prove to be a more useful approach in the relevant applications as needed and that the model is a fundamental step in the study of many-bodied quantum mechanics.

Simulating Entanglement in the Coherent Ising Machine

Discipline: Physics & Astronomy
Subdiscipline: Physics

Shraddha Anand*; Edwin Ng; Ryotatsu Yanagimoto and Hideo Mabuchi, *Stanford University*

Abstract: Solutions to combinatorial optimization problems, like the Travelling Salesman problem, have numerous applications from analysis of large data sets, circuit design to drug discovery. From a theoretical perspective, this class of problems includes many NP-hard problems: problems for which no classical polynomial-time algorithms currently exist. Due to the existence of mappings, solving one NP-hard problem efficiently would enable us to solve all NP problems, with polynomial overhead. Consequently, several attempts have been made to find alternatives to the current von-Neumann architecture to improve computational power. A novel machine called the Coherent Ising Machine (CIM) uses networks of coupled optical parametric oscillators to represent a fully-connected spin network of the Ising problem. Since the Ising problem is NP-Complete, one can map NP problems onto the CIM. However, its current implementation relies on local operations and classical communication, and is devoid of entanglement which can potentially be leveraged to reduce computation time. While non-Gaussian effects are possible in the single-mode basis with the entire system dynamics being simulable, the simulation becomes intractable on adding entanglement. As a compromise, we perform a model-reduction of the CIM based on the quantum projection filter formalism assuming that optical states are approximately Gaussian, as expected in a system with low non-linearities. By construction, we cannot claim exponential speed-up, but we may observe a polynomial speedup. Additionally, we have developed a simulation based on our formalism to probe the computational consequences of adding entanglement between the initial vacuum states of the system via an entanglement swapping protocol.

Understanding Phosphate-Based Structures in b-Li3PS4/Polyethylene Oxide Composite

Discipline: Physics & Astronomy
Subdiscipline: Physics

Jeremy Barrios*, *Hunter College, City University of New York*; Daniel Morales, *Graduate Center of City University of New York*; Lauren O'Donnell, *Hunter College of City University of New York* and Steve Greenbaum, *Hunter College of City University of New York, Dept of Physics*

Abstract: b-Li$_3$PS$_4$ is a solid-state ceramic electrolyte with a promising conductivity but poor interface interaction between electrode and electrolyte. Polyethylene Oxide (PEO) is a polymer-based electrolyte with an insufficient ionic conductivity on its own but suitable interface interactions. Nuclear Magnetic Resonance (NMR) spectroscopy is used to determine the structural characteristics of the electrolytes composite. This gives insight on possible changes resulting from different ratios of PEO to b-Li$_3$PS$_4$ and thermal treatment temperatures.

Magic Angle Spinning NMR is used to probe changes in molecular structure resulting from mixing different ratios of Li$_3$PS$_4$ and PEO. Three samples treated at 45 ^{o}C had PEO percentages of .2%, 1% and 5%, and two treated at 140 ^{o}C where had PEO percentages of 1% and 5%. These samples provided by Oak Ridge National Laboratory where packed in an argon filled glovebox and the Phosphate Spectra was examined using MAS NMR.

There peaks found at 86.2 ppm denoting presence of b-Li$_3$PS$_{4.}$ Additionally, peaks at 83 ppm represent PS$_3$O^{3-} and PS$_4^{3+}$. The wide curvature with an apparent peak near 93 ppm shows presence of the P$_2$S$_7$. The spectrums showed peaks at 88.6 ppm which what is consistent with where g-Li$_3$PS$_4$ is seen. g-Li$_3$PS being a different phase of Li$_3$PS with a crystalized structure as opposed to b-Li$_3$PS$_4$ ceramic one. It also displays much lower ionic conductivity than its beta counterpart. The presence of g-Li$_3$PS within the samples was unexpected and requires further questioning into how it arose in our samples

Exact Sum Rules for Approximate Ground States

Discipline: Physics & Astronomy
Subdiscipline: Physics

Ken Luu*[1]; Calvin Johnson[1] and Yi Lu[2], *(1)San Diego State University, (2)Qufu Normal University*

Abstract: Electromagnetic, weak, and other transitions tell us a great deal about the structure of atomic nuclei. Yet it is often easier to compute the ground state, if only as an approximation, than a full spectrum of excited states, which makes testing transitions difficult. One alternatives are through sum rules, in particular the non-energy-weighted and energy-weighted sum rules, which can be written as the expectation value of an operator. To explore this, we compute the sum rules for a variety of nuclei, comparing the numerically exact full configuration-interaction shell model, as a reference, to Hartree-Fock, projected Hartree-Fock, and, where practical, the nucleon pair approximation.

Automatic Leptonic Tensor Generation for Beyond the Standard Model (BSM) Models

Discipline: Physics & Astronomy
Subdiscipline: Physics

Diego Lopez Gutierrez*, *Macalester College* and Joshua Isaacson, *Fermi National Accelerator Laboratory*

Abstract: The Standard Model (SM) is one of the most accurate theories of nature that explains most, but not all, of the phenomena in the universe. Beyond the Standard Model (BSM) theories seek to describe the realm of new physics outside the SM. Neutrinos are particles at the forefront of research because of their potential to give us information about BSM physics. Starting this decade, experiments such as the Deep Underground Neutrino Experiment (DUNE) will answer fundamental questions about neutrinos. With colossal amounts of data, testing of our neutrino BSM models will be crucial for the analysis. First, however, we need to know what we are looking for, but BSM processes can be too complex to calculate by hand. Thus, we employ event generators to simulate the physics of our theory and perform calculations. These event generators require two components (a hadronic and a leptonic tensor) to make predictions that physicists can compare to experiments. For neutrino event generators, the hadronic tensor is the same in all cases, so we expect new physics to appear in the leptonic tensor. Unfortunately, the time to implement a BSM theory in an event generator can take up to a year. With many BSM theories, this time constraint is unfeasible. Hence, we seek to develop a program that automatically calculates the leptonic tensor, and that can be interfaced with any neutrino event generator, including those that DUNE will use. Thus, our Python program significantly reduces the time to implement BSM theories and make useful predictions.

The Search for the Fourth Neutrino at Daya Bay

Discipline: Physics & Astronomy
Subdiscipline: Physics

Jessica Cmiel*[1]; David Ernst[2] and Noah Austin[2], *(1)University of Georgia, (2)Vanderbilt University*

Abstract: Neutrinos are fundamental particles that interact only via the weak interaction. They exist as three “flavors”: electron, muon and tau. The neutrino flavor varies between these three as it propagates through space; these variations are called neutrino oscillations. In the standard model, neutrinos are massless and do not oscillate; their oscillation is the only known phenomenon that lies outside the standard model. The experiment at Daya Bay is a predominantly Chinese-US collaboration comprised of six nuclear reactors and eight antineutrino detectors. Daya Bay experimentalists have developed models for the three neutrino case, yielding results for the phenomenological parameters that govern the oscillations. There exist experiments that may not fit into the three neutrino picture; these may be explained by postulating the existence of a fourth neutrino, referred to as the “sterile neutrino”. The additional neutrino(s) must oscillate much faster and interact much less than the already known flavors. Daya Bay experimentalists have extended their three neutrino model up to higher frequencies, but not to the frequencies that the Vanderbilt Group is finding evidence of the sterile neutrino. Our aim is to develop a model that would produce results at these higher frequencies. We have tried a number of models that combined the forty-eight different baselines into subgroups, but none have worked. We believe this is not an adequate approximation, so we are attempting to expand the model to treat each baseline individually, which is computationally challenging and will require some assumptions, given the limited information we have from the experimentalists.

Creation of a Monolayer Ferroelectric Using Substitutional Impurities

Discipline: Physics & Astronomy
Subdiscipline: Physics

Nicholas G. Richardson*[1]; Andrew O'Hara[2] and Sokrates T. Pantelides[2], *(1)Fairfield University, (2)Vanderbilt University*

Abstract: Two-dimensional materials, including single-atom-thick monolayers, have shown great promise in recent years for applications in nanotechnology and electronics. One particular area of interest is ferroelectric materials and their potential for use in computer memory and sensing due to their switchable electric dipoles. As one of the few wide-bandgap insulating 2D materials, hexagonal Boron Nitride (h-BN) is an important material for electronic and opto-electronic applications. While h-BN is not naturally ferroelectric, we explored inducing ferroelectricity by incorporating isovalent substitutional impurities that are larger than the host atom they replace. This disparity is expected to cause a buckling of the impurity, either up or down, which amounts a dipole with two equivalent orientations, ultimately creating the ferroelectric phase that we seek. To investigate this idea theoretically, we performed quantum mechanical calculations using density functional theory (DFT). We incorporated isovalent impurities (e.g. Al for B, P for N, etc) and optimized the centrosymmetric and distorted structures. Using these structures, we then calculated the switching energy barrier to move the impurity from one side of h-BN to the other as well as the magnitude of the dipole in order to determine if any substituents have a small but not insignificant barrier. We are performing additional calculations to understand the strain response and multidefect coupling properties of the impurities. Based on the initial results, we conclude that aluminum, gallium, and phosphorus substituents show the most promise for creating a stable ferroelectric h-BN.

Elliptic Flow in C+C Collisions from Ampt Simulations

Discipline: Physics & Astronomy
Subdiscipline: Physics

Everett Prichard* and Shengquan Tuo, *Vanderbilt University*

Abstract: Relativistic heavy ion collisions of sufficiently high energy produce quark-gluon plasma (QGP) whose macroscopic behavior can be accurately described by hydrodynamics. Thus, when a system of QGP is initially azimuthally anisotropic, it experiences elliptic flow, v_2, which is described by the second coefficient of the azimuthal Fourier decomposition. The initial state anisotropy of the QGP in a relativistic heavy ion collision depends on many factors, one of them being the participant ions in the collision. The CMS collaboration at CERN has only studied systems with larger ions like lead+lead, proton+lead, and xenon+xenon collisions. In this study, we use A Multi-Phase Transport model with string melting to model carbon+carbon collisions and, if time permits , proton+carbon, deuterium+carbon, and Helium-3+carbon collisions at center of mass per nucleon energies $\sqrt{s_{NN}}$ = 7 TeV. We will then analyze the v_2 using the event plane method to build a deeper understanding of the elliptic flow of smaller systems and to help the CMS collaboration make a more informed decision on which experiments to run at CERN in the future.

Simulations of Scintillation on Zinc Oxide Nanowire Induced By 511 Kev Radiation

Discipline: Physics & Astronomy
Subdiscipline: Physics

Kenneth Marcelino*, *Loyola University Maryland* and Richard Haglund, *Vanderbilt University*

Abstract: Positron emission tomography (PET) scanners are used to map and visualize the highly metabolic areas of the body where tumors reside. This project focuses on developing a novel scintillator material to improve the spatial resolution of PET scan images. This new material would comprise a dense carpet of vertical zinc oxide nanowires feeding silicon CCD detectors and improve scintillator efficiency in two ways. First would be light yield: Light emission in crystalline scintillators is omnidirectional; on the other hand, The ZnO nanowires embedded in a polymer, act as waveguides, forcing unidirectional emission regardless of the trajectory of the ionizing radiation ensuring virtually all the emitted light will reach the detector. The second improvement is related to improving the time resolution of scintillators. The scintillator response time dictates the spatial resolution of the image. The current best scintillators have a response time of order 10 ns, while ZnO has a 10 ps response time, reducing the uncertainty in the spatial resolution of the scans from 6 cm to 0.2 cm. I use Lumerical® simulations in both finite difference time domain and finite element eigenmode solvers, to find the optimal parameters for maximum light yield in ZnO nanowire arrays and use these parameters to design the detectors. The

improvements in the light yield and spatial resolution of ZnO nanowires will allow detection of smaller tumors which would enable earlier medical intervention.

This work is supported by the NSF REU grant number 1852158.

Creating Interactive Web-Accessible Real Time Electrocardiac Simulations of the Heart

Discipline: Physics & Astronomy
Subdiscipline: Physics

Jorge Ramirez Ortiz*[1]; Abouzar Kaboudian[2] and Flavio Fenton[2], *(1)University of Maryland, College Park, (2)Georgia Institute of Technology*

Abstract: This summer research project seeks to develop interactive web-based electrocardiac simulations that will be used to better study electric potentials and ion transmissions in cardiac cells coupled in tissue, as well as used by educators to demonstrate how the heart functions from the cellular level to the whole organ. The interactive simulations will improve understanding of the electrical systems that control how the heart beats, with aims to observe chaos and nonlinear dynamics in cardiac models. The simulations will place a focus on showing ion transmissions and currents across cardiac cell membranes, creating user-placed voltage nodes to show how an electrocardiogram (ECG) signal varies throughout the heart, and allow for physiological changes on the cell's dynamics that can have a significant changes in the heart's dynamics from normal to arrhythmic. The simulations are based in WebGL which is a language that allows direct access to a machine's GPU by web-browsers, making these programs available to run in real time and independent of operating system and device, so simulations can be run even on smart-phones.

Modeling Carbon Nanotube Networks

Discipline: Physics & Astronomy
Subdiscipline: Physics

Joshua Maldonado* and Ruth Saunders, *Humboldt State University*

Abstract: Current industrial applications of semiconductors largely use a 'top-down' approach to creating small scale devices, etching features painstakingly into a material such as Silicon, using expensive and time-consuming precision lithographic processing. The emergence of a 'bottom-up' approach - such as in the growth of semiconductor nanowires using guided self-assembly fabrication - is an exciting innovation. Carbon Nanotubes (CNTs) are rolled up sheets of graphene on the order of microns long. have many potential applications. While we are unable to actually build well ordered circuits from CNTs as we can not yet accurately pick them up and place them somewhere, we are able to make networks of randomly distributed CNTs. Even though the CNTs make a random network, the overall average properties are reproducible. The electrical properties of these networks, how electrons make the journey from an electrode on one side to the other, are altered by the presence of charged biomolecules. This project will model the electrical properties of these CNT networks by creating a computational simulation that generates a network of wires and examines the electrical response. We will further study the addition of the presence of charged biomolecules and the impact on the electrical response. Computational simulation is an excellent mechanism to explore this topic. Creating the CNT networks is time consuming, so using a simulation where parameters are easily altered is greatly beneficial to creating optimal devices.

Developing a Convolutional Neural Network for Scanning Tunneling Microscopy Image Analysis

Discipline: Physics & Astronomy
Subdiscipline: Physics

Daniel Glazer*[1]; Kevin Honz[2]; Anna Binion[2]; Riju Bannerjee[2] and Eric Hudson[2], *(1)Carnegie Mellon University, (2)The Pennsylvania State University*

Abstract: Local measurements of electronic properties, enabled by scanning tunneling microscopy (STM), have led to a better understanding of 2D materials such as graphene and MoC2. The impact of local strain on these properties has been of great theoretical and experimental interest. However, correlating these electronic properties with local strain has proven challenging, as directly measuring strain - determining picometer-scale offsets of atoms from their unstrained locations – is non-trivial. Here we present the development of a convolutional neural network to assign atom locations and local strain values to STM topographies of hexagonal lattices. We will discuss improvement of model accuracy through increasingly realistic simulated training sets, and the outlook for quick and reliable characterization of local strain using this method.

Gap Statistics and Localization in a Cubic Lattice

Discipline: Physics & Astronomy
Subdiscipline: Physics

Niko Reed*, *University of Delaware* and Jorge O. Sofo, *Pennsylvania State University*

Abstract: Electrical conductivity is an important property of materials, but it is difficult to model because it is caused by random and thermal disorder. An interesting phenomenon known as Anderson localization is that, at a certain level of disorder, otherwise metallic materials become insulating. We compare the electronic energy spectrum of materials to electron localization to see if the energy spectrum of a material can be used as a computationally efficient tool to examine this phenomenon. We used a tight binding model in which the solid is represented by a set of atomic orbitals at each lattice

position and a probability of jumping to adjacent sites. Disorder is introduced though the randomization of the energies at the lattice sites, and diagonalization of the resulting Hamiltonian provides energy eigenvalues and wave functions. Localization of wave functions is analyzed using the inverse participation ratio which measures how spread the wave function is among lattice sites. We observe a change in the probability of energy-spectrum gaps as a function of disorder strength. When these are scaled by the median, curves for low disorder coalesce into one single functional form called the "Wigner surmise." Beyond that disorder, the system transitions to a Poisson distribution. Our results show distinct localized and delocalized phases which correspond to modes observed in the energy spectrum. This suggests that the energy spectrum may serve as a useful indicator of localization, which could allow for faster computation of electrical properties of solids.

The Mechanisms of Electrical Sensitivity in Carbon Nanotube Network Field Effect Transistors

Discipline: Physics & Astronomy
Subdiscipline: Physics

Savannah Silva*, *California Polytechnic State University, San Luis Obispo* and Colleen A. Marlow, *California Polytechnic State University*

Abstract: Carbon Nanotube (CNT) field effect transistor (FET) aptasensors show promise as state-of-the-art biosensors because of their sensitivity to electrical changes in the environment at the molecular level. It has recently been demonstrated that individual metallic-semiconducting (m-s) CNT junctions are sensing hotspots in CNT FETs and likely responsible for the network sensitivity. Recent studies, however, also show the importance of the structural properties, such as network length, tube density, tube length, and the percent of semiconducting versus metallic tubes. The aim of this study is to better understand the influence of network morphology on the role CNT junctions play in network sensitivity. We have approached this problem in two complementary ways. First we created a scanning gate microscopy setup using a conductive atomic force microscope (AFM) tip as a movable, localized electrostatic gate and a multichannel lock-in amplifier to measure the change in device current when a given region is electrically stimulated. The resulting data is presented as a conductive map which reflects the network's most sensitive regions. In parallel, we developed computational methods to simulate an array of CNT networks with varying morphological parameters. We tested them for electrical sensitivity by changing the properties of individual junctions and measuring the change in network current to map the network sensitivity. Our results verified that m-s tube junctions have a large influence on network sensitivity, but they also showed that morphological characteristics also play a role. By optimizing these two features, we can improve the sensing capabilities of CNT FET aptasensors.

The Interplay of Childhood Physical Abuse and Maternal Depression on Children's Reward Responsiveness

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Jaime Sosa* and Katie Burkhouse, *University of Illinois at Chicago*

Abstract: The Reward Positivity (RewP) is an ERP-component of reward responsiveness. Reduced RewP predicts depression in at-risk youth, and could be a neural marker for depression. Maternal depression history is one component associated with the reduced RewP in offspring. Another component associated with reduced reward responsiveness, but also increased it in some cases in offspring, is the childhood physical abuse (CPA). Studies that examine the interplay of maternal depression and CPA on offspring's RewP have not been done. This work could identify common neural reward phenotypes of depression vulnerability or find that maternal depression and CPA predict distinct neural reward responsiveness patterns in children. Participants included 125 diverse mothers and their children (M = 12.36 years, 9-16 years; 71.2% female). Participants were split into two groups: high-risk group with 76 participants that included youth whose mothers had histories of depression and 49 participants into a low-risk group that consisted of youth whose mothers had no past psychopathology. The RewP was measured at frontal electrodes (FCz, Fz) from 250ms-350ms following reward feedback. The HR group displayed significantly reduced RewP relative to the LR group when CPA was high (B = -4.63, t = -2.12, p = .04). Youth depression and RewP were not associated (β = .07, p = .51). LR and HR groups did not differ in CPA histories (F = 1.56, p = .22). We found youth with both maternal depression and physical abuse exposures demonstrated reduced RewPs, but maternal depression and physical abuse did not uniquely predict youth's RewP.

Systemic and Interpersonal Factors Impact the Mental Health Outcomes of Transgender Latinas in the United States

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Yazmin Meza Lazaro*, *Department of Psychological Science, Pomona College* and Guadalupe Bacio, *Departments of Psychological Science and Chicana/o-Latina/o Studies, Pomona College*

Abstract: Aim: To investigate the systemic and interpersonal factors that impact the mental health of transgender Latinas. Method: A secondary analysis of the 2015 U.S. Transgender Survey with self-identifying Latinx transgender or gender non-

conforming participants (N = 953). We predicted that experiencing systemic and negative interpersonal factors would predict worse mental health outcomes, and the positive interpersonal factors would be protective. Logistic regression models were conducted for each of the following: psychological distress, alcohol use, binge drinking/illicit drugs use, suicidal ideation, and suicide attempts. Results: Serious psychological distress was predicted by being out of the labor force or unemployed and having an individual income of $1 to $9,999. An individual income of $1 to $9,999 decreased the likelihood of alcohol use, but experiencing discrimination increased the likelihood of alcohol use. Additionally, having an income of $50,000 to $99,999 decreased the likelihood of binge drinking/illicit drug use compared to those who made $100,000 or more. Experiencing discrimination in places of public accommodation predicted both suicidal ideation and attempts. Finally, both housing discrimination and a lack of family support predicted suicide attempts. Discussion: Overall, systemic factors (i.e. employment status and income) were predictive of serious psychological distress and substance use, while interpersonal factors (i.e. discrimination and a lack of family support) were predictive of alcohol use, suicidal ideation, and suicide attempts. Future interventions should address both the systemic and interpersonal factors that negatively impact the mental health of transgender Latinas, such as increasing employment and housing opportunities.

Preschool-Aged Children’s Irritability Is Related to Problematic Sleep Habits and Parental Depression

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Cheyenne Bates*[1]; Edith Jimenez[1]; Lea Dougherty[2] and Sara Bufferd[3], *(1)California State University San Marcos, (2)University of Maryland, (3)University of Louisville*

Abstract: Children’s irritability, a facet of children’s mood, is associated with a range of psychological difficulties. Children’s sleep and parental depression are two factors that may be related to child irritability, but these associations are largely understudied in early childhood. This study aimed to contribute to the knowledge by assessing associations between these variables in a large community sample of preschool-aged children. It was hypothesized that parental depression and child irritability would be positively correlated and that problematic sleep habits in children would be positively correlated with parental depression and child irritability. To assess these relationships, 592 parents of 3-5-year-old children completed the Center for Epidemiologic Studies Depression Scale (CES-D; parental depression), Affective Reactivity Index (ARI; child irritability), and Children’s Sleep Habits Questionnaire (CSHQ). Pearson’s correlation analyses supported the hypotheses, such that parental depression was positively related to child irritability (r=.31,p<.001). Additionally, children’s problematic sleep habits were positively related to child irritability (r=.35,p<.001) and parental depression (r=.33,p<.001). In a multiple linear regression analysis with parental depression and children’s sleep as independent variables, both remained significantly associated with child irritability (dependent variable) (b=.07,SE=.01,β=22,p<001;b=.03,SE=.004,β=28,p<001, respectively; F(2,585) = 59.10,p<.01) suggesting both variables are important correlates of child irritability. The interaction between parental depression and sleep was not associated with child irritability, p=.28. Implications of this study include the importance of increased monitoring of parental depressive symptoms, and alertness to increases in child mood difficulties and sleep behaviors. Future research should investigate causal relationships between these variables and examine potential racial/ethnic and socioeconomic differences.

The Relationship between Oxytocin and Coping Skills on Conflict Resolution in Couples

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Aileen Kangavary*[1]; Elizabeth Santa Ana[2]; Julianne Flanagan[2] and Jeffrey Korte[2], *(1)California State University, Northridge, (2)Medical University of South Carolina*

Abstract: Oxytocin is a neuropeptide known for its anxiolytic, prosocial, and pair-bonding effects. However, the literature is mixed regarding how oxytocin affects human behavior depending on contextual and individual characteristics. Previous literature indicates that oxytocin might increase positive communication among normative couples. Other literature reports, however, that oxytocin might enhance detrimental behaviors such as competitiveness, aggression, and anxiety when administered to individuals with pre-existing interpersonal difficulties that often accompany substance misuse. The present study sought to examine whether coping skills moderate the effect of oxytocin on a couples' laboratory-based conflict resolution behaviors compared to placebo. Participants were 30 different-sex couples (n=60) consisting of at least one partner with recent substance misuse. Participants were randomly assigned in a double-blind manner to 40 IU intranasal oxytocin or placebo. Couples completed the Brief COPE (Carver, 1997) and a 10-minute laboratory conflict resolution task. Conflict behaviors were observationally coded by independent raters into positive or negative categories. Based on literature, we hypothesized that: a) adaptive coping skills will interact with oxytocin resulting in greater frequency of positive conflict resolution behaviors, and reduced frequency of negative behaviors; and b) maladaptive coping skills will interact with oxytocin resulting in reduced frequency of positive behaviors, and increased frequency of negative behaviors. Results showed that overall, oxytocin had a stronger effect on men compared to women. A moderation analysis was conducted and showed that men with higher scores on maladaptive coping showed a decrease in negative behaviors during the couples' task. Overall, oxytocin had no significant effect on women.

Effects of Daily Heterosexism and Positive Sexual Minority Identity on Posttraumatic Cognitions and PTSD Symptoms in a Trauma-Exposed Sample of Sexual Minorities

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Lisbeth Rubi*, *Hunter College of the City University of New York* and Danielle S. Berke, *Hunter College of the City University of New York, CUNY Graduate Center*

Abstract: Sexual minority individuals face identity-specific obstacles such as daily heterosexist experiences which present a unique set of stressors. Heterosexism has been associated with psychological distress, including elevated symptoms of posttraumatic stress disorder (PTSD). Individuals may experience negative posttraumatic cognitions including negative beliefs about the self and the world and may blame themselves for their trauma. Holding more positive thoughts and feelings about sexual minority identity may buffer individuals against negative appraisals about themselves after heterosexist experiences. However, research on the role of protective identity-specific factors in the development of posttraumatic cognitions or PTSD symptoms for sexual minorities is lacking. To address this gap, the present study examined the effects of positive sexual minority identity processes on the relationships among daily heterosexism, posttraumatic cognitions, and PTSD symptoms. A total of 51 trauma-exposed LGBTQ+ individuals (60.8% female-identified, ages 18-62) completed measures of daily heterosexism, sexual minority identity, posttraumatic cognitions, and PTSD symptom severity. Results revealed a negative and significant main effect of sexual minority identity superiority on posttraumatic self-blame (ß = -0.33; $p < 0.05$), over and above the effects of daily heterosexism. We also found a significant positive association between posttraumatic self-blame and PTSD symptom severity ($r = 0.32$, $p = 0.02$). Together, these findings suggest that individuals who believe that sexual minority identity is preferable to heterosexual identity may be protected against the pathogenic consequences of blaming oneself for heterosexist harms.

Disruption of Medial Prefrontal Cortex Induces Epoch Specific Deficits in Spatial Delayed Alternation Performance

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Mauro Torres*; Kevan Kidder; Jesse Miles; Victoria Ivanova; David Gire and Sheri Mizumori, *University of Washington*

Abstract: Neuropsychiatric disorders such as Alzheimer's, schizophrenia, and major depressive disorder are linked with deficits in decision making abilities. Research suggests deficits may arise due to faulty communication between brain areas involved in decision making such as the hippocampus (HPC) and medial prefrontal cortex (mPFC). Therefore, investigating phenomena which underlie effective neural communication could reveal insights that bring us closer to developing treatments to help those suffering from disorders that involve impaired neural communication. Past research reveals task-dependent fluctuations in oscillatory activity between HPC and mPFC, such as increases in theta (4-12Hz) rhythm activity when animals deliberate at choice points. This increased oscillatory activity is thought to reflect increased communication. Our research sought to investigate whether disrupting the mPFC at specific epochs of a delayed-alternation task would reveal spatial working memory deficits specifically at epochs where HPC-mPFC communication is highest. Using a closed-loop optogenetic system we disrupted the mPFC in three distinct task-epoch conditions (delay, choice, and reward). Results revealed significant choice accuracy deficits when the mPFC was disrupted during the choice epoch compared to all other epochs. Considering findings from past studies that HPC-mPFC communication is strongest during the choice point, our findings support the view that impaired communication between HPC and mPFC when making decisions leads to an impaired decision-making ability, revealed by choice accuracy deficits. This suggests that spatial working memory involves a unique, epoch specific role for HPC-mPFC interactions at choice points which doesn't exist while animals are receiving reward or waiting during a delay.

Analyzing Auditory Neural Response Patterns in Autism Spectrum Disorder, Fragile X Syndrome, and Phelan-Mcdermid Syndrome

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Saramarie Azzun* and Lauren Ethridge, *University of Oklahoma, Norman*

Abstract: Fragile X Syndrome (FXS) and Phelan-McDermid Syndrome (PMS) are neurodevelopmental disorders associated with Autism Spectrum Disorder (ASD) that cause a range of lifelong symptoms. While FXS and PMS are monogenic disorders, there is no genetic test for ASD. However, studies have shown that the three conditions share similar patterns in the neural oscillations within the cortex. These neural oscillations include gamma waves, theta waves, and other patterns in brain activity. Sensory reactivity can be measured and compared for a better understanding of the relationship between FXS, PMS, and ASD. We hypothesize that the auditory neural response patterns will be similar between the three conditions. Dense-array electroencephalograms (EEGs) are great tools in measuring the symptomatic brain activity for diagnosis. MATLAB® software will be the primary tool in collecting raw data to isolate brain activity. We can measure the neural oscillation patterns that exist between a subset within each of the three groups in response to a comparable auditory stimulus. Statistical analysis tests will be run to determine the significance within and between groups, and we

anticipate our results to be consistent with our hypothesis. With these results, we can analyze the similarities and differences in neural activity between the three disorders and potentially identify their biomarkers. These biomarkers can become relevant at the clinical level as possible targets in drug treatment and other remedies.

The Role of Excitatory Projection Neurons in Interference-Based Actions

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Mariela Lopez Valencia*; Mr. Christian Cazares and Christina Gremel, *University of California, San Diego*

Abstract: Flexible decision-making is important for daily-life function. The orbitofrontal cortex (OFC) has been identified to play a key role in goal-directed or inference-based decision-making. However, whether OFC computations for decision-making flexibility when direct information about ongoing processes and future consequences is not readily available remains unknown. Here, we adapted the instrumental task of action differentiation, where a mouse must continuously infer and hold a lever press down for a fixed, minimum duration in order to get a reward. We assessed daily performance differences following selective OFC excitatory projection neuron lesions using a viral caspase strategy. Our results indicated that OFC-lesioned mice can readily acquire similar levels of lever pressing and hold down performance for food. To directly assess the behavioral strategy controlling decision-making performance in our task, we used an outcome devaluation procedure and found that both control and OFC-lesioned reflected an insensitivity to outcome value change and thus habitual control. This suggests that excitatory projection neurons might not be necessary for performing interference-based actions, suggesting that other prefrontal areas might be contributing to decision-making computations to make up for the loss of OFC contributions.

Investigating Deep Artificial Neural Networks Trained to Do Ecological Tasks As a Normative Model for Pitch Perception

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Bryan Medina*[1]; Mark Saddler[2] and Josh McDermott[2], *(1)University of Central Florida, (2)Massachusetts Institute of Technology*

Abstract: Pitch perception is an important aspect of human hearing thought to underlie complex auditory tasks, such as separating concurrent sounds, recognizing voices, and following melodies. While pitch is traditionally considered the perceptual correlate of fundamental frequency, naturally-behaving listeners are rarely asked to explicitly report the pitch of a sound. Thus, in order to investigate how human pitch perception may have been shaped by the demands of ecologically-important tasks, we trained deep artificial neural networks to perform different combinations of three tasks that are ecologically important to humans (speech, voice, and environmental sound recognition) using simulated cochlear representations of speech excerpts superimposed on recorded auditory scenes. We then interrogated networks for learned representations of pitch by training linear classifiers on the networks' internal activations to perform psychophysical experiments, such as two-tone pitch discrimination. These classifiers enabled us to measure thresholds from networks trained to perform arbitrary tasks. We compared the effect of stimulus manipulations previously used in psychoacoustic experiments (e.g. inharmonic vs. harmonic tones, low vs. high-numbered harmonics, sine vs. random phase) between network and human listeners. These comparisons can shed light onto how pitch perception facilitates everyday auditory tasks. Comparisons between networks trained on different tasks also provide hypotheses for potentially distinct pitch mechanisms specialized for different aspects of audition.

Differences in Cortical Anatomy Are Associated with Anxiety Symptom Severity in Adults with Autism

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Ryan Tung*; Annika Linke; Jiwandeep Kohli; Ralph-Axel Müller and Ruth Carper, *San Diego State University*

Abstract: In anxiety disorders, alterations of underlying brain anatomy have been linked to anxiety severity and to treatment response. Behavioral evidence shows high prevalence of anxiety in autism spectrum disorders (ASD). We previously examined adults with ASD and found atypical functional connectivity of brain regions implicated in anxiety, which was correlated with anxiety symptom severity. The current study examined whether adults with ASD also show changes in the anatomy of those brain regions. Twenty-three adults with ASD (40-63 years; 19 males) and twenty-four typical controls (TC; 40-64 years; 20 males) completed the Beck Anxiety Inventory and a T1-weighted anatomical MRI scan. Images were pre-processed using Freesurfer, and surface area (SA) and cortical thickness (CT) measures were extracted from 12 regions of interest. The ASD and TC groups were matched on age, handedness, sex, total brain volume and image Contrast to Noise Ratio (CNR). Group differences were examined using independent samples t-tests.Partial correlations (controlling for age and CNR) were conducted to test for relationships between SA, CT and anxiety symptoms in the ASD group. As expected, anxiety symptoms were elevated in the ASD group ($t(42)=-4.11, p=.0002$). In the ASD group, SA was significantly reduced in the left anterior insula and left ventromedial prefrontal cortex, and CT was higher in the left anterior insula . SA of the anterior insula correlated negatively with anxiety symptoms but not with autism symptom severity, mirroring results previously identified for functional connectivity of the anterior insula in the same participants.

Investigating Differences in Cognitive Function in Individuals from Different Racial and Ethnic Backgrounds & Its Interactions with Resilience

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Morgan Montoya*; Jyoti Mishra and Gillian Grennan, *University of California, San Diego*

Abstract: Neuro-cognition is the ability of the brain to perform appropriate cognitive functions, such as paying attention and working memory, which are associated with specific neural pathways in humans. The ability to neuro-cognitively respond to everyday life demands is a shared experience across all races and ethnicities. Additionally, the ability to overcome hardship, defined as resilience, is needed for daily life. We studied how race and ethnicity influence neuro-cognitive abilities and how these relationships are in-turn shaped by self-reported resilience. To bridge this gap in knowledge, we used the Brain Engagement (BrainE) digital platform developed at NEATLabs, UC San Diego, which comprised of a suite of game-like assays to study attention, working memory, and conflict processing in and outside of emotional context. We collected demographics (age, gender, socio-economic status) from all participants as well as acquired ratings of resilience measured by the Brief Resilience Scale (BRS). The 248 adult participants reported as Caucasian (53.2%), Asian (27.4%), and Other (19.4%), which also composed of Hispanic (15%), Non-Hispanic (83%), and Unknown (2%) ethnicities. Using generalized linear mixed models, we found that race was an important factor predicting working memory capacity and efficiency, and ethnicity was an important factor predicting conflict processing in the context of emotions. Resilience alone was not significant in these models; however, we found that resilience interacted with race/ethnicity variables. Understanding how race/ethnicity, resilience, and neuro-cognition are indispensable to mental health outcomes will improve the quality of care given to diverse Americans, and consequently decrease mental health care disparities.

A Sex Difference in the Flexibility of Circadian Clocks: Does It Depend on an Exercise Wheel?

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Vanessa Cervantes*, *University of California, San Diego* and Dr. Michael R Gorman, *Department of Psychology and Center for Circadian Biology, University of California, San Diego*

Abstract: Humans have internal clocks facilitating synchronization (or entrainment) to regular day-night variations in environmental conditions. These clocks are not easily shifted such that shift workers, people working under abnormal conditions, are poorly prepared to meet their physiological and environmental demands. Mice housed under certain 24h light:dark:light:dark (LDLD) cycles can adapt their behavioral rhythms to two activity periods and two resting periods per day, an entrainment pattern known as bifurcation. Female mice can adapt to this unusual 24h cycle more readily than male mice, suggesting greater flexibility entraining to their environment. Studies demonstrated running wheels, a commonly used tool to monitor day-night activity levels, have feedback effects on various aspects of circadian entrainment. Little is known about wheel access effects on bifurcation abilities of mice or if sex differences are induced by its presence. The current study focuses on the necessity of running wheel access for bifurcated entrainment, and if prior sex differences in entrainment are observed in absence of running wheels. Male and female mice were placed under a previously validated 59 day assay for bifurcation with passive infrared (PIR) motion detectors to measure rest-activity cycles. Some animals without a wheel did bifurcate indicating it is not necessary for bifurcation. However, bifurcation was less robust than in animals with wheels. On average, female mice without a wheel bifurcated more readily than male mice suggesting sex differences are not wheel dependent. By further understanding sex differences and running wheel effects, translating these results could improve health and productivity of human shift-workers.

Comprehensive Analysis of Open Source Software for Mouse Behavioral Phenotyping.

Discipline: Psychology & Social Sciences
Subdiscipline: Cognitive Neuroscience

Arthor Bernal*, *University of California, Riverside* and Amir Zarrinpar, *University of California, San Diego*

Abstract: Behavioral phenotyping in mice is a common way to assess neurocognitive abnormalities in response to experimental interventions in the study of health and disease. Human assessment of video recordings of behavioral tests can be time consuming and unreliable with high interindividual and inter-institution variability that would require hours of training to make reproducible. Thus, there is a need for automated, reliable scoring tools. Software suites frequently used by behavioral experts, including Ethovision XT, can be cost prohibitive. We hypothesize that open source software can reliably reproduce findings across multiple study paradigms, indicating value in application across mouse models and institutions. The aim of this study was to evaluate several open source video processing programs (e.g. ezTrack, Tracktor) to assess the best one for its ease of use and reproducibility of data. Of the programs tested, eZtrack was selected for further analysis in the present study. Behavioral metrics that were evaluated include attention, grooming, rearing, locomotor behavior, and anxiety-like behavior. Wild type C57Bl/6 specific-pathogen free mice from various experimental groups were evaluated. We identified several strengths and weaknesses associated with each method assessed and proposed a suggestion for researchers aiming to select an ideal scoring program. Ultimately, we select an open source program that

best meets our criteria for ease of use and is capable of reproducing previous findings generated by hand scoring and Ethovision XT software for several neurocognitive tests of short term memory and anxiety-like behavior in mice.

Cultural Differences in Children's Attentional Patterns during a Joint Activity

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Vanessa Barragan*; Sylvia Liu and Lucia Alcala, *California State University, Fullerton*

Abstract: Previous research suggests that children from diverse cultural backgrounds develop keen attention and are more likely to learn by observing than middle-class children (Correa-Chavez & Rogoff, 2009). This study examined cultural differences in children's attention patterns during a semi-structured interview. 17 sibling pairs, 7 European American heritage sibling pairs and 10 Mexican American heritage sibling-pairs, were interviewed at home regarding their after-school activities. The interviews lasted 5 minutes on average and were segmented into 10 second fragments for analysis. The analysis started with an ethnographic description of the videos examining attentional patterns and related behaviors (attention, interruption, gaze, cohesion) as children simultaneously responded to the interview. Our preliminary findings suggest that Mexican American heritage sibling pairs engage in shared eye contact, and show more sustained attention during the interview. Moreover, Mexican American heritage children were more likely to engage as a cohesive unit, allowing the other sibling to talk with little interruptions, as well as supporting their sibling if they had trouble responding. The younger sibling was more likely to turn to the older sibling for social referencing support and engaged in more physical contact. European American heritage sibling pairs responded more individually, were more prone to engage in interruption, and more likely to disengage when not being addressed by the research assistant. They were more likely to sit away from their sibling and either faced away from each other or more towards the research assistant. Findings from this research can inform educators and policy makers working with diverse families.

Morocco and Algeria: A Comparative Case Study on the Treatment of Human Rights for the Amazigh Population

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Yamina Sfiat* and Peter Jacques, *University of Central Florida*

Abstract: In this study, I use a comparative analysis of the political standing and treatment in Morocco and Algeria, ranging from strict oppression to reconciliation of Amazigh identity, including practices like herding and pastoral rights, the role of geography (e.g., rural versus urban), and the policies regarding the use of Tamazight. Early comparisons indicate that the Amazigh are treated poorly in the mountains and have similar pastoral rights in both countries but enjoy broader constitutional rights in Morocco that they do not have in Algeria. The political conditions for the Amazigh appear to be a result of different historical conditions and inherited colonial policies, which indicate a lingering inequality that has lasted for a long time. They are consistently excluded from linguistic and political representation yet included in national and cultural identity among Moroccans and Algerians. In relation to environmental studies, this work focuses on historical management of Amazigh land for pastoralism and access to water. Colonial structures of privatization and government regulation of land has reduced Amazigh peoples' abilities to herd and maintain cultural traditions. Previous policies that regulated the distribution of land to pastoralists were colonial in nature. Decolonizing policies regarding responses to loss of indigenous land is imperative in maintaining Indigenous identity and traditions. The importance of understanding and recognizing the issues of the Amazigh not only aids in the reconciliation of a violation of human rights, but also provides an example of (some) cooperation with indigenous groups across Africa.

Differences in Website Design and the Effect on Users Impressions across Varying Demographics

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Sophia Chadsey*, *University of California, Berkeley* and John Hugyik, *SLAC National Accelerator Laboratory*

Abstract: Prior research has shown that website design affects user's overall impressions, time spent, and prolonged use of a website. With limited research on how a user's demographics affect their impressions of a website, this study aims to find if there are any differences in user impressions across varying demographics. Using a survey to collect participant's age, gender, educational level, time spent using technology, and overall technological literacy will find if there are any significant results. The expected results are those that are above the mean age, below the mean educational levels, below the mean time spent using technology, and below the mean technological literacy level will have the same impression across different web designs. Conversely, those with opposing demographics are expected to have varying levels of impressions across different web designs and prefer more stylized versions. The findings can be used to alter a website's design for its intended demographic to increase positive impressions and therefore use of a website. With COVID-19 making remote education and work activities prevalent these findings can be especially useful to increase user's overall use of their respective institution's websites.

The Role of Reward Signaling in Responses to Ethanol in Male and Female Rats

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Kylie Foster* and Yada Treesukosol, *California State University, Long Beach*

Abstract: In 2018, 6.6% of adults reported heavy alcohol use within the past month (NIH). There is some evidence of sex differences in alcohol-related behavior in humans (HSDUH, 2014) and rats (Hilderbrand & Lasek, 2018). Here, male (n = 17) and female (n = 14) rats were tested in a brief-access lick procedure (10-s trials, 30-min sessions). This procedure allows for some segregation of the appetitive and consummatory (here measured by number of trials and licks respecirvely) components of behavior towards ethanol. Rats were presented 1, 2, 4, 8, 16, and 32% ethanol in randomized blocks over 5 sessions. Rats could initiate as many trials as possible during each session. To assess the role of opioidergic signals on reward-related responses to ethanol, 0.1 or 1.0 mg/kg naltrexone, an opioid receptor antagonist, or saline control was administered 30 minutes before each test session. Regardless of sex, licks decreased as EtOH concentration increased suggesting sex differences in ethanol intake are not driven by differences in consummatory components of behavior. In contrast, males initiated more trials than females suggesting that males were more motivated than females to respond to EtOH. Naltrexone decreased trials in both males and females in a. The 1.0 mg/kg naltrexone decreased number of licks for males, but not females. Collectivelythese findings suggest opioidergic pathways are involved in consummatory and appetitive components of behavior towards ethanol for males but primarily only the appetitive component of behavior for females. These results provide possible explanations for sex differences observed in ethanol intake.

Effect of Linguistically and Culturally Tailored Web-Programs on Nutritional Intake and Well-Being of Latina Breast Cancer Survivors

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

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Abstract: Breast cancer is the most commonly diagnosed cancer among Latina women, and compared to non-Hispanic whites, Latina breast cancer survivors (BCS) experience worse health-related quality of life (HRQOL) and well-being. High quality dietary intake is associated with improved HRQoL, and observing nutritional intake patterns among Latina (BCS) can uncover pathways for improving well-being. The web-programs, My Guide and My Health, are culturally and linguistically adapted to Latina BCS HRQoL concerns and well-being. This project explores the effect of these web-programs on changes to nutritional intake and well-being among Latina BCS.

A 6-week randomized control trial was conducted comparing two web-programs. My Guide focused on HRQoL; My Health contained evidence-based guidelines on general health. Participants completed the Functional Assessment of Cancer Therapy-Breast (FACT-B) and nutritional intake questionnaires at baseline, 6-weeks and 8-weeks after baseline.

Eighty women were recruited for the study: 64% were Spanish speakers and 71% were born outside of the U.S. Results revealed greater reduction in fat intake of My Health participants compared to My Guide (F= 4.57, p=0.036). A positive correlation between reduction in fat intake and improvement in well-being scores was also observed (r=0.243, p=0.04; n=72).

The differences between My Health and My Guide in their ability to improve nutritional intake suggest that the topics presented by the My Health web-based program to the participants may be influential on lifestyle choices. The results of the My Guide and My Health study offer direction for designing web-programs targeting nutrition and well-being of Latina BCS.

Association between Mmpi-2-RF Somatic/Cognitive Scales and Conceptually Relevant Medical Diagnoses Among Forensic Psychiatric Inpatients

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Zaida Lopez*[1]; Lea Carrasco[1]; Ethan Mach[2]; Sebastian C. Lopez[2]; Lauren E. Lopez[2]; Danielle Burchett[1] and David Glassmire[2], *(1)California State University, Monterey Bay, (2)Patton State Hospital*

Abstract: Clinicians rely on patient self-reported symptoms to aid in accurate diagnosis. Studies of the psychometric properties of self-report psychological and somatic symptom measures can help professionals determine whether tests reliably and validly aid the diagnostic process. We used independent samples *t*-tests to compare mean scores on four Minnesota Multiphasic Personality Inventory-2-Restructured Form (MMPI-2-RF) Somatic/Cognitive Scales (Gastrointestinal Complaints, Head Pain Complaints, Neurological Complaints, and Cognitive Complaints) for 907 forensic psychiatric inpatients. Specifically, we compared mean scores for patients with conceptually relevant medical diagnoses versus those (1) without conceptually-relevant diagnoses and (2) without *any* medical diagnoses at all. For all analyses, we hypothesized those with relevant diagnoses would score higher on self-report scales than those without them. Those with head pain and

neurological diagnoses had statistically significantly higher scores on Head Pain Complaints and Neurological Complaints than those without these respective diagnoses, with medium effects (Hedges' *g*s ranged from .46 to .59). Comparing patients with relevant versus no medical diagnoses, a similar pattern emerged, although Gastrointestinal Complaints was also statistically significant with a small effect (*g* = .28). In sum, Head Pain Complaints and Neurological Complaints—and to a lesser degree, Gastrointestinal Complaints—were particularly associated with relevant medical conditions in a forensic inpatient setting. These results provide psychometric information about associations between the MMPI-2-RF Somatic/Cognitive Scales and documented medical diagnoses. Clinicians can have greater confidence that MMPI-reported head pain and neurological complaints are related to genuine medical problems, but should look to alternative tools for valid self-reported cognitive or gastrointestinal complaints.

Association between Mmpi-2-RF Somatic/Cognitive Scales and Pain-Related Medical Diagnoses Among Forensic Psychiatric Inpatients

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Lea Carrasco[*1]; Zaida Lopez[1]; Ethan Mach[2]; Sebastian Lopez[2]; Lauren Lopez[2]; Danielle Burchett[1] and David Glassmire[2], *(1)California State University, Monterey Bay, (2)Patton State Hospital*

Abstract: Accurate assessment of pain-related dysfunction is important for clinicians to make appropriate treatment plans that best serve their patients. Psychological assessment tools such as the Minnesota Multiphasic Personality Inventory-2 Restructured Form (MMPI-2-RF) Somatic/Cognitive Scales offer reliable methods for assessing for self-reported physical complaints. In this study, we examined whether 267 forensic psychiatric inpatients with pain-related physical health diagnoses scored higher on the MMPI-2-RF Somatic Cognitive Scales than patients (1) without pain-related medical diagnoses (*n* = 640) and (2) with no medical diagnoses at all (*n* = 552) using independent samples *t*-tests. In all analyses, we hypothesized that patients with pain-related medical conditions would score higher on all five scales: Malaise (MLS), Gastrointestinal Complaints (GIC), Head Pain Complaints (HPC), Neurological Complaints (NUC), and Cognitive Complaints (COG). Results indicated that those with pain scored statistically significantly higher on GIC, NUC, and COG as compared to those without pain-related diagnoses and compared to those with no medical diagnoses at all, but the associated effects were negligible to small in size (Hedges' *g* range: 0.15-0.20). Given these very small differences, the MMPI-2-RF Somatic/Cognitive Scales do not appear to be particularly effective indicators of pain-related medical diagnosis. Thus, clinicians should consider alternative tools with greater predictive validity to help guide a reliable approach to self-reported pain symptom assessment.

Are Perceptions of Behavioral Phenotypes and Social Value Influenced By Perceptual Cues to Mortality Risk?

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Aaron Lukaszewski and Vanessa Bruno[*], *California State University, Fullerton*

Abstract: Formal theoretical models predict that variation in behavioral strategy is calibrated in response to an individual's mortality risk. For instance, individuals with greater mortality risk are expected to be more present-oriented (e.g., high impulsivity, high short-term mating orientation) than individuals with lower mortality risk. Pilot data lend support for these theoretical models regarding variation in behavioral strategies via individual mortality risk. Participants with reported life insurance policies from Amazon MTurk (N = 272) completed the Life History Rating Form (LHRF; = 0.88), to assess various indicators of present- vs. future-orientation, and items from the Socio-sexual Orientation Inventory (SOI; = 0.77), to assess mating strategy. Mortality risk rating was correlated with expected age of death (r = -.13, p = .038), SOI (r = .16, p = 0.001), and the LHRF (r = -.18, p = .004). These results suggest that people with higher mortality risk are expected to die younger, are more likely to pursue uncommitted mating strategies, and exhibit a range of present-oriented behavioral indicators. The current study's primary goal is to test whether mortality risk estimates taken from individual life insurance policies predict behavioral indicators of present- vs. future-orientation and whether observers can detect other individuals' mortality risk based on visual cues (i.e., standardized photos and videos). If predictions are supported, this would not only help develop a new method for the empirical assessment of mortality risk, but it would also suggest that cues to mortality risk are essential factors in how we perceive others.

The Development of Children's Resilience: Relations between Parent and Child Response Styles

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Samaria Stovall[*], *University of Colorado at Denver* and Katherine Casillas, *University of Colorado Anschutz*

Abstract: According to the National Scientific Council on the Developing Child, resilience is defined as positive, adaptive responses in the face of significant adversity. While not all children face *significant* adversity, all children do face at least intermittent stressors and challenges to which they must respond. Learning positive, adaptive responses to such events is one necessary factor in the development of resilience, yet how are such response styles attained? One of the most

important factors that influences children’s emotional and behavioral responses—especially for young children—is the parenting to which they are exposed. While the centrality of the parent here is not surprising, the specific mechanisms by which a parent influences children’s response styles is less clear. Social learning theory would say that parents shape their children’s behavior through modeling. Yet, a review of the literature provides mixed results on the direct relation between parent and child response styles, at least when focused on direct dyadic interactions between parent and child. Perhaps the field has focused too narrowly on situations directly tied to parent-child dyadic interactions? Instead, our current work takes a more holistic view of the role of the parent. We argue that the influence of the parent is more cross-contextual—across the many settings from which the child is watching and learning, parenting and otherwise. We propose that adult response styles—avoidant and overreactive—are key in the development of child response styles—internalizing and externalizing. We expect that parents holistically impact the development of their children’s resilience.

Psychological State before, during and after Hurricane Maria

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Genesaret Flores Roque*, *Universidad de Puerto Rico en Cayey* and Julio Cammarota, *University of Arizona*

Abstract: The issue of mental health in Puerto Rico is something that becomes invisible on the island, since vulnerability is not recognized. The objective of this research is to recognize what were the negative psychological effects caused by Hurricane Maria in Puerto Ricans. Data collection was carried out through nine semi-structured interviews with different Puerto Ricans between the ages of 20-75 years, the majority being students. We investigated the experiences of each of the interviewees regarding their life before, during and after Hurricane Maria. The results of this research showed that the greatest impact, in terms of mental health, was during the months after the hurricane. As most of the participants mention, the despair of seeing that nothing was back to normal and that the basic necessities -water, electricity, food, etc.- were scarce, created a collective hysteria and a great trauma in the Puerto Rican community. In conclusion, the Puerto Rican people have not yet overcome the adversities that Hurricane Maria brought. During the investigation we were able to observe how there are still people who have not recovered mentally or psychologically after this natural disaster. In recognition of our observations, there are numerous people in need of professional psychological help, which is not recognized as it is a taboo subject, therefore, it is time to take action and start working on this situation on the island.

In Vivo synapse Tracking of Transgenic Zebrafish (*danio rerio*) Larvae Utilizing a Gal-4/UAS System to Visualize the M-Cell

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Trevor Zimmerman-Thompson*; Anjum Hussain and Adam Roberts, *California State University, Fullerton*

Abstract: Understanding the physical basis of memory formation is a major goal in neuroscience; therefore, model systems have been developed to promote an understanding of the neural structures that mediate memory. To investigate learning-related structural changes, zebrafish larvae are useful due to their relatively reduced nervous system, translucency, and expansive molecular toolkit. As long-term memory tends modify neural structure more than short-term memory, we developed a protocol to induce a robust and long-term form of habituation using larval zebrafish. Habituation is a nonassociative memory in which the organism learns to decrease a response to repeated stimuli. In our protocol, zebrafish are exposed to repeated acoustic stimuli to induce an escape response that is mediated by a well-defined and simple neural circuit— attributes necessary to finding and observing learning-related changes in neural structure. Using this behavioral protocol, we will use a double transgenic line of zebrafish to track synapses within this escape-related neural circuit to observe (*in vivo*) changes in synapses related to memory formation. We expect that the number and/or size of synapses will change as the fish undergo habituation training. When completed, we hope that these studies will provide a greater understanding of the synaptic basis of memory.

Intercultural Differences Influences Maternal Stress in Emerging Adulthood

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Krystal Alvarez-Hernandez* and Kimberly D'Anna-Hernandez, *California State University San Marcos*

Abstract: In the United States emerging adulthood (18 to 25 years of age) is described as a time of transition. Additionally, research has proposed that emerging adulthood exists from cultural knowledge and cultural construct. However, little is known about the outcomes of emerging adults who become pregnant and how these outcomes may differ upon cultural orientation and assimilation. The current study aims to examine socioemotional outcomes of pregnant Mexican American women and the influence of cultural orientation and assimilation on emerging adulthood. We hypothesize that women less assimilated to American society with high Mexican orientation will differ in pregnancy experience and maternal stress. Furthermore, we predict that Mexican American women who are highly assimilated to American society will be more likely to experience higher rates of maternal stressors during and after pregnancy, as a result of an alteration in the expectancy of emerging adulthood. To test this, pregnant Mexican American women (*N* = 310) were recruited from a community clinic in Southern California. To assess Mexican orientation, assimilation, and pregnancy experience, mothers completed surveys.

We found a strong positive correlation between the two age groups and the ratio of hassles: upbeats frequency, suggesting that as age of the mother increased so did the frequency of negative pregnancy experiences. Additionally, results indicated that higher levels of assimilation were associated with a higher frequency of positive pregnancy experiences over negative experiences. The findings support the importance of examining pregnancy during emerging adulthood and intercultural differences impact the role of maternal stress.

The Combined Influence of Post-Traumatic Stress Disorder and Depression on Somatization Among Post-9/11 Veterans

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Gabrielle Earley*, *Univeristy of Texas at San Antonio*; Alicia Swan, *University of Texas at San Antonio* and Mary Jo Pugh, *The University of Utah School of Medicine*

Abstract: Previous research has shown that veterans who have post-traumatic stress disorder (PTSD) and/or depression report likewise poorer physical health relative to their unafflicted peers. However, the post-9/11 era encompasses veterans that are more racially/ethnically diverse than ever before. Given the increasing diversity of the current veteran population, it is imperative to examine the combined influence of PTSD and depression among this unique veteran population. The objective of this study is to explore somatization among post-9/11 veterans with and without PTSD and depression, while accounting for socio-demographic characteristics, deployment experiences (e.g., wounded during hostile actions), and self-reported resilience. Generalized linear models (GLM) were used to assess the unique contribution of PTSD and/or depression on reported somatization among post-9/11 veterans while controlling for socio-demographic characteristics, deployment experiences, history of traumatic brain injury (TBI), and self-reported resilience (Reaction to Stressful Experiences scale; RSES). Comorbid PTSD and depression was found to be associated with significantly greater somatization relative to those with depression only, PTSD only, or neither diagnosis. African-American and Hispanic veterans reported greater somatization relative to their Caucasian counterparts. Veterans with history of TBI likewise reported greater somatization relative to their peers who had no evidence of TBI. These results indicate that minority groups and veterans with history of TBI may be at increased risk for physical comorbidities or have limited access to clinical care, and that clinical care programs may benefit from conducting more nuanced assessments of mental and physical health burdens that account for socio-demographic considerations that influence outcomes.

Study of Emotions in the Teaching-Learning Experience with Virtual Platforms: A New Theoretical and Methodological Point of View

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Derek Torres* and Antoinette Alom, *Universidad de Puerto Rico en Cayey*

Abstract: Universities have begun an extensive implementation of information and communication technologies such as virtual platforms (VP's), as a means of acclimating to new educational demands. VP's are software applications that integrate a set of tools: texts, multimedia, and activities, to enhance the experience of courses or training programs. The integration of VP's triggers the development of complex emotional processes in individuals, which need to be studied. In education, emotions have been studied as susceptible variables of direct quantitative measurement and homogeneously operationalized. This study explores the emotions portrayed by students and professors in their academic experiences through VP's based on Gonzalez-Rey's historical-cultural theory of subjectivity. This theoretical framework understands subjectivity in its dialectical relationship between individuals and society. Furthermore, emotions are understood to be subjective senses, units of symbolical and emotional processes, in continuous construction by the individual. To examine the subjective senses of students and professors involved in the study, we partook in a conversational dynamic in the form of semi structured interviews and a written composition, to look at how their emotions impacted their teaching-learning process. Additionally, sociodemographic sheets were used to capture their backgrounds. By using the constructive-interpretive methodology, derived from the theoretical framework, the ongoing research has revealed that subjectivity presents itself as a genuine cognitive affective unit, which integrates the individual history with current experiences. Therefore, subjective senses should be considered essential elements of research in education as a means to attend to the diversity of individuals in times of teaching and learning through VP's.

Social and Cognitive Development in Play: Observing Family Experiences at a Children's Museum

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Natassia Aleman*[1]; Brandon Garcia[2] and Jennifer Dyer-Seymour[1], *(1)California State University, Monterey Bay, (2)CSU, Monterey Bay*

Abstract: It is known that certain learning competencies and concepts, like gender-type play differences, develop early. We wanted to understand how local families experienced a play-based setting and its influences on children's social and cognitive development. In this study 71 families were observed and 49 caregivers were interviewed in a free pop-up

museum over a two-month period. Researchers used time sampling in three-minute snapshots for a total of fifteen-minutes of observation. Snapshots included participants exhibit choice, action being performed, who each participant was with, and who directed the activity. Exhibits were categorized post-hoc by gender-type play activity: Female, Male, and Neutral. Results revealed children spent most of their time interacting (77%) than the other observed actions: talking (18%), watching (3%), separating (2%), and cellular devices (0%). Frequency of caregiver's actions were spread more evenly: interacting (39%), watching (32%), talking (28%), separating (6%) and devices (8%). Interviews gathered caregiver's motivations to visit the museum was so their children could have fun, socialize, and play. Chi-squared tests found a significant difference between child's gender and exhibit choice. Girls favored feminine exhibits and boys favored masculine (X2(2)=30.32, p<.05). Adults showed no significant difference in exhibit choice in the first four snapshots, but in the fifth women preferred feminine exhibits and men preferred male exhibits (X2(2)=8.266, p<.05). Evidence could suggest that the museum had high levels of engagement and children significantly gravitated to exhibits based on gender. Further study is needed to understand the relationship between gender-type choices and the implications of the patterns found.

Gender Differences in Mathematical Equivalence Learning and Reasoning

Discipline: Psychology & Social Sciences

Subdiscipline: Psychology (general)

Dominique Giambalvo*; Maleeha Chughtai; Usaid Mahmud; Kimberly Bruckman; Ruth Church and Andrew Young, *Northeastern Illinois University*

Abstract: Research has shown gender differences in mathematics skills. Many children struggle with math but studies show that including gesture in math instruction can make learning easier. I ask whether gestures used in math instruction can increase math learning for young females. Past research has shown that instructional gestures can improve children's understanding of mathematical equivalence but there has been little research on whether gestures can reduce gender differences. However, research has yet to consider the role of gender in mathematical equivalence understanding. Our research examines three factors, (1) gesture accompanying speech instruction, (2) mathematical equivalence and (3) gender. To do this we conducted an online pretest-instruction-posttest protocol for children learning mathematical equivalence. I hypothesize that gender biases begin early in development and may result in males outperforming females in math pretest, but females will benefit more from instruction. Preliminary data shows that males perform significantly better than females before instruction as they come into instruction knowing more about mathematical equivalence than females (male $M = 6.24$ vs. female $M = 2.46$, $p = .029$). Importantly, instruction closed this performance gap at posttest (male $M = 8.67$ vs. female $M = 6.77$, $p = .25$). Ongoing research examines whether instruction with gesture is particularly beneficial for females. This research furthers our understanding of gesture as an instructional tool to improve math learning and support gender equality in math achievement. This research furthers our understanding of gesture as an instructional tool to improve math learning and support gender equality in math achievement.

The Role of Bilingualism and Instructional Gesture in Math Learning

Discipline: Psychology & Social Sciences

Subdiscipline: Psychology (general)

Princess Maleeha Chughtai*; Usaid Mahmud; Kimberly Bruckman; Dominique Giambalvo; Breckie Church and Andrew Young, *Northeastern Illinois University*

Abstract: Bilingual children who are still learning English tend to struggle with math learning in the U.S. Research suggests including non-verbal gestures with math instruction can greatly improve the math learning of school-aged children (Koumoutsakis, 2016; Alibali et al., 2015). Research has not yet examined whether children's mastery of English affects their learning from instruction with gestures. However, bilingual children gesture more when speaking English than native English speakers, suggesting gesture may be an important scaffold for bilingual children's communication and understanding (Church et al., 2004; Fernandes et al., 2017). We examined 34 bilingual and monolingual English speaking elementary schoolers in a pretest-instruction-posttest design. Children were randomly assigned to one of two instructional videos designed to teach the meaning of the equal sign: (1) speech instruction with gesture or (2) speech instruction without gesture. We hypothesized that bilingual children would learn more from instruction with gestures than monolingual children. As predicted, bilingual students improved more from pretest to posttest from instruction with gesture ($M = 2.00$ additional items correct) than monolingual students ($M = 1.67$), who benefited most from speech only instruction ($M = 5.00$). Ongoing data-collection and analyses investigate whether the directionality of bilingual children's native language (right to left vs. left to right) affects learning from gesture. This study may have the potential for decreasing the gap in math understanding through the use of instructional gestures, thus making math education and STEM careers more accessible for bilingual students.

Mathematical Equivalence Learning: Differences between High and Low Resource Schools

Discipline: Psychology & Social Sciences

Subdiscipline: Psychology (general)

Kimberly Bruckman*; Dominique Giambalvo; Maleeha Chughtai; Usaid Mahmud; Andrew Young and Breckie Church, *Northeastern Illinois University*

Abstract: The U.S. underperforms in math compared to other industrialized countries, putting many marginalized and under-resourced individuals at risk for entering STEM careers. Research suggests that an early mastery of mathematical equivalence (understanding the equal sign) predicts later mathematical achievement (McNeil et al, 2017). One factor that can support math learning is the use of representational gesture during math instruction (Alibali et al., 2015; Novack & Goldin-Meadow, 2015). Gesture engages students' attention as a visual representation that clarifies speech (Cook et al., 2013). However, few studies have examined gesture's impact across diverse populations. Research suggests students at high-resource schools have greater math achievement than students at low-resource schools (Lubienski & Lubienski, 2006). We ask whether gesture-enhanced instruction can reduce this gap. Thirty-four children from 31 U.S. elementary schools completed an online pretest-instruction-post test protocol. Children were randomly assigned to watch a 3-minute instructional video that included speech and gesture or a video with only speech. We measured children's learning from pretest to post test on equivalence problems that assess understanding of the equal sign (3+4+5=_+5). Children from high-resource schools performed better (M = 5.58 correct out of 12) at pretest than children from low-resource schools (M = 3.80). However, instruction improved both low-resource and high-resource children's performance from pretest to post test ($ps < .01$). Ongoing data-collection and analyses investigate whether gesture-enhanced instruction is more beneficial for low-resource children than high-resource children. Implications for creating equity in math performance across diverse populations and teaching remotely during a pandemic will be discussed.

Younger Children Know More about Mathematical Equivalence Than Older Children

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Usaid mahmud*; Kimberly Bruckman; Dominique Giambalvo; Maleeha Chughtai; Breckie Church and Andrew Young, *Northeastern Illinois University*

Abstract: Gesture is a form of non-verbal communication that has been shown to support math proficiency in the United States (Alibali et al,. 1993). In particular, previous research shows that when gesture is experimentally manipulated in math instruction, children are significantly more likely to learn when gesture is present than when it is not (Cook, 2013). What remains unclear is whether the age child learners interacts with exposure to math instruction with and without gesture. Some studies suggest that older children become inflexible in their understanding and less likely to benefit from instruction (McNeil, 2007). Our research investigates the effects of gestures in math instruction, with respect to age of the child learner. We studied children ages 7-11 who watched video tutorials on mathematical equivalence (understanding the equal sign) either with or without gesture. Children significantly improved their mathematical equivalence understanding from before to after remote video instruction ($p < .001$). However, 7-to-8-year-old children had greater mathematical equivalence understanding at pretest than 8-to-11-year-old (younger M = 6.19 vs. older M = 3.56 items correct). Our video instruction closed this gap between older and younger children, bringing older children to the same level of understanding as the younger children at posttest (younger M = 7.88 vs. older M = 8.00). Ongoing analysis considers the interaction between instructional gestures and child age on learning. We hypothesize that the younger children will benefit more from gesture in instruction than older children.

Study Habits, Trait Anxiety, and Socioeconomic Background of STEM Undergraduates

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Zachary Ngo*; Mya Arellano and Amira Ibrahim, *California State University Channel Islands*

Abstract: Undergraduate students pursuing science, technology, engineering, or mathematics (STEM) fields of study need to pass several lower-division courses before continuing. Previous research has demonstrated that students with higher academic confidence, lower academic anxiety, and higher socio-economic backgrounds (SEB) are more likely to succeed in STEM. However, it is still unclear if STEM students' SEB relates to general trait anxiety, if this further influences their study habits, and if study habits predict success in STEM coursework. We aim to determine 1) whether studying in a group leads to better grades than studying alone, 2) whether SEB predicts study habits, and 3) if SEB is associated with trait anxiety in STEM majors. 111 participants were recruited from a physics course at California State University, Channel Islands. Instructors provided the link to surveys on their online learning management system containing items assessing trait anxiety, study strategies, and demographic information . Final grades were provided by instructors. Participants were asked how much of their study time for the course was dedicated to studying alone versus in a group. Trait anxiety was measured using six items from the State-Trait Anxiety Inventory, where participants rated how often they experience scenarios, for example "I take disappointments so keenly that I can't put them out of my mind". We hypothesize that higher course grades will be associated with more time studying in groups, that lower SEB is a predictor of more time studying alone, and that there will be a negative relationship between SEB and student's trait anxiety.

The Impact of a Compassionate Love Writing Intervention on State Attachment to God

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Kaitlyn Knight* and Anna Harper, *Southern Nazarene University*

Abstract: Attachment has been a topic that has been explored through research for many years by various researchers. From prior research we have been able to see a correspondence between a childs attachment to their caregivers and their relationship with God. The purpose of the current study is to determine whether or not reflecting on past experiences of giving or receiving compassionate love has made an impact on state attachment to God. In the present study there were three hypothesis that were tested. The first hypothesis was reflecting on an experience of giving and receiving compassionate love will result in less state attachment anxiety toward God, compared to reflecting on an everyday experience. The second hypothesis was reflecting on an experience of giving and receiving compassionate love will result in less state attachment avoidance toward God, compared to reflecting on an everyday experience. The last hypothesis was Reflecting on an experience of giving and receiving compassionate love will result in greater state attachment security toward God, compared to reflecting on an everyday experience. The participants were asked to answer a series of questions including the attachment to God scale and then were asked to take 5 minutes to reflect on an assigned prompt. There were 3 different prompts that included giving compassionate love, receiving compassionate love, and an everyday experience(control). My analyses will include three one-way ANOVA's testing how reflecting on giving/receiving compassionate love will impact state attachment to God.

The Influence of Latinx Acculturation and Ethnic Enclaves on Alcohol and Illicit Substance Use Among Latina Adults

Discipline: Psychology & Social Sciences
Subdiscipline: Sociology

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Abstract: Background: This study tests the hypothesis that less acculturated, female-identified Latinas and Latinas living in Latinx ethnic enclaves will be less likely to use alcohol and drug use than more acculturated Latinas and Latinas living outside of ethnic enclaves.

Methods: EMR data were extracted from Latina patients who had received care at a federally qualified health center (FQHC) in Chicago, Illinois from between 2012 to 2017. From the EMR and national neighborhood datasets, we abstracted data on demographics, acculturation (preferred language),lifetime history of alcohol and illicit substance use, and neighborhoods(% Latinx residents).

Results: The range of our 1282 patients' ages was 23 to 77. Among our sample, 38% of patients preferred to speak Spanish and 33% of patients lived in neighborhoods with ≥83% of residents identifying as Latinx. Approximately 29% of patients had a lifetime history of alcohol use and 5% had a lifetime history of illicit substance use. Compared to English-speaking women, Spanish-speaking women have lower odds of alcohol use, OR = 0.39, 95%CI[0.29, 0.53], p <.0001, and illicit substance use,OR= 0.47, 95%CI [0.23, 0.93], p = .03. Women living in ethnic enclaves/predominantly Latino neighborhoods also had lower odds of alcohol use relative to their counterparts, OR=0.70, 95%CI [0.50, 0.97], p = .04.

Discussion: Acculturation appeared to have positive health effects in terms of alcohol and illicit substance use. Future studies should examine if this relationship is similar among Latino men and other Latinx individuals, who may experience different social norms.

H2A Guest Workers in the Salinas Valley and Central Coast during the Covid-19 Pandemic

Discipline: Psychology & Social Sciences
Subdiscipline: Sociology

Angie Tran; Xenia Enriquez* and Lorenzo Covarrubias, *California State University of Monterey Bay*

Abstract: The purpose of this project is to investigate the working and living conditions of agricultural guest workers in the Salinas Valley and Central Coast during the Covid-19 Pandemic. The research is especially interested in the promises made by the growers to the guest workers through the H-2A program and if those promises still withstand during the Covid-19 Pandemic. The project will use data conducted from interviews, observations, press coverage, and archival research. The research question is the extent to which the living and working conditions of H2A guest workers have worsened during the pandemic. Research is still ongoing, but as anticipated, our current information already shows that H2A workers are in fact facing more challenges during the pandemic and are particularly vulnerable. Studies show that many workers who speak out, strike, or attempt to unionize for better living and working conditions are not rehired for the following year. Due to the potential backlash and consequences, H2A workers fear speaking out. In conclusion, this research is important to give a voice to the H2A guest workers who are underrepresented and under-resourced.

High Impact Practices in the Mathematics Classroom

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Circe Gedeon* and Maria Mercedes Franco, *Queensborough Community College*

Abstract: The purpose of this research project is to collect, digitalize, organize, and analyze data from sections of mathematics courses taught at an urban community college with and without the use of High Impact Practices (HIPs) and to

attempt to capture and compare the student experience in these varied settings. Aspects of the student experience that are being examined relate to student participation and satisfaction with the course (e.g. attendance, withdraw rates, student evaluations) and student learning outcomes (e.g. final grades, proficiency on final exam questions/topics covered on both traditional and HIP courses). Preliminary results about the student experience will be discussed.

Improving the Understanding of Energy Conservation in Hawai'i's Community

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Nikki Arakawa* and Herve Collin, *Kapiolani Community College*

Abstract: Hawai'i is setting the pace for renewable energy and sustainability in the US. By 2045, Hawai'i plans to generate 100% of its electricity solely using renewable sources. Renewable energy generation in Hawai'i stood at 27.6% by 2017 according to the Hawai'i State Energy office. In meeting these goals, it is important for Hawai'i residents to first understand energy usage, so they can be better equipped to support the state's goals by reducing their personal energy consumption. The purpose of this research is to increase the understanding of energy conservation and the need to reduce its consumption by engaging participants in a renewable energy-based project. Participants will learn how energy is generated, converted, and saved, how to determine its usage rate, and how to visualize its acquisition and its usage. Participants will employ two 12V solar panels connected to a battery charge controller and a 12V lead-acid battery. A battery monitoring device will be used to measure the power produced and an inverter will charge the physical electrical system. By the end of the project, students will be able to better understand their electric energy usage and how it can impact Hawaii's Clean Energy initiative.

Physical Science in Elementary Schools: Is It Happening

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Dermont Donnelly; Iliana Borges* and Phillip Tapia, *California State University, Fresno*

Abstract: Elementary students are naturally curious about the world around them, but often receive limited Physical Science instruction in schools. The introduction of the Next Generation Science Standards (NGSS) is an effort to support Physical Science instruction at younger grade levels, yet little is known about the impact of the NGSS at such grade levels. This study used the Theory of Planned Behavior (TPB) to investigate what factors influence elementary teachers' intentions to teach Physical Science. Data was collected using a questionnaire with credential-candidate teachers (n=21) and nine interviews with other stakeholders including teacher educators, professional development providers, and practicing elementary teachers. We found that teacher candidates did not make any lesson plans focused on Physical Science during their credential school placements. Such a finding was further supported by stakeholder interviews where most stakeholders believed that less than 25% of elementary teachers teach any Physical Science to their students. Using TPB we identified three factors that restrict most teachers from teaching Physical Science: most administrations are not giving the teachers time to focus on science, the teacher's personal knowledge and confidence of the subject, and the lack of materials and lessons of the subject. This presentation will consider the implications of these findings for teacher education and systemic challenges facing successful integration of the NGSS in meaningful ways.

Gender and Ethnic Differences in Parental Motivations for STEM Event Involvement

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Remi Ali Khan*[1]; Kaylen Sanchez[1]; Tasmia Alam[1]; Dr. Argero Zerr[2]; Philip Hampton[1] and Ian Villalta[3], *(1)California State University, Channel Islands, (2)California State University Channel Islands, (3)San Diego Mesa College*

Abstract: This study examines parental motivations for attending a family science, technology, engineering, and mathematics (STEM) event, including potential gender and ethnic differences. Parental involvement in children's STEM achievement increases persistence in STEM careers (Ing, 2014) and parental attitudes towards science predict higher aspirations in science (Dewitt & Archer, 2015). However, parents of daughters are less likely to believe their child is interested in science and more likely to believe that science is difficult for their child (Tenenbaum & Leaper, 2003). Sons also perceive more parental support in STEM than daughters (Fernandez-Garcia et al., 2019). Participants in the study included 160 caregivers of 218 children (54% girls) who attended a university-affiliated family STEM event. Families were 42% Latino, 24% White, 14% multiethnic, 7% Asian and 10% other. The most common reason caregivers reported attending was wanting to expose children to science (49%), followed by: the child(ren) wanting to come (43%), the caregiver wanting to learn about science activities (26%), and other (14%). Caregivers who brought sons were more likely (18%) to report "other reasons" for attending compared to those who brought daughters (5%; χ 2 = 4.99, p = .03). Latino families were marginally more likely to attend with sons (69%) than daughters (31%; χ 2 = 2.67, p = .08), while

there was no gender difference for White families. Additional qualitative analyses will further examine “other reasons” for attendance. Findings from this study will help to understand parental involvement in family STEM activities and inform future STEM events.

Creation of Coupled-Multiple Response Test Items for Use in an Adaptive, Online Formative Assessment in Introductory Mechanics

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Christina Yee* and Laura Rios, *California Polytechnic State University, San Luis Obispo*

Abstract: Mechanics courses are full of non-intuitive, conceptually difficult principles that are difficult to correct. In order to help students with conceptual growth, we first must determine student's prior resources and tailor supplemental instruction to the student's unique needs. To do this, we are using coupled-multiple response (CMR) questions in introductory mechanics. Coupled-multiple response (CMR) tests are assessments that use a nuanced rubric to examine underlying reasoning elements students may have for decisions on a multiple-choice test (e.g., Wilcox and Pollock, 2015). Here, we describe how we converted 6 free-response formative assessments into CMR items that can be used in an online format for use outside the classroom, and the specific conceptual difficulties they are tailored to address.

Botanical Garden Installation Planning Project

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Trinity Gomez* and Victoria Derr, *California State University Monterey Bay*

Abstract: California State University Monterey Bay (CSUMB) was built on the grounds of the decommissioned Fort Ord Army base and opened in 1995. Since then the campus has changed significantly but despite these improvements, many students and faculty still describe the campus as lacking in green spaces. Faculty in the Applied Environmental Science (AES) department and Psychology department, have been exploring the potential to develop spaces on campus as ecological learning laboratories and for outdoor wellness use. One idea that emerged was to create a botanical garden on campus that could be used for both education and student wellness. The goal of this research is to discover the limitations and necessary components that may come with creating this garden at CSUMB, along with gathering stakeholder perspectives from the AES department and campus planners on garden use, location, and other factors related to the garden. Qualitative research methods such as semi-structured and key informant interviews were created and based off data collected from cross theme document analysis of the CSUMB Master Plan, 2020 Sustainability Plan, and a Landscape Ecology Capstone. The semi-structured interviews are used to gather the viewpoints of the stakeholders previously mentioned. Currently, we are working on analyzing interviewee answers with qualitative data software, Nvivo, to compile common themed data. Results from these analyses will contribute to the creation of a project proposal for a botanical garden that not only fills the lack of green spaces on campus, but will also fulfill CSUMB Master Plan requirements, and address stakeholder concerns.

Seeds in STEM: Generation STEM Program

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Louisa Nickerson*[1]; Aurabel Sandoc[1]; Stephanie Carpintero[1] and David Gillette[2], *(1)California Polytechnic State University, San Luis Obispo, (2)California Polytechnic State University San Luis Obispo*

Abstract: Generation STEM is an inclusive and self-sustaining program that aims to introduce fifth graders in Santa Maria to coding and the many possibilities within STEM using robots and storytelling. Santa Maria is a city thirty minutes south of San Luis Obispo where 89% of students in the elementary school district received free and reduced-price meals in 2017-2018. Students begin the two-hour Generation STEM activity by first watching an animation to learn about the engineering design process and then working in pairs on two engineering design challenges. The students are then split up into seven groups, with each group facilitated by a high school mentor from the Generation STEM Mentorship Program, and led through a story that asks students to assist various STEM professionals with a challenge they are currently facing in their careers as computer programmers, mechanical engineers, physicists, mathematicians, etc. Through the story, the students learn details about the professionals’ fifth grade interests that sparked their entry into a STEM career and work together to block code the robot to complete the challenge.

All materials used in the Generation STEM program are hosted on a website in order to provide teachers with free access to the activities. Surveys were taken before and after each activity. The data implies that the Generation STEM activity provided students with an increased understanding of STEM and an introduction to coding.

Evaluating the Effect of the Covid-19 Pandemic on Learner Engagement in the Mitx 7.05x Biochemistry Mooc

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Martha A. Castro*[1]; Monika Avello[2]; Darcy Gordon[2] and Mary Ellen Wiltrout[2], *(1)Pomona College, (2)Massachusetts Institute of Technology*

Abstract: The COVID-19 pandemic has caused many academic institutions to migrate to the virtual world. However, many online course providers existed before the pandemic, like edX, a platform that hosts thousands of MOOCs (massive open online courses) created by institutions across the world. MITx Biology has produced seven MOOCs, ranging from introductory biology to upper-level molecular biology courses, which run regularly, sometimes multiple times a year. These courses are free to audit and require just an internet connection, increasing access and affordability to learners worldwide. One MITx Biology MOOC, 7.05x Biochemistry: Biomolecules, Methods, and Mechanisms, began a new run in April 2020 during the pandemic. Given its extreme disruption to daily life, we seek to understand how the COVID-19 pandemic has affected learners in 7.05x. We hypothesize that the pandemic has caused an increase in learner engagement during the 2020 run in comparison to three prior runs in 2019. To test this hypothesis, we will compare learner data, including enrollment, success in assessments, and completion of practice questions and course videos across runs. We will use Microsoft Excel, Tableau, and Python 3 to perform quantitative and visual comparisons across runs. Enrollment in the 2020 run of 7.05x appears two-fold higher than previous runs, with similar increases in video, problem, and forum activity. Interestingly, while the absolute number of learners interacting with the course increased, preliminary analyses show the proportion of engaged learners decreased, signifying that higher enrollment does not necessarily correspond to greater course engagement.

Workplace Climate for LGBT+ Physicists:

Discipline: STEM Education & Learning

Subdiscipline: Other STEM Education & Learning Research

Matthew Mikota*, *DePaul University* and Ramón Barthelemy, *The University of Utah*

Abstract: An ever-growing number of our future physicists identify as a part of the Lesbian, Gay, Bisexual, Transgender/Transsexual Plus (LGBT+) community and therefore it is important that we understand their experience and how to best support them. Specifically our question of study was: what role does workplace climate play on the degree of outness of LGBT+ physicists? We analyzed the climate experiences of LGBT+ physicists through an online survey (N=324) collected by the committee on LGBT+ physicists for the American Physical Society. Results demonstrated the impact of workplace climate (positive and negative), the observation and experience of exclusionary behavior, and status as a student on how out physicists were about their LGBT+ identity. We found that being a student, exposure to exclusionary behavior, and both positive and negative workplace climate were significant predictors of outness to coworkers. The climate model can explain 22% of the variance in outness using these significant features. The results indicate that a positive workplace climate is a strong predictor of outness suggesting the further importance of proactively inclusive physics communities.

Ciencia Para Todos: Making the Psyche Mission Accessible to Spanish Language Speakers

Discipline: STEM Education & Learning

Subdiscipline: Other STEM Education & Learning Research

Christian Trujillo*[1]; Adriana Talamante[2] and Catherine Bowman[2], *(1)Humboldt State University, (2)Arizona State University*

Abstract: Western science often has not been inclusive of other cultures, especially when it comes to people who speak different languages. The integration of language diversity into our institutions and outreach is necessary for the inclusion of underrepresented groups in science, especially as many of our scientific efforts have global reach. NASA has some existing Spanish resources (such as https://ciencia.nasa.gov/, https://spaceplace.nasa.gov/sp/, @NASA_es, etc.) but, with about 50 million Spanish-speakers in the U.S. (and ~500 million worldwide), additional resources in Spanish have the potential to increase learning and engagement among traditionally underrepresented groups in STEM. Translating documents into Spanish for NASA's Psyche mission contributes to this goal, adding to work being done by an undergraduate-led group called Ciencia Para Todos (Science For All). Our first step was to translate the mission's "FAQs." Critical to this was acknowledging that translation, particularly of technical information, involves more than translating each word. In many cases, we found that new phrasing was needed to ensure accuracy and comprehensibility. Additionally, with so many variations of Spanish spoken, we sought reviews from Spanish speakers on the Psyche mission team (those from around the world and those from the U.S. who speak Spanish with their families) to ensure that the language would be understandable to as many people as possible. We will provide examples of concepts and vocabulary that required rephrasing for inclusivity to demonstrate the importance of engaging a diverse group of speakers when translating scientific and technical information.

Analyzing Interviews with Team Members: A Comparative Analysis of Team Member's Perceptions

Discipline: STEM Education & Learning

Subdiscipline: Other STEM Education & Learning Research

Hannah Castro*[1]; Amreen Thompson[1]; Alice Olmstead[1]; Andrea Beach[2]; Charles Henderson[2] and Diana Sachmpazidi[2], *(1)Texas State University, (2)Western Michigan University*

Abstract: Existing research has shown that the use of research based instructional strategies can improve the quality of instruction and students' academic performance in undergraduate STEM courses. The redesign and improvement of STEM courses can be done through the use of instructional change teams. Although there is existing research about business teams and teams in general, there is limited research about how teams can effectively make change in a higher educational setting. The goal of our overall project is to develop guidance for leaders of instructional change teams through research involving interviews and surveys. A postdoctoral researcher and I have been conducting interviews with team members from several different teams. We have been asking them to react to our existing model of instructional change teams and consider how the model applies to their own teams. The main parts of the model include 5 team inputs, 5 team processes, 3 emergent states, and 4 team outcomes. We will eventually use these interviews to develop a survey to run a qualitative analysis on a larger group of team members. A sub-goal of the research that I will be focusing on will analyze interviews from team members from the same team by comparing and contrasting their individual perceptions of their team's dynamic with particular focus on power. This analysis will also consider possible explanations for why differences across team members' perceptions may have emerged and how these findings can support future research about instructional change teams.

Integrating Native Hawaiian Pedagogies into a Virtual Summer Bridge to Increase Diversity in Engineering

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Kiana Fuller* and Hervé Collin, *Kapiolani Community College*

Abstract: Native Hawaiians are one of the most underrepresented groups in engineering in Hawaiʻi. In 2015, only 5.8% Native Hawaiian students majored in engineering and only three received their Ph.D. at the University of Hawaiʻi at Mānoa. While programs that incorporate cultural pedagogies to keep students engaged in engineering exist, few exist in Hawaiʻi. Hawaiian pedagogies — such as ʻāina (land)-based learning and moʻolelo (stories) told through song (mele) and chants (oli) — are foundational ways that Native Hawaiians learn and pass on knowledge, and many student support programs use them to successfully increase retention. The objective of this project is to show how Native Hawaiian pedagogies can be integrated into an engineering program. A six-week online summer bridge program for underrepresented engineering students at a community college was chosen to trial methods and collect observations and feedback. A cultural peer mentor integrated cultural activities such as chanting and met with students daily to create a space where they could find and express their cultural identity. Students were asked to create a sustainability-based engineering project and work with the mentor to connect it Hawaiian culture. The mentor met with the program's mentors, faculty, and coordinator to share the significance and effects of the integrated pedagogies. Results will discuss the implementation's successes and challenges, especially in an online environment. Future work includes assessing its effects on student retention and incorporating it into the curriculum in order to understand how cultural integration is foundational to diversify engineering.

Social Emotional Learning and Precollege STEM Education: What Is the Intersection between Inclusion and STEM?

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Metzin Rodriguez* and Susan Rowe, *Oregon State University*

Abstract: It is important to not overlook the intersection of Social Emotional Intelligence (SEL) in STEM, specifically, pre-college programs. SEL is described as the social behavior by which students achieve goals, the way they feel including but not limited to empathy. When looking at pre-college programs in the nation, their curriculums and initiatives centralize around equity, inclusion, and accessibility for student groups, sometimes excluding underrepresented audiences. Studies have shown STEM popularity within the last few years, but obsessing too much in the training of individuals instead of discovery tools in the field. In the following case study, we will investigate three areas of STEM: Inclusion, technical curriculum, and teaching style at Oregon State University. Including the leaders from pre-college programs, including SMILE.We will utilize a mixed-methods quantitative approach - a structured survey for pre-college program experts (N=20), part A focusing on STEM approaches and part B on student enrollment. The second piece is qualitative - personal meaning maps with a subgroup of the participants (N=30) representing different STEM focus. We will analyze the expected results and detect any similarities and differences between the intersection of shared definitions; or missions for the implementation for enhancement through professional development and SEL. Being able to understand the student and current state of learning will inform future research on this topic, the implementation of programs that empowers students, especially amplifying underrepresented voices in science. To innovate the foreground makeup of Social Emotional Learning to integrate into the STEM curriculum, during the novel COVID-19 era.

Ocean Acidification Toolkits: Keeping Ocean Acidification in the Public Eye in the Pacific Northwest

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Annalise Guthrie*, *Kansas University* and Libby Jewett, *National Oceanic and Atmospheric Administration*

Abstract: The National Oceanic Atmospheric Administration's (NOAA) Ocean Acidification Program is developing educational outreach toolkits to meet goals outlined in its Educational Implementation Plan. Toolkit development will increase engagement of target audiences and enhance community resilience to ocean acidification (OA). A toolkit was designed for the NOAA Northwest Fisheries Science Center (NWFSC) that uses effective strategies in expanding awareness around OA, NOAA OA research, and community-based actions that can help mitigate OA. The NWFSC OA outreach toolkit was informed by the Framework's Institute Strategic Frame Analysis to understand effective approaches in translating OA foundational knowledge and research to empower student audiences with solutions. Consisting of four modules, the toolkit explains our ocean's carbon cycle, OA as a chemical change over time, effects of OA on pteropods such as *Limacina helicina, Oncorhynchus kisutch* olfaction, and food web implications. All modules discuss the cause of OA, along with actions audience members can take to mitigate OA. The modules were piloted to three student audiences: undergraduates, 3rd and 4th graders, and 7th through 9th graders. Effectiveness of the toolkit was evaluated using pre- and post surveys taken by each audience. Preliminary results suggest the audience exhibited increased knowledge of OA concepts aligned with the modules. The NWFSC OA educational outreach toolkit was adapted based on these evaluations and prepared for distribution. Continued development and refinement of toolkits will be based on pre- and post-presentation evaluations for various NOAA centers around the country.

Cultivating Empathy in STEM: Emerging Themes from Student Reflections about the Thirty Meter Telescope Controversy

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Alexander Vasquez*; Brianne Gutmann; Daniel Barringer and Alice Olmstead, *Texas State University*

Abstract: It is important for STEM students to develop ethics knowledge, yet this is rarely taught in STEM classes. We are addressing this limitation in our physics classes at Texas State University. Here, we focus on teaching about the ethics of building the Thirty Meter Telescope (TMT) in Hawaii for an observational astrophysics class. We developed resources for students to make informed decisions about this complex issue. The unit encompasses an introduction of the TMT, a local perspective in San Marcos, a history of Hawaii, and perspectives about the TMT relative to formal ethical frameworks. We will present data from this new unit in Spring 2020, including post-class interviews with students and their written reflections from class. Our preliminary analysis of students' written work indicates that students experienced an increased understanding of the complexity of the issue, increased empathy with the protesters, and a desire for a compromise. Based on this and our ongoing analysis, we will highlight what worked well in our design and what could be improved in order to support the community of STEM educators and education researchers in teaching about ethics in STEM classes.

The Symbiologist: Examining the Power of Science Communication through Narrative Storytelling

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Arya Natarajan*, *University of California, San Diego* and Laurel Allen, *California Academy of Sciences*

Abstract: There are many works of children's literature exploring scientific topics through fictional characters (e.g. *The Magic School Bus*) that serve as everyday vessels for STEM education. However, there are far fewer such stories geared toward teens and adults; science writing for these older audiences often remains within the realm of news articles, editorials, and informational books. *The Symbiologist* series aims to create a compelling outlet for sharing science stories and provides a vehicle to investigate how fiction-based narratives of real science resonate with broader audiences. This publication provides descriptions of natural phenomena through the lens of fictional writer Tara Anand as she adds to her field journal. Each entry contains personal, sensory, and scientifically accurate accounts of various symbiotic relationships accompanied by hand-drawn illustrations, all from Tara's perspective as a woman of color and emerging scientist. *The Symbiologist* is hosted online as a blog (*https://bit.ly/symbiologist*) but will also be published as a printed book or zine. Blog posts are supplemented with a newsletter (*https://symbiologist.substack.com/*) providing extended sources, additional scientific research interpretation, and supplementary illustrations. Online surveys will be used to elicit audience response, assess information retention, and ultimately determine the effectiveness of narrative storytelling for science communication purposes. In its exploration of creative science storytelling, *The Symbiologist* seeks to instill a deep appreciation for the natural world's interconnectedness, as well as inspire wonder and curiosity in people of diverse ages while making scientific research and concepts accessible and part of everyday life.

Physical Science in Elementary Schools: Is It Happening?

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Phillip Tapia* and Dermot Donnelly, *California State University, Fresno*

Abstract: Elementary science teaching curriculum in contemporary society has faced many challenges overtime with pre- and in-service teachers not receiving sufficient training or support. Many adolescents are not exposed to Physical Science until their middle/high school years. Studies have shown that many elementary teachers are uncomfortable teaching Physical Science and it is questionable if the implementation of the Next Generation Science Standards (NGSS) will result in

broader changes. To this end, we conducted a questionnaire with credential-completing teachers (n=21) and nine in-person interviews with teacher educators, professional development providers, and elementary teachers to examine what factors impact the teaching of Physical Science. We used the “Theory of Planned Behavior” model to analyze our data and identified three main components to why elementary teachers have difficulty teaching Physical Science: 1.) They have restricted time to teach science, 2.) they have a lack of confidence in their knowledge of the subject, and 3.) they lack sufficient materials and support from their school systems. In light of the goals of the NGSS, these results illustrate the continued difficulties faced by elementary teachers in teaching Physical Science. This presentation will discuss the nature of these difficulties and consider possible future directions to support Physical Science in elementary schools.

The History of Latinx Women Reaching Higher Education

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Alondra Castaneda* and Ellen Kittell, *University of Idaho*

Abstract: The purpose of my research is to evaluate how women from a marginalized population are achieving higher education over the past two centuries. I will carry this on by examining women who identify as Latinx and first generation. I will examine between the nineteenth and twenty-first centuries, comparing how their histories were similar and how they were different. One of the questions I wish to investigate is whether stereotypes impact women in higher education and if they do, to what extent? Then I will conclude what I have examined throughout the history found in articles, book, archives and interviews. To Ultimately prove the impact that stereotypes have/have had on women for the past centuries. The significances of my research is to serve as a key for women who identify as Latinx and first generation in the process to achieve higher education knowing that this a reality is essential to the progress and growth of these community with marginalized population, we must strive to motivate women to continue "taking up spaces" and using there voices my research is the backbone.

Strengthening the Guardians of Living Water Program through Integration of Indigenous Knowledge

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Catalina Rosales* and Vanessa Simonds, *Montana State University*

Abstract: Water is vital for all living things and the current worldwide environmental crisis affects us all. These crises are the reason why it is crucial for us to educate the next generation, on the importance of Indigenous and Western science combined. We have held 5 summer camps and a 4 year-long after school programs that have enhanced the knowledge of the participants on culture, history and water contamination. The objective of this research project was to refine and adapt the Guardians of the Living Water facilitator guides. Our main goal was to strengthen the Native science aspects of the curriculum. The research team met weekly to discuss readings on Indigenous Science, Decolonizing Research, and to review existing environmental health curriculum. We developed a list of best practices among the existing materials to apply to the Guardians of the Living Water facilitator guides. The research team also developed an interview guide to elicit feedback from experts. We compiled and analyzed the data and then brought it back to our community advisory board. We developed a process for adapting this curriculum to other unique cultural communities. We found that incorporating Indigenous science into this curriculum is beneficial for communities. The development of this curriculum is an initial step we can take as a society to give new energy to Western science.

Painting the Pacific: A Comparative Analysis of the Lightfastness of Watercolors Made from Indigenous Plants in the Pacific Region

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Michael Fernandez* and Mari Marutani, *University of Guam*

Abstract: Pacific Islanders have traditionally used plants and other natural resources to craft paints, dyes, and other colorants. However, much of society today has transitioned to more accessible, inexpensive colorants which oftentimes contain toxic pigments and harmful solvents that can be detrimental to human health and the environment. This study will explore using phytochemicals of plants indigenous to the Pacific as safe, natural watercolor paints. The objective of this study is to test the lightfastness or permanence of watercolors made from *langiti* (*Ochrosia mariannensis*), *ladda* (*Morinda citrifolia*), *binalo'* (*Thespesia populnea*), and *kaffo*' (*Pandanus tectorius*) — plants which are heavily rooted in the Pacific arts.

In this experiment, water-soluble pigments were extracted from the plant materials through solvent extraction, rotary evaporation, and freeze drying. The extracted compounds were then bonded to a colorless mordant, potassium aluminum sulfate, through chemical precipitation. The resulting pigment was then dried and made into traditional natural watercolors using a mixture of gum arabic and honey. To test for lightfastness, the natural watercolors and name-brand ASTM compliant watercolors were subjected to an accelerated UVA and UVB exposure test for 21 days. Furthermore, sections of the color swatches were covered to analyze color intensity without exposure to any UV light. Color differences were measured in CIE L*a*b* coordinates in two-day intervals using a spectrocolorimeter. Data obtained from the triplicated samples were compared by analysis of variance and mean and standard deviation were calculated.

Research is currently being conducted and results will be examined and published at a later date.

Graduate Poster Presentations

Developing Bioanalytical Tools to Sequence Guanine Oxidation Products in RNA

Discipline: Chemistry
Subdiscipline: Analytical Chemistry

Nicole Mathewson*; Aaron Fleming and Cynthia Burrows, *University of Utah*

Abstract: RNA is susceptible to oxidative damage caused by reactive oxygen species (ROS). Exposure to ROS can result in modifications of the free nucleobases, nucleosides, or nucleotides in RNA. Our interests lie in modifications arising from guanine (G) oxidation, as G has the lowest standard reduction potential of the four canonical bases, making G a major site of ROS-mediated oxidation. Interestingly, guanine oxidative modifications in RNA has only recently been studied as methods developed for investigating G oxidation in DNA cannot be directly applied to RNA. In this work, we aim to develop bioanalytical methods to sequence the major guanine oxidation products in RNA, 8-oxo-7,8-dihydroguanine (OG) and spiroiminodihydantoin (Sp). We will use reverse transcription of RNA containing OG or Sp to perform insertion assays for initial method development. This initial study will provide the foundation for developing a method to sequence OG or Sp in RNA by following characteristic mutation signatures. After initial studies, we will perform Sanger sequencing to identify the sequencing signatures for OG and Sp in RNA. Last, we will use the developed methods on an *in vivo* RNA sample to demonstrate we can use the characteristic signatures for use in next-generation sequencing. This study will provide a more complete analysis of guanine oxidation in RNA, which could further aid in mechanistic insight of RNA damage and provide useful bioanalytical tools to identify oxidative modifications in RNA. The ability to identify specific modifications may provide knowledge into how a modification affects gene regulation or other cellular responses.

Characterization of Copper Hyponitrite Complexes Using X-Ray Absorption Spectroscopy

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Brenda Henriquez*[1]; Pokhraj Gosh[2]; Subrata Kundu[2]; Timothy H. Warren[2] and Dr. Chantal Stieber[1], *(1)California State Polytechnic University, Pomona, (2)Georgetown University*

Abstract: Nitrous oxide (N_2O) is the main contributor to the ozone layer depletion, has almost 300 times the warming potential of carbon dioxide, and lingers in the atmosphere for an average of 114 years. Biological systems can both produce N_2O via NO reductive coupling, and reduce N_2O through reactions at copper and iron centers, but not at sufficient rates to mitigate pollution. The mechanisms are not fully understood. Hyponitrite ($O_2N_2^{2-}$) intermediates are proposed, but there are few isolated examples. In the current work, discrete b-diketiminate (^{i}PrNNF$_6$) copper complexes formed in solution from NO coupling were analyzed by X-ray absorption spectroscopy (XAS) to determine the metal oxidation state, coordination environment, and assess hyponitrite formation. The X-ray absorption near edge structure (XANES) analysis determined the oxidation state of the complexes $[(^i\mathrm{PrNNF}_6)\mathrm{CuO}_2\mathrm{N}_2][\mathrm{CoCp}_2]$ and $(^i\mathrm{PrNNF}_6)\mathrm{CuO}_2\mathrm{N}_2$ to be +1, while $(^i\mathrm{PrNNF}_6)\mathrm{CuO}_2\mathrm{N}_2\mathrm{Ph}$ has an oxidation state of +2. The $[(^i\mathrm{PrNNF}_6)\mathrm{CuO}_2\mathrm{N}_2][\mathrm{CoCp}_2]$ complex had a lower rising edge feature making the oxidation state assignment more nuanced. The extended X-ray absorption fine structure (EXAFS) allowed for the copper coordination environment to be determined, using $(^i\mathrm{PrNNF}_6)\mathrm{CuO}_2\mathrm{N}_2\mathrm{Ph}$ as a comparison for which the 3-D atomic structure is reported. The EXAFS for $[(^i\mathrm{PrNNF}_6)\mathrm{CuO}_2\mathrm{N}_2][\mathrm{CoCp}_2]$ suggest dimer formation. The EXAFS for $(^i\mathrm{PrNNF}_6)\mathrm{CuO}_2\mathrm{N}_2$ are consistent with O_2N_2 bound to copper, and suggest that the hyponitrite complex was synthesized and isolated. This has implications for understanding reactivity and reduction of N_2O and NO. Future work includes understanding the mechanism by studying other intermediates formed in NO coupling reactions and has implications for understanding pollutant reduction.

The Modification of Metal-Organic Frameworks for Drug Delivery

Discipline: Chemistry
Subdiscipline: Inorganic Chemistry

Alberto Smith*; Willmer Flores; Brandon Liu and Yangyang Liu, *California State University, Los Angeles*

Abstract: Metal-organic frameworks (MOFs), with high storage capacity, biocompatible and low cytotoxicity, have emerged as possible drug carriers. Direct administration of drugs for cancer treatment is not practical in biological systems because these drugs often lack selectivity. Previous research has shown that the incorporation of acid-responsive polyethylene glycol (PEG) by surface modification of UiO-66 MOF improved its drug delivery properties. We aim to develop a post-synthetic method compatible with a variety of zirconium-based MOFs with different pore sizes and geometries. The incorporation of PEG to each MOF is achieved by the functionalization of MOFs using the solvent-assisted ligand incorporation (SALI) of an organic linker, followed by a “click” reaction. The drug encapsulation and release properties of PEGylated MOFs is studied by observing drug-release in neutral pH and slightly acidic pH to mimic healthy and cancer cell environments. This project explores approaches to improve the stability and drug-release control for a variety of MOFs in biological systems.

Modular System for Transition Metal-Single Chain Polymeric Nanoparticles

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Thao Mee Xiong* and Steven Zimmerman, *University of Illinois at Urbana-Champaign*

Abstract: The current field of conducting transition metal-catalyzed bioorthogonal reactions inside cells shows important applications in intracellular drug synthesis and bio-labeling. This requires the catalyst to function under mild conditions (air, water, room temperature) and extremely low concentrations. One strategy to improve catalytic activity in the complex biological environment mimics metalloenzymes by folding a polymer chain around a metal center to form single chain nanoparticles (SCNPs). In 2016, our group reported Cu-SCNPs that catalyze the azide-alkyne cycloaddition (CuAAC) reaction in water and inside cells. We are working toward expanding the library of catalysts by developing a modular approach via supramolecular chemistry – a SCNP formed from induced self-folding of an amphiphilic polymer under highly dilute aqueous conditions to form unimolecular micelle-like structures for selective binding of catalysts and substrates. The polymers were synthesized from free radical polymerization and characterized by GPC, TEM, and DLS. The SCNP's ability to increase the catalytic activity of CuAAC and Ru-catalyzed cleavage of allylcarbamate groups was studied by fluorescence kinetic studies. We observed faster rates of reaction and higher yields than that of free catalysts. We also observed trends between the structure of the metal-ligand complex and its catalytic activity in the presence of a SCNP. Our results demonstrate the potential of this system as a general scheme to obtain functional transition metal-SCNPs.

Tracking Degradation in Niobium Pentoxide Thin Films across 10,000 Lithiation/Delithiation Cycles

Discipline: Chemistry
Subdiscipline: Other Chemistry

Heriberto Flores Zuleta*; Gaurav Jha; Chaitanya Gadre; Joshua Ziegler; Ilektra Andoni; Mingjie Xu; Vivian Chen; Xiaoqing Pan and Reginald Penner, *University of California, Irvine*

Abstract: Niobium pentoxide (Nb_2O_5) is a metal oxide that has garnered attention as a battery material due to its high theoretical energy capacity and fast Li^+ (de)insertion kinetics. Like other battery materials, Nb_2O_5 electrode performance diminishes over extended periods of cycling until it can no longer store charge. Electrode degradation is a complex process involving the operation of several interdependent processes including surface passivation, the loss of crystallinity caused by repetitive strain, and the loss by leaching of metal, from the oxide, altering its stoichiometry. Multiple characterization methods are typically required to elucidate these processes. Electrochemical impedance spectroscopy (EIS) is a powerful *in-situ* tool that exposes the electrical properties of an energy storage material during cycling, and over long periods of time during which degradation may be occurring. We have acquired EIS data sets for Nb_2O_5 films prepared by electrophoretic deposition in this study. These data sets are fitted to an equivalent circuit model originally used to describe conducting polyaniline films. Using this model, some preliminary trends emerge when the circuit element values are plotted as a function of cycle number which provide insight into how the Nb_2O_5 film degrades. For the full picture, EIS is coupled with x-ray photoelectron spectroscopy, Raman spectroscopy, and *ex-situ* scanning & transmission electron microscopy to monitor the degradation evolution of electrodeposited Nb_2O_5 thin films subjected up to 10,000 charge/discharge cycles.

Symmetry-Breaking Charge Separation in Solid State Tetraphenoxy Perylene Diimide Films for Use As Active Layers in Organic Photovoltaics

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Carolyn Ramirez* and Michael Wasielewski, *Northwestern University*

Abstract: In organic photovoltaics, the light-absorbing layer absorbs photons which create excitons (bound electron-hole pairs). To separate these opposite charges with organic molecules (and extract them from the device), separate electron donor and acceptor molecules are needed to conduct each charge, which can lead to engineering challenges. Through symmetry-breaking charge separation (SB-CS), only one material is needed to generate excitons and separate charges. SB-CS can occur when one organic molecule is photoexcited while coupled to a neighboring molecule. The complex undergoes charge transfer where one molecule is oxidized while the other is reduced, breaking the charge-neutral symmetry and resulting in one cationic and one anionic molecule. This phenomenon is generally not energetically favored in the solid-state.

We show for the first time SB-CS in solid-state films of 1,6,7,12-tetra(phenoxy)-perylene-3,4:9,10-bis-(dicarboximide), or tetraphenoxy-PDI (tpPDI). Films of three different tp-PDI derivatives (with different tails at imide positions: octyl-tpPDI, cyclohexyl-tpPDI, and hydrogen-tpPDI) are made by spin-coating solutions of each molecule in chloroform on sapphire substrates and then solvent-vapor or thermally annealing. Single crystal and grazing incidence x-ray diffraction/scattering reveal π-π stacking in all derivatives and intermolecular hydrogen-bonding only in H-tpPDI, revealing that H-tpPDI films are most ordered. A mixture of excimer and charge transfer (CT) character is observed by transient absorption and time-resolved fluorescence spectroscopies. More CT character is seen in H-tpPDI, more excimer character in octyl-tpPDI, and a mixture of both in cyclohexyl-tpPDI films. These trends match nicely with coupling expected from x-ray data and show that H-tpPDI is the strongest candidate for photovoltaic applications.

Vibrational Sum Frequency Generation Spectroscopy of Clay Nanoscrolls

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Ariel Vaughn*; Angelo Montenegro; Sabrina Falcon; Muhammet Mammetkuliyev; Brent Melot and Alexander Benderskii, *University of Southern California*

Abstract: Nanoscrolls are rolled up sheets of materials on the nanometer scale with applications ranging from technology to catalysis. Techniques like SEM and TEM are typically required to analyze the surface structures of nanoscrolls. Clay minerals are layered structures that can form as platelets or scrolls where the shape influences the properties of the material - for example talc and asbestos. Detailed knowledge of the surface structure of these minerals is key to understanding their properties. Surface specific spectroscopy techniques including vibrational Sum Frequency Generation (SFG) spectroscopy can be applied to understand the structure of clay nanoscrolls. Vibrational SFG identified four unique hydroxyl features in the clay mineral nickel phyllosilicate. Orientational analysis of the hydroxyls determined that 280 - 328 degrees of the scroll is uncompensated. These results demonstrate the application of vibrational SFG spectroscopy to morphology of nanomaterials.

Using Pnetcdf and Beegfs to Improve I/O of Large Scale Geophysical Simulations

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Jared Brzenski*; Chris Paolini and Jose E. Castillo, *San Diego State University*

Abstract: Large scale geophysical modeling uses high performance computing systems to expedite the solutions of very large, complex systems. High disk latencies, low IOPS, and low read/write data transfer rates are relegating many numerical simulations to I/O bound jobs, where the run time is bound not by CPU rate, but by I/O rate. In this work we seek to improve the I/O of two geophysical modeling applications and take full advantage of the parallel nature of the programs, as well as the file management system for the large output files. Parallelizing output for these programs is achieved using PnetCDF, a parallel implementation of the netCDF format, and BeeGFS, an open source parallel file system. Using these solutions, we have significantly decreased the amount of time spent saving data to disk, and we compare the parallel to the serial implementation of each model, and give analysis of the features used.

Diversifying College Admissions through Machine Learning

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Barbara Martinez-Neda* and Sergio Gago-Masague, *University of California, Irvine*

Abstract: STEM fields like computer science have the highest drop-out rates, with minority students being more likely to drop out. Socioeconomic status can impact students' level of knowledge about fields and options available to them. Additionally, students' admission decision is determined by a review committee that may be influenced by cognitive bias, and some universities focus heavily on standardized testing even though it may not accurately predict disadvantaged students' success.

Furthermore, some students may choose an alternative major even if they are qualified to succeed in their ideal program choice. Others may be denied admission due to bias in the review committee. We hypothesize that the use of new tools based on statistical models with machine learning can improve the current selection process for college admissions.

Based on our research, there are no reported previous efforts to increase representation and success rates in STEM by utilizing machine learning in the admissions process, making our project a leading study in the field. Our project consists of training and implementing a model with students' data regarding their admission and their success in their initial program choice. The goal of the project is to prove that the proposed tools can increase graduation rates in students' first program choice, reduce bias when reviewing applications, and in turn increase diversity in computer science. By suggesting the best-fit program for students from their selections in their applications, this project could reduce drop-out rates in computer science.

Development of Antibiotic-Conjugated Gelatin Type-a for Wound Healing Applications

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Yoliem S. Miranda Alarcón*; David I. Shreiber and Elani Hillman, *Rutgers University, Department of Biomedical Engineering*

Abstract: According to the World Health Organization, in low- and middle-income countries, surgical site infections (SSIs) are the most frequent type of health care-associated infections. The current treatments for SSIs include high doses of antibiotics, additional surgery, or possible implant removal, all of which happen after the patient has begun showing symptoms of infection. The systemic introduction of antibiotics increases the chances of antibiotic resistance developing. Instead, we propose to introduce antibiotic properties to gelatin type-A using proprietary methods to generate bacterial-resistant scaffolds for applications in tissue engineering and drug delivery. Gelatin, the denatured version of collagen, is a biologically-derived polymer that retains the unique chemistry of fibrous collagen to communicate and guide cells during

the remodeling process. This protein serves as a building block for the development of cellular scaffolds, drug delivery systems, and wound healing treatments, among many other products. We aim to tether antibiotics from the β-lactam family, due to their chemical structure and broad-spectrum bacterial inhibition, to gelatin type-A and have it presented within the gelatin scaffold. Herein, we confirm the synthesis and bactericidal activity of our antibiotic-bound gelatin.

Simulation of the Electric Field Intensity and Dielectrophoresis Forces Generated By a Microelectrode Array Influenced By Insulator Coverage for Recovery of Circulating Cancer Biomarkers

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Ramona Luna*; Daniel Heineck and Stuart Ibsen, *Oregon Health and Science University*

Abstract: Tumors are known to shed nanoparticles into circulation throughout their development, even in early stages. These nanoparticles could be used for cancer screening applications, however recovering them from plasma and analyzing them for cancer specific biomarkers is a challenge due to their small size and low density. Microfluidic chips, purchased from Biological Dynamics, that contain microelectrode arrays can be used to create a dielectrophoretic (DEP) force on the desired particles and preferentially recover them from blood plasma samples when an alternating electric field is applied. These electrodes are coated with a protective hydrogel layer that forms a dome over the electrode when electrified. The material inside the dome is unknown but enhanced particle collection is observed in their presence. We hypothesize that the presence of the hydrogel dome effects the electric field distribution and enhances collection of particles. Using COMSOL Multiphysics simulation software, we have modeled the electric fields around the DEP electrode array considering different dome geometries and internal material compositions including gas and diluted blood plasma. Our results suggest that the presence of the dome under certain conditions does effect the spatial distribution of the electric field. Some of these effects should increase collection efficiency. These modeling results better define the relationship between dome formation and enhanced biomarker collection and will help optimize collection techniques and protocols for low nanoparticle concentrations observed in early stage cancer. Further studies will involve analyzing the effect of the dome on convective flow and the effect in particle path during DEP collection.

Single Compartment Membraneless H_2O_2 Fuel Cell Anode Fabrication & Characterization

Discipline: Engineering
Subdiscipline: Chemical Engineering

Menelik James* and Xiaolin Zheng, *Stanford University*

Abstract: Single compartment hydrogen peroxide cells have the potential to revolutionize the energy supplied to micro-electronics. This communication investigates the exploitation of nickel electrodeposited on copper mesh as the anode for performance testing in a single compartment membrane-less fuel cell utilizing hydrogen peroxide as both fuel and oxidant. The nickel electrodeposition on copper mesh procedure is presented here in addition to the performance characterization of the fabricated anode. An open circuit potential of 310mV and max power density of 0.46 mW cm^{-2} has been obtained. Once fully developed, this technology shows a promising application for power supply to electronic micro-devices. The major challenges of today include the development of innovative environment-friendly technologies for energy generation, storage, and conversion. The efficient and clean conversion of chemical energy to electrical power utilizing renewable energy sources with highly active, cost-effective, and readily available catalyst materials is an important technology to develop for the sustainable future of the planet. Single compartment hydrogen peroxide fuel cells are a promising technology for power generation to help address these global challenges.

Redox-Functionalized Electrodes for Electrochemically-Mediated Reactive Separation of Perfluorooctanoic Acid

Discipline: Engineering
Subdiscipline: Chemical Engineering

Paola Baldaguez Medina*; Kwiyong Kim; Johannes Elbert and Xiao Su, *University of Illinois at Urbana Champaign*

Abstract: Per- and polyfluorinated alkyl substances (PFASs) are persistent contaminants that have severe effects to the human body. In water, they exist in low concentrations and, therefore, are considerably hard to remove via conventional methods. Traditional treatment methods lack molecular selectivity, have low energy-efficiency, and require the addition of new chemicals that promote the occurrence of secondary products. Here, we develop a redox copolymer to selectively and electrochemically adsorb perfluorooctanoic acid (PFOA), one of the most abundant PFAS. The copolymer combines poly(4-methacryloyloxy-2,2,6,6-tetramethylpiperidin-1-oxyl) (PTMA) and poly(4-methacryloyloxy2,2,6,6-tetramethylpiperidine) (PTMPMA), denoted as PTMA-co-TMPMA. The implementation of amine functional groups promotes the affinity towards the anionic PFOA, and the redox active radicals provide electrochemical control towards adsorption and desorption. The oxidation degree of PTMA-co-TMPMA tunes the electrostatic, hydrophobic, and affinity interactions, which provides a pathway for optimal adsorption and regeneration, leading to a high uptake capacity of up to 1,000 mg PFOA/g adsorbent. Then, the incorporation of boron-doped diamond (BDD) as counter electrode allows a tandem configuration where separation and destruction of PFOA occurs within the same system. In sum, this work demonstrates an incorporation of

redox functionalized copolymers for the removal of PFOA as well as combining advanced oxidation process to achieve reactive separation of PFOA.

Nano Limestone Concrete

Discipline: Engineering
Subdiscipline: Civil Engineering

Lochana Poudyal*, *Texas Tech Univresity* and Moon Won, *Texas Tech Univeristy*

Abstract: This research aims in reducing the CO_2 emission especially from cement production without compromising the quality of concrete. Limestone dust has been largely used to replace certain percentage of cement in the construction until fly ash was introduced to the concrete industry. Addition of limestone dust increases the early strength of concrete due to early hydration in concrete. On the other side, higher replacement percentage reduces the strength of concrete in later stages. Meanwhile, environmental regulations for coal burning industries has led to decreased production of fly ash. Thus, there is a dire need for a sustainable and economical alternative technology in the concrete industry. Use of nanotechnology in concrete industry is an emerging field that shows higher potential of developing new generation concrete. This research targets in producing a cement with 15% or more limestone dust without reducing the strength of concrete. One of the most promising techniques in this regard is the use of nano calcium carbonate. Nano calcium carbonate mainly helps in providing the nucleation site for the formation of Calcium Silicate Hydrate (CSH) and filling the nanopores in concrete. Different testing methods including fresh, hardened, and durability properties of nano limestone concrete were evaluated. Addition of nano $CaCO_3$ at 1% increased the compressive strength of PLC (Portland Limestone Cement) at 3 days by 6% and at 56 days by 2%. Furthermore, the chloride penetration, resistance to alkali silica reaction, and scaling resistance improved drastically with the addition of nano calcium carbonate for both cement types.

Reducing Detectability of QS-CDMA Signals Via Pattern Randomization Techniques

Discipline: Engineering
Subdiscipline: Electrical Engineering

Chryssalenia koumpouzi*[1]; Predrag Spasojevic[1] and Fikadu Dagefu[2], *(1)Rutgers, the State University of NJ, (2)U.S Army Research Laboratory*

Abstract: In various scenarios tactical military, first responder or civilian ad-hoc communication networks usually require quick and flexible deployment. Those networks suffer from poor synchronization due to lack of coordinating infrastructure which may render communication unreliable. In addition to flexible deployment, security -in terms of covertness- is another essential property of such systems. In order to cope with bad synchronization, Quasi-synchronous (QS) Direct Sequence Code Division Multiple Access (DS-CDMA) has been proposed to enable reliable communication in the presence of imperfect synchronization. QS-DS-CDMA systems rely on spreading codes that are characterized by a Zero-Correlation Zone (ZCZ) which allows maintaining orthogonality up some delays, thus enabling loose synchronization. Even though CDMA is inherently a low probability of detection (LPD) scheme due to its property of spreading transmission in the frequency domain making it appear like white noise, sophisticated adversaries employing feature detectors may still detect the existence of transmission due to the periodic (cyclostationary) nature of the transmitted signals. We reduce the cyclostationary features of a QS-DS-CDMA signal - quantified in terms of the Degree of Cyclostationarity (DCS) - by disturbing its periodic structure via random time dithering, random spreading sequence selection or combination of the two. This approach enables both loose synchronization and improved resilience to sophisticated. All types of proposed randomization do not require knowledge on the receiver part, thus further enhancing security. We show that by employing such pattern randomizing schemes, the DCS can be reduced up to half while maintaining reliable communication.

The Design, Fabrication, and Testing of a Cooling Garment

Discipline: Engineering
Subdiscipline: Mechanical Engineering

Richard Garza* and Noe Vargas, *University of Texas Rio Grande Valley*

Abstract: Temperatures in the Rio Grande Valley are high compared to other parts of the world nearly year-round. Despite this, construction is a necessary part of modern life, and construction workers cannot afford to work only on days when the heat is less oppressive. A serious concern for anyone spending time outdoors in the sun, but especially for construction workers, is heat stroke. There are dozens of deaths and thousands of cases of illness reported in the United States each year due to heat. The aim of this research is to design a device or technology capable of cooling the user – for example a construction worker – in a manner as convenient as putting on a jacket. The feasibility of using the Peltier effect – a phenomenon in which two dissimilar semi-conductors heat up and cool down with the application of an electric current – for this application will be tested. Measurements of input and output temperatures, heat absorption rates, and battery life will be measured, as well as opinions on comfort, in an attempt to validate a potential product. Methods of measure include the use of thermocouples and heat transfer fundamentals. Expected results include a measure of technology readiness and a comparison with current existing solutions. The potential impact of a successful product could be a reduction in the number of lives lost to heat illness, as well as increased productivity for construction workers.

Reliability-Based Spare Parts Management

Discipline: Engineering
Subdiscipline: Other Engineering

Alejandro Najera-Acosta*, *New Mexico State University* and Delia J. Valles-Rosales, *New Mexico State University, Main Campus, Las Cruces*

Abstract: In a competitive production environment, only those companies that consider all aspects of processes or systems performance remain competitive. An important aspect of systems performance is maintenance. Different studies have indicated that for many components in a system, maintenance accounts for as much as 60% to 75% of their overall life cycle costs. Management of spare components is a key feature for the performance of maintenance activities. Spare parts constitute an essential element in all industries, they are designed for a specific use, its useful life is random, and its propagation is difficult to determine. Therefore, spare parts inventories are established to allow rapid replacement of failed parts and ensure a continuity of the operations.

However, the management of spare parts inventory is a significant challenge because these parts have characteristics that differentiate them from other products. For the current work, it is proposed a reliability-based approach, to estimate the failure risk of an equipment when it is subjected to its working conditions. The results show that the number of spare parts required for an equipment can be effectively predicted on the basis of its reliability performance. According to the outcomes obtained, is concluded that the system's working conditions has a significant influence on the system's reliability characteristics and therefore on the management of spare components.

The Bofedales: An Atlas of the High-Altitude Wetlands of the Andes from the Space

Discipline: Geoscience
Subdiscipline: Earth Science

Gabriel Zeballos Castellon* and Bryan Mark, *The Ohio State University*

Abstract: This project integrates the use of satellite imagery with extensive botanical field assessments to produce the first map and spatio-temporal characterization of the highest hydro ecosystems in the Andes. To date, a comprehensive map and inventory of the bofedales of this region are yet inexistent due in great part to their remoteness, inaccessibility, and scattered distribution, but also for lack of effectively integrating remote sensing tools with expert ground assessments. Moreover, because of climate change these wetlands are drying out without the scientist fully understanding how, when or where exactly this degradation is taking place. Consequently, pastoralists are migrating to the cities, most times in highly precarious conditions. This project aims to determine the number, size and location of the bofedales in the Central Andes, and to understand what geomorphological and climatological drivers are affecting their health and variability. My integrated methodology involved the interpretation of multi-petabyte satellite imagery, and the acquisition of hundreds of field-validation data points. The present project is an effort to direct the conservation strategies to protect these ecosystems in order to improve the lives of hundreds of thousands of people that depend on them to survive.

Greenhouse Gas Emissions from California Agricultural Soils Amended with Dairy Manure Biochar and Anaerobic Digestate

Discipline: Geoscience
Subdiscipline: Earth Science

Michael Rodriguez* and Francesca Hopkins, *University of California, Riverside*

Abstract: In California, dairies generate about 60% of greenhouse gas (GHG) emissions from the agricultural sector. The production and land application of biochar & anaerobic digestate (AD) may allow for greenhouse gas (GHG) emissions offsets while improving soil health and sequestering carbon. However, the GHG emissions and temperature sensitivities for these materials from dairy manure feedstocks are not fully understood. The goal of this research is to determine which manure management strategies have the most potential for soil GHG emission reductions across California and under different temperatures. In laboratory incubation experiments, three California (Riverside, Tulare, Marin counties) dairy soils were amended with solid dried dairy manure, manure derived biochar, or anaerobic digestate (AD) and solid manure mixture, at ambient (23℃) & elevated temperatures (28℃) while kept at 65% water holding capacity. CO_2, N_2O, & NH_3 fluxes were measured using cavity ringdown spectroscopy in either a closed or dynamic chamber system and soil was sampled for total carbon and nitrogen. Application of manure biochar significantly decreased CO_2 and N_2O emissions from Riverside & Tulare soils at both temperatures compared to solid manure application. Application of AD with manure decreased CO_2 emissions from only the Tulare soil but increased N_2O emissions. Application of AD generated significant NH_3 emissions especially from Tulare soil. Further research on site differences, temperature sensitivity, and emission mechanisms is necessary to quantify GHG emissions from these systems. Field application of biochar and digestate may allow opportunity for California dairies to meet climate regulations while moving toward sustainable production.

Environmental Origin of a Major Marine Invertebrate Clade, the Rhynchonelliform Brachiopods

Discipline: Geoscience
Subdiscipline: Earth Science

Kayla Irizarry* and Mark Patzkowsky, *Pennsylvania State University*

Abstract: Global marine biodiversity does not increase linearly over time, instead it is punctuated by periods of intense diversification and extreme loss of biodiversity (mass extinctions). The question of what drives these extreme and irregular changes is not resolved. In order to understand environmental causes of the diversification, this research focuses on the early Paleozoic (520 to 480 million years ago), a time of tremendous ecological diversification in the marine realm.

Environmental patterns of marine invertebrate taxa suggest that new clades and communities tend to originate in nearshore environments, while relict taxa reside in offshore environments. This study examines the Middle Cambrian origins of a successful clade of brachiopods, the Rhynchonelliformea. A database of Middle and Late Cambrian marine invertebrate faunal assemblages in North America was compiled using museum collections, digital databases, and literature sources. These data were vetted and collections were assigned to onshore-offshore depth-related habitat zones. Multivariate analysis was used to determine the habitat preference for rhynchonelliform brachiopods and co-occurring taxa on the onshore-offshore environmental gradient. We expect that these analyses will show that the earliest rhynchonelliform brachiopods diversified and became ecologically dominant in nearshore, well-oxygenated environments in the Cambrian long before they rose to dominate marine benthic assemblages across the onshore-offshore gradient for the remaining 230 million years of the Paleozoic.

Analysis of the Geochemical Spatial Variation in the Volcanic Rocks of the Toro-Ankole Volcanic Province

Discipline: Geoscience
Subdiscipline: Earth Science

Sofia Johnson-Gutiérrez*[1]; Tanya Furman[1]; Wendy Nelson[2]; Erica Pitcavage[3] and Peggy Kulyanyingi Kalegga[4], *(1)The Pennsylvania State University, (2)Towson University, (3)University of Houston, (4)Makerere University*

Abstract: The Toro Ankole Volcanic Province (SW Uganda) hosts a large cogenetic suite of geochemically rare mafic lavas (e.g. kamafugites and carbonatites) and accompanying mantle xenoliths (Rosenthal et al. 2009; Lloyd et al. 1985; Lloyd 1981). The lava and mineral geochemistry is extremely variable, and have limited in-depth synthesis of metasomatic and melting processes to discrete location-based studies rather than broader regional analysis. Two distinct metasomatic fluids (one carbonate and one silicate) have affected the subcontinental lithospheric mantle and the records are preserved in the unusual mineral phases (phlogopite, titanite and perovskite) of the Toro Ankole mantle xenoliths (Pitcavage et al. 2019; Rosenthal et al. 2009; Lloyd et al. 1996; Rudnick et al. 1993). The present study compiled all published geochemical data, metadata and sampling locations of Toro Ankole volcanic rocks from the past 90 years to identify large-scale patterns in rock and mineral compositions. The database was then imported into GIS software to project the spatial distribution of all the recorded major, minor and trace element abundances of each sample within the province. The database will help evaluate the distribution and movement of fluids and melts within the lower lithosphere and upper mantle of Toro Ankole by allowing us to temporally and spatially track their geochemical signatures. The resulting scale(s) of metasomatic heterogeneity will be integrated with geodynamic models to better understand continental rift systems and processes.

Constraining Ice Shelf Basal Channel Evolution and Melt Rates

Discipline: Geoscience
Subdiscipline: Earth Science

Allison Chartrand* and Ian Howat, *Byrd Polar and Climate Research Center, The Ohio State University*

Abstract: Ice shelves, or the floating extensions of glaciers that drain the Antarctic and Greenland ice sheets, provide a buttressing control on the flow of ice from the ice sheet, but they are vulnerable to mass loss from surface and basal melt as well as the calving of icebergs. Basal channels, deep longitudinal grooves carved into the base of ice shelves that can entrain meltwater, are poorly understood in their behavior and evolution, and in their impact on ice shelf buttressing capacity. We investigate how basal channels in both Antarctica and Greenland behave and change through time and estimate basal melt rates in order to help quantify their impact on ice shelf stability. We investigate basal channel evolution using a suite of high-resolution remote-sensing data from the early 2000s to the present, including ice surface elevation, thickness, and velocity data from NASA and the Polar Geospatial Center. Basal melt rates are estimated from surface elevation data using the assumption of hydrostatic equilibrium, as the ice above basal channels settles to form surface depressions that reflect the shape and size of the channels below. We have already identified a number of evolutionary behaviors, including channel deepening, lengthening, and migration, often coincident with high basal melt rates, and stagnation. We continue to investigate and characterize additional basal channel behaviors and estimate melt rates so that ice shelf dynamics may be more accurately accounted for in ice sheet models, leading to more accurate predictions of sea level rise.

Assessment of Magma Viscosity Using Juvenile Glass Composition at Telica Volcano, Nicaragua: Insights into Persistent Restlessness and Explosive Activity

Discipline: Geoscience
Subdiscipline: Geology

Victor Garcia* and Maureen Feineman, *The Pennsylvania State University*

Abstract: The Telica volcano in northwestern Nicaragua is considered a persistently restless volcano (PRV). The hydrothermal system that drives the low frequency seismicity paired with low-level eruptive activity characterize the Telica complex, with recent noteworthy low-explosivity eruptions occurring in 2011 and 2015. The 2011 single-episode eruption of Telica was characterized as a phreatic eruptive event because of lack of deformation in the edifice, small net changes in SO_2 flux, and the lack of juvenile material in the accretionary lapilli and ash. Meanwhile, the 2015 three-episode eruption consisted of larger ballistic blocks, and higher eruptive columns than that of 2011 while exhibiting similar fluctuations in low-frequency (LF) and high-frequency seismic events (HF) preceding eruptive activity. In addition, the 2015 eruption in its later phases involved the mobilization of magma in the shallow volcanic system, shown by the presence of fresh glass (≤10%) in ash samples, and has been characterized as a phreatomagmatic eruption. The near-constant low-level seismic activity at Telica provokes the question of when and how a persistently restless volcanic system transitions from “stable” to “unstable” behavior. By utilizing various techniques such as Electron Probe Microanalysis (EPMA), Laser Ablation Inductively Coupled Plasma Mass Spectrometry (LA-ICP-MS), and Fourier-Transform Infrared Spectroscopy (FTIR), we will be able to fully characterize the glass composition and volatile content, and crystallinity and crystal composition in ash samples from both eruptions, to better understand the behavior of magmatic systems and predict potential eruptions at Telica and other PRVs.

Rising from the Ocean: The Uplift and Evolution of the Aleutian Islands Using (U-Th)/He Thermochronology.

Discipline: Geoscience
Subdiscipline: Geology

Anahi Carrera* and Emily Cooperdock, *University of Southern California*

Abstract: Uplift and erosion studies in volcanic arcs, such as the Andes, S. America, and the Cascades, N. America, link exhumation with tectonic and/or climatic forces. It is important to understand which mechanisms drive exhumation in arcs since these feedbacks lead to some of the highest topography and erosion rates in the world. The Aleutian Islands are an example of an oceanic volcanic arc extending from Russia to Alaska, composing the northern segment of the Ring of Fire. Although the timing for uplift and erosion has been proposed based on field geology and seismic surveys, its exhumation history has never been directly dated or assessed. A systematic thermochronology study on samples collected along 1400 km of the Central Aleutians can help resolve this. Particularly, the use of multiple chronometers (i.e., apatite fission track and zircon (U-Th)/He) with different temperature sensitivities within the same sample can constrain uplift and erosion rates over time. This data set provides a regional framework to quantitatively asses the various proposed mechanisms for Aleutian Arc exhumation, such as, 10° Pacific plate rotation, subduction of the Kula ridge, and pluton emplacement. Each of these mechanisms would result in predictable and testable geographic age trends. Preliminary (U-Th)/He zircon data vary from 6 to 24 Ma across the arc without a discernible geographic age trend, supporting the prediction that plutonism controls exhumation. More data from multiple chronometers and erosion rates still need to be calculated in order to make a robust assessment.

Reconstructing the Paleoclimatology of Cuba from Oxygen Isotope Stalagmite Precipitation Records

Discipline: Geoscience
Subdiscipline: Geology

Leah Travis Taylor* and Martin Medina Elizalde, *Auburn University*

Abstract: Anthropogenic climate change is a dire issue humanity faces today on a planetary scale, particularly concerning its effects on hydroclimate extremes. More intense hydrologic events, such as droughts, flooding, and tropical cyclones (TCs), have dramatic impacts and may soon become routine; however, the historical record is insufficiently long and incomplete to enable the firm attribution of observed extreme hydrological events to an anthropogenic cause and/or to internal modes of climate variability. As an interface between the Caribbean and Gulf of Mexico regions with an extensive cave system and a frequent path for TCs, Cuba is a prime location to reconstruct paleohydroclimate. Here we conduct an innovative study of speleothems from the Majaguas Cave System in Cuba by producing multi-proxy stalagmite precipitation records, spanning on glacial to interglacial time scales. The $\delta^{18}O$ composition of Cuban stalagmites is expected to reflect precipitation amount when in isotopic equilibrium with drip water $\delta^{18}O$, thus allowing for reconstruction of past precipitation variability. Preliminary U/Th geochronology results indicate that the first analyzed stalagmite specimen spans 202-187 kyr BP during the transition from the peak interglacial MIS7 to glacial MIS6, thus a time when there was a large shift in the atmospheric composition of greenhouse gases. We hypothesize that 1) stalagmite $\delta^{18}O$ will provide a record of precipitation variability in the Caribbean region, and 2) these paleoclimate records will provide empirical information of the frequency and magnitude of regional hydroclimate change and the mechanisms driving this variability before human interference with the climate system.

Developing Age-Specific Normative Values for Dichotic Digits and Dichotic Sentence Identification in Older Adults without Significant Hearing Loss or Cognitive Decline

Discipline: Health

Subdiscipline: Other Health

Genoveva Hurtado* and Susan Naidu, *University of Utah*

Abstract: Auditory changes naturally occur with age. Two clinical tests examining auditory processing, Dichotic Digits (DD) and Dichotic Sentence Identification (DSI) Randomization F by Auditec, have established values for adults under the age of 60 years, but not for older adults. This study obtained normative limits on adults over 60 years of age for the DD and DSI. Testing, completed at the University of Utah Speech-Language-Hearing Clinic, followed typical audiometric parameters. The Montreal Cognitive Assessment (MoCA) Version 8.1 English was used to verify normal cognitive abilities. Audiometric testing confirmed hearing sensitivity. The DD and DSI were presented following the established protocol, with a varying testing sequence.

Statistical analysis was completed using a rationalized arcsine unit (RAU) transform. Comparing right and left ear scores showed a statistically significant right ear advantage (higher score) for both dichotic tests. A significant correlation between age and hearing sensitivity was found. There was a significant negative correlation between hearing sensitivity and the DD, such that the higher sensitivity, the lower the DD score. There was a significant positive correlation between the DD and the DSI. For clinical use, the mean and standard deviation of raw scores were calculated. The results are consistent with what was expected based on knowledge within the field of audiology. The results show that older adults perform comparatively well to the established adult (<60 years) data. However, there are important differences, such as the greater right ear advantage. This information will be used clinically at the University of Utah Speech-Language-Hearing Clinic.

Food and State Nutrition Policy: A Systematic Review of Nutrition Policies Introduced in California to Address Obesity between 1999 - 2019

Discipline: Health
Subdiscipline: Public Health

Kesia Garibay* and Denise Payan, *University of California, Merced*

Abstract: Studies have previously examined patterns and predictors of obesity and physical activity legislation, however, none have focused on state nutrition legislation to address obesity. This study describes the results of a systematic search for nutrition-related legislation to address obesity in California between 1999-2019. We systematically searched for obesity prevention and reduction bills introduced in California's legislature between 1999-2019. Two research assistants searched and reviewed all related legislative documents, and abstracted key bill information (topic, target population, setting, political variables, behavioral assumptions of policy, enactment outcome). We used the Behavioral Assumptions Framework to examine the policy content of the bills. The search yielded N=346 bills (29 excluded for non-relevance). 24.3% were related to nutrition, 19.1% to physical activity, 4.0% to health care, 2.9% to breastfeeding, and 41.3% to a miscellaneous topic. Between 1999 and 2019, 42.9% of nutrition bills were enacted. Half of those enacted targeted children suggesting policies focused on children may be more likely to be successful than bills aimed at the general population. Sugar-sweetened beverage tax bills were introduced multiple times in the state's legislature, however, these bills were not successful, indicating authority policies face more barriers to passage than other types of nutrition-related bills. This systematic review of state nutrition policies to address obesity will advance our understanding of policy change to promote healthier, more equitable communities at the state-level. Future research includes examining determinants of state nutrition policy and investigating the role of advocacy coalitions involved in the state health policymaking.

Vape Pen Product Placement and Imagery in Popular Music Videos

Discipline: Health
Subdiscipline: Public Health

Marlene Huerta*, *California State University of Los Angeles* and Patricia Escobedo, *University of Southern California*

Abstract: Introduction: Given the increasing use of vape pen products among young adults, it is crucial to identify possible sources of vape pen product marketing exposure in media popular among young adults. For years research has focused on tobacco product placement in television and film, however few studies have documented vape pen marketing in music videos. The objective of this study was to determine the extent of vape pen and combustible product placement and use in popular music videos.

Methods: Songs on the Billboard Hot 100 list during the weeks of June 16 through September 22, 2018 with official music videos were identified (n = 180) and coded for number of views (as of October 25, 2018), genre, theme, vape pen and combustible product content.

Results: Vape pen product placement, devices or vapor appeared in 7 (3.8%) music videos and viewed over 1.6 billion times. Among music videos featuring vape pen product placement, devices or vapor, the most prevalent theme was *Image/Lifestyle/Sociability* (e.g., ostentatious lifestyle, partying) and the most prevalent musical genre was Hip Hop. Product placement for vape pen products (Kandypens, Mig Vapor) and combustible tobacco products (RAW) were observed.

Conclusion: Findings indicate that vape pen product placement appears in popular music videos receiving views in the billions. Music videos should be included when assessing vape pen and tobacco marketing exposure among priority populations. Future research should examine how viewing product placement in music videos influences tobacco use and susceptibility among young adults.

Keywords: e-cigarettes, marketing, music videos, image/lifestyle/sociability, placement

Self-Reported Symptoms of Illness and Treatment-Seeking in Western Kenya

Discipline: Health
Subdiscipline: Public Health

Valerie Madera-Garcia*[1]; Jenna E. Coalson[2]; Maja Subelj[3]; Melanie L. Bell[1]; Mary H. Hayden[4]; Maurice Agawo[5]; Stephen Munga[5] and Kacey C. Ernst[1], *(1)The University of Arizona - Mel and Enid Zuckerman College of Public Health, (2)University of Notre Dame, (3)University of Ljubljana, (4)University of Colorado, (5)Kenyan Medical Research Institute*

Abstract: Timely treatment-seeking behavior can reduce mortality due to infectious diseases. Patterns of treatment-seeking behavior can differ by access to health care, and perceptions of disease severity and symptoms. Our study objective was to determine the level of treatment-seeking behavior at last illness of selected households in lowlands and highlands of Western Kenya. We analyzed cross-sectional data from households in Western Kenya from 2015 using logistic regression models adjusting for other covariates separately. In the highlands, participants self-reporting fever, aches, and digestive symptoms at last illness were significantly more likely to seek treatment than those with just fever and aches (OR = 3.65, 95% CI: 1.80, 7.39). Participants from the lowlands self-reporting fever, aches and digestive symptoms (OR= 2.99; 95%CI: 1.65, 5.41) had significantly higher odds of seeking treatment compared to participants self-reporting fever and aches. These ORs did not change dramatically upon adjustments for age category, malaria severity perception, or sex. Self-reported fever, aches and digestive symptoms were associated with higher odds of formal treatment-seeking [OR = 1.40, 95% CI: 0.74, 2.64] in the highlands. In the lowlands, self-reporting fever only was associated with higher odds of formal treatment-seeking [OR = 1.50, 95% CI: 0.63, 3.59]. The number of self-reported symptoms at last illness was associated with treatment-seeking behaviors in the highlands and lowlands of Western Kenya, and frequency of treatment-seeking differed considerably between the highlands and lowlands sites. Understanding the drivers of treatment-seeking behavior after febrile illness are important to control and treat infectious diseases in the community.

MOF-Encapsulated Vaccines Improves the Stability and Enhance the Adaptive Immune Response

Discipline: Life Sciences
Subdiscipline: Biochemistry

Michael A. Luzuriaga*; Sarah Popal and Jeremiah Gassensmith, *University of Texas at Dallas*

Abstract: Many vaccines use a weakened or inactivated form of a pathogenic virus to strengthen our immune system against a real infection from that virus. Being proteinaceous therapeutics, however, these vaccines denature when exposed to elevated temperatures. In 2016, we published a communication showing how the surfaces of virus-like-particles could nucleate the growth of a crystalline porous coordination polymer called zeolitic-imidazolate-framework-8 (ZIF-8). In addition, we showed that the ZIF-8 shell can stabilize tobacco mosaic virus (TMV) against harsh conditions and after the shell is removed by EDTA exfoliation the virus retains its rod-like shape. In our recent publication, we showed that the encapsulated TMV (TMV@ZIF) does not denature the antigens required to elicit an antibody response. Further, the enzyme-linked immunosorbent assay (ELISA) indicated that the ZIF-8 shell improves the surface stability of TMV compared to the unencapsulated virus when boiled in water for 20 min. We also showed that the ZIF does not need to be removed prior to injection into the subcutaneous region. With these results, we are now comparing three injections of TMV vs one injection of TMV@ZIF to show similar or enhanced immune response. We also begun injecting mice with TMV and TMV@ZIF heated at different temperatures to mimic shipment around the world. We will show TMV@ZIF activates the adaptive immune system by measuring the antibody production by ELISA and measuring T-cell count by flow cytometry. We believe our method of encapsulation can remove the need for multiple injection, offer long-term immunity, and remove the need for refrigeration.

Exploring Chemoresistant Pathways Mediated By t-Darpp/Darpp-32

Discipline: Life Sciences
Subdiscipline: Biochemistry

Herbert Castillo* and Jamil Momand, *California State University, Los Angeles*

Abstract: Herceptin (chemical name: trastuzumab) is a chemotherapeutic drug that prevents tumor cell growth in HER2+ breast cancer. After one year of administering Herceptin, most patients show resistance to the treatment. Resistance has been shown to be due to activation of the PI3K/AKT1 pathway resulting in cell survival. Patients that develop resistance often show an overexpression of the PPP1R1B gene which encodes for two protein isoforms: Darpp-32 and t-Darpp. t-Darpp is sufficient for conferring resistance in breast cancer cells. Previous crosslinking and size exclusion chromatography data indicates that t-Darpp/Darpp-32 forms high molecular weight complexes. Proteins that co-purified with t-Darpp/Darpp-32 were identified by mass spectrometry. Co-immunoprecipitation (Co-IP) of t-Darpp/Darpp-32 followed by immunoblotting was used to confirm the identity of these binding proteins. In initial Co-IP assays, I was unable to identify the co-purifying proteins. I performed capture optimization tests to maximize the immunoprecipitation of t-Darpp/Darpp-

32 in order to make the epitopes of t-Darpp more available for antibody capture. Increased t-Darpp capture was achieved by increasing the incubation period to 24 h. Even under optimized conditions, the Co-IP experiments failed to confirm the identity of the selected target proteins. This suggests that either the proteins that co-purified with t-Darpp were artifactual or my methods are still not optimized sufficiently to capture these proteins in Co-IP. Moving forward, proximity ligation assays (PLA) will be used to confirm that the mass spectrometry-identified t-Darpp-associated proteins bind to t-Darpp in breast cancer cells. PLA is used for detection of endogenous protein-protein interactions with high specificity and sensitivity.

Self-Assembling Peptides (Q11) As a Platform to Create New HPV Vaccine Candidates

Discipline: Life Sciences
Subdiscipline: Biochemistry

Crystal Morales* and Dr. Naomi Lee, *Northern Arizona University*

Abstract: Self- assembling proteins commonly occur in nature and have shown potential as a vaccine platform with displayed peptide antigens. Beta-strand peptides that alternate hydrophobic and hydrophilic amino acids self-assemble into a beta-sheet bilayer. This format could cause an immunogenic response and therefore be an effective vaccine for HPV. Current HPV vaccines are virus-like proteins which are not as robust or as easily stored as the peptides. In addition, current HPV vaccines do not protect against all types of HPV. The goal is to be creating Q11 (Ac-QQKFQFQFEQQ-NH2) peptide sequences so that HPV antigens and PADRE will be added on in a linear fashion and it is theorized that it will cause an immune system response with T cells. Standard Fmoc solid phase peptide synthesis will be utilized to synthesize all peptides. The Q11 and HPV peptides will be co-assembled followed by chemical conjugation of the PADRE sequence. The project was started in January 2019. Thus, results consist of peptide synthesis, HPLC purification, MALDI-TOF and CD spectroscopy, and TEM imaging. TEM is used to characterize fibril morphology which will be followed by animal studies. The animal models will be used to test the immunogenicity and effectiveness of the vaccine. Mice will be injected with cancer-causing HPV types after one month of being vaccinated and results will be assessed using ELISA assays. In conclusion, self-assembling peptides with multivalent display of antigens could be an efficient way to not only make next generation HPV vaccines but vaccines for other diseases as well.

The Influence of Seasonal Variability and Winter Ice out on Mercury Trophic Ecology in High Mountain Lakes

Discipline: Life Sciences
Subdiscipline: Biology (general)

Elliott Dominguez*[1]; Frank von Hippel[1]; Catherine Propper[1] and Sudeep Chandra[2], *(1)Northern Arizona University, (2)University of Nevada, Reno*

Abstract: Mercury (Hg) is a toxic metal and global pollutant that poses a significant threat to ecosystems. Upon methylation, Hg readily bioaccumulates in individuals and biomagnifies in food webs, posing a significant health risk to wildlife and human populations. Our research aims to determine how the date of ice out affects methylmercury (MeHg) concentrations in aquatic vertebrates of a subalpine lake. Because earlier ice out leads to increased secondary production of benthic invertebrates, we anticipate early ice out to be positively correlated with higher concentrations of MeHg in lake fish. Samples were collected from Castle Lake, California and stored until analysis. Determination of Hg was performed using cold-vapor atomic absorbance spectroscopy on a FIMS-100 mercury analyzer (PerkinElmer). δ^{13}C and δ^{15}N stable isotope ratios were quantified by the University of New Mexico Center for Stable Isotopes. High-elevation lakes, such as Castle Lake, are useful indicators to determine the effect of changes in global Hg emissions on local Hg bioconcentration rates and to help assess ecological risk. Seasonal variability and winter ice out are not normally considered in monitoring programs; therefore, the findings of our research will be used to improve existing Hg bioaccumulation models through the assessment of seasonal variability and winter ice out. Moreover, because over 80% of fish consumption advisories in the United States are due to MeHg contamination, our work aims to limit MeHg exposure and mitigate health risks to wildlife and people through the improvement of monitoring programs.

Restoration of Native Skin Properties in a Recellularized Porcine Skin Model

Discipline: Life Sciences
Subdiscipline: Biology (general)

Dominic Dominguez* and Robert Kellar, *Northern Arizona University*

Abstract: Burns requiring medical attention are ranked fourth among all global injuries. Furthermore, a high percentage of deaths caused by burns occur in low- and middle-income countries, highlighting the need to better understand and develop effective treatments. Third-degree burns lead to destruction of the epidermis, dermis, and hypodermis, causing limited wound healing and increasing the risk of environmental or nosocomial infection. The standard of clinical care in such wounds includes debridement, antibacterial treatments, and skin grafts to aid wound healing. One common type of graft used is an allogeneic skin graft, recovered from cadaveric tissue. However, cadaveric tissue may contain major histocompatibility (MHC) antigens, thus increasing the potential for host immune rejection. While allogeneic skin grafts can be decellularized to mitigate this, decellularization has also been shown to disrupt the architecture and mechanical properties of tissue. Fibroblasts contribute to the mechanical strength of the skin and are the predominant dermal cell type removed during decellularization. The potential impact of recellularizing a decellularized graft with a patient's native fibroblast, lacking MHC antigens, has yet to be studied. Recellularized skin may be developed into a skin replacement that better matches the mechanical properties as native skin. The mechanical properties of freshly excised, decellularized, and recellularized porcine skin will be compared. Recellularization of skin grafts using fibroblasts will mimic the mechanical strength and be a beneficial treatment used in wound healing for treating third-degree burns.

Poxvirus Decapping Enzymes and Their Roles in 5'-Poly(A) Leader-Mediated Translation

Discipline: Life Sciences
Subdiscipline: Biology (general)

Candy Hernandez*; Fernando Cantu; Erick Cheng; Josh Spradlin and Zhilong Yang, *Kansas State University*

Abstract: Poxviruses comprise a large family of viruses, with many causing serious diseases in humans and other animals. Decapping enzymes remove mRNA 5'-cap, which renders an mRNA susceptible to ribonuclease-mediated degradation. Vaccinia virus (VACV), the prototype poxvirus, encodes two decapping enzymes, D9 and D10. Decapping enzymes are thought to be negative regulators of mRNA translation by eliminating the translation template and suppressing the translation process. Surprisingly, our results indicate that VACV decapping enzymes are required for efficient translation of VACV post-replicative mRNAs, which all have a 5'-poly(A) leader in their 5'-untranslated regions (5'-UTR). Notably, D10 expression in cells without VACV infection promotes 5'-poly(A) leader-mediated mRNA translation. We surveyed the D10 homologs in the poxvirus family, African swine fever virus, and human, and compared their genetic relationship. We further chose representative D10 homologs from each genus of poxviruses, as well as African swine fever virus and human. These decapping enzymes were first codon-optimized for expressing in mammalian cells. Their effects on 5'-poly(A) leader-mediated translation were examined using an RNA-based translation reporter assay. The results indicate that only some D10 homologs promote 5'-poly(A) leader-mediated translation. We further identified the domains in VACV D10 that are responsible for the 5'-poly(A) leader-mediated translation enhancement. Our findings identified an unexpected function of poxvirus decapping enzymes to selectively promote poxvirus mRNA translation.

Increasing Antimicrobial Proteins and Lipids of Alveolar Type II Cells through Pro-Inflammatory Cytokines

Discipline: Life Sciences
Subdiscipline: Biology (general)

Cindy Toscano*, *California State University, Los Angeles* and Edith Porter, *California State University of Los Angeles*

Abstract: Tuberculosis is a disease caused by *Mycobacterium tuberculosis* (Mtb) and approximately 10 million people die each year from tuberculosis. Current vaccines targeting macrophages and T helper cells as well as anti-tuberculosis drugs have limited efficacy and are further compromised by the emergence of multidrug and extensively drug resistant strains of Mtb. Epithelial cells in the lungs, alveolar cells, are among the first host cells to have contact with inhaled Mtb. Epithelial cells are capable of producing antimicrobial peptides (AMPs) such as human beta defensins (HBDs) and antimicrobial lipids (AMLs). Proinflammatory cytokines including IL1β made by macrophages and IL17 &IL22 secreted by T helper cells are known to increase production of AMPs in epithelial cells, but their effect on the production of AMLs is unknown. We hypothesized that these cytokines can increase the production of both, AMPs and AMLs in lung alveolar type II cell and subjected A549 cells grown at air-liquid interface to cytokines alone or in combination for 24 or 48 h. IL17 combined with IL22 significantly increased the production of HBD2 as determined by immunofluorescence after 48 hours ($n = 3$, $p = 1.458e\text{-}08$). To quantify intracellular lipid accumulation, cells were stained with the lipophilic fluoroprobe Bodipy. Preliminary data ($n = 2$) suggest that IL1β treated cells contain more lipids than the control after 24 h, but less lipids than the control after 48 h possibly reflecting enhanced lipid production and secretion. This research may lead to novel approaches to control tuberculosis.

The Effect Rhizobia on Flowering Time and Fitness of Trifolium Bar. Plants.

Discipline: Life Sciences
Subdiscipline: Biology (general)

DeMarcus Turner*, *Norfolk State University* and Maren Friesen, *Washington State University*

Abstract: Undergraduate Researcher: DeMarcus Turner

Faculty Advisor: Maren Friesen

Home Institution, Major, Class Standing: Norfolk State University, Biology, Senior

Atmospheric nitrogen is inaccessible to most species of plants, so they rely on microbes known as rhizobia to provide usable nitrogen through nitrogen fixation. However, the presence of these microbes may also have a profound effect on other key plant traits, such as flowering time. A plant's flowering time can have significant effects on fitness, health, and lifespan. Here, we test the effect of rhizobia on flowering time of *T. barbigerum* plants. and determine how this affects fitness. In a greenhouse experiment, a single genotype of *T. barbigerum* was inoculated with 80 different strains of rhizobia to see which strains provide the greatest fitness benefit. The flowering time and number of flowers on each plant were recorded during the first 8 weeks of growth. The plants were grown for 10 weeks before being harvested and the number

of seeds produced was recorded. Since the same plant genotype is used, any variation is likely due to genetic variation within the rhizobia. This data will show which strain of rhizobia provides the greatest influence on the *T. barbigerum* plants' flowering and the largest impact on fitness. If certain strains of microbes improve plant flowering and fitness, it will provide significant research on microbially mediated plant functional traits.

Understanding the Biosynthesis and Biological Roles of Diterpenes in *Magnaporthe Oryzae.*

Discipline: Life Sciences
Subdiscipline: Biology (general)

Ayousha Shahi* and Sibongile Mafu, *University of Massachusetts*

Abstract: Plant-pathogenic fungi harbor diverse and highly bioactive specialized metabolites. Understanding the roles of specialized metabolites in survival, adaptation, and virulence of fungi could pave a way for the discovery of novel fungicides. Our research is focused on understanding the role of specialized metabolites, terpenes, in a model plant-pathogenic fungus *Magnaporthe oryzae.* Ten terpene biosynthetic gene clusters have been identified in *M. oryzae.* However, the biosynthesis and biological roles of these compounds remain unexplored.

To understand the terpene diversity in the fungus, we carried out in-silico and biochemical characterization of terpene synthase genes. Briefly, the codon-optimized synthetic constructs of terpene synthases were cloned to an expression vector and co-transformed with their precursor gene into engineered E. coli host cells for recombinant expression of each terpene synthase. The subsequent analysis of the resultant products by GC-MS revealed the formation of two diterpenes, a sesquiterpene and a sesterterpene. Among them, two diterpene synthase scaffolds-manoyl oxide and pimaradiene scaffolds are our focus of study. The diterpene scaffold, manoyl oxide is an intermediate to cAMP activator molecule forskolin with a potential role in fungal development. Similarly, the pimaradiene scaffolds are known to have roles in asexual reproduction in Aspergillus. Besides, these two diterpenes are present in most of the host-specific lineages (pathotypes) of *M. oryzae* suggesting their potential role in fungal fitness. The comparative assessment of gene regulatory network, phenotype, and metabolites of the mutants under abiotic stresses and host pathogenicity will enable us to decipher the roles of terpenoids in *M. oryzae*.

A Tuft Understanding of Pancreatic Cancer Progression

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Daniel Salas-Escabillas*[1]; Meggie Hoffman[2] and Howard Crawford[2], *(1)University of Michigan, Cancer Biology Training Program, (2)University of Michigan, Molecular and Integrative Physiology*

Abstract: Pancreatic cancer is on its way to becoming the second leading cause of cancer related death and has a 5-year survival rate of only 10%. Currently, there is a strong initiative to understand more about the microenvironment in the diseased pancreas. Recent studies have shown that tuft cells are a cell type that is hypothesized to act as a cancer stem cell in other organs. Tuft cells are also known to be chemosensory cells, utilizing the taste sensory system to signal to both the immune and nervous systems. Interestingly, when we ablate the sensory system, pancreatic transformation is accelerated.

To understand the role tuft cells play in the progression of pancreatic cancer, we have used a unique dual inducible recombinase system to lineage trace tuft cells in a pancreatic cancer model to determine if they act as putative cancer stem cells. We find that tuft cells do not expand in benign neoplasia, suggesting they do not act as a stem cell in this context. However, when we trace tuft cells within malignant cancer, we see tuft cells transdifferentiate to a neuroendocrine-like cell type that is associated with tumor aggressiveness. We hypothesize that during benign neoplasia, tuft cells secrete acetylcholine to prevent pancreatic tumorigenesis, but tuft cells can also become malignant express markers such as Synaptophysin and Chromogranin A. These markers along with our reporter and the absence of tuft cell markers are used to identify this novel malignant cancer cell type.

Determining the Therapeutic Effectiveness of Synthetic Notch-Gated Chimeric Antigen Receptors in Mouse T Cells Targeting Glioblastoma

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Jessica Briones*, *San Francisco State University* and Joseph Choe, *University of California, San Francisco*

Abstract: Human synthetic Notch-gated chimeric antigen receptor T cells (SN CAR-T) have shown promise in treating glioblastoma (GBM), the deadliest form of brain cancer, with previous research demonstrating complete clearance of human GBM tumors in immunodeficient mice. Although immunodeficiency prevents rejection of transplanted human T cells and tumors, the lack of an immune system fails to represent the true physiological and immunological state of GBM patients. Developing a SN CAR-T system compatible with an immunocompetent mouse model is critical for understanding its clinical implications and therapeutic potential. I aim to engineer a mouse SN CAR-T therapy targeting mouse GBM and demonstrate its anti-tumor effectiveness *in vitro.* Mouse T cells will be transduced to express a SN-CAR receptor circuit that recognizes and kills mouse GBM cells. I will assess the mouse SN CAR-T's therapeutic strength and duration through a series of co-culturing assays in which the proportion of killed cancer cells will be measured using flow cytometry. Successful

tumor clearance is expected due to precise antigen-recognition of the mouse T cell's synthetic Notch and CAR receptors, and therapeutic effects are expected to decrease over time due to cell exhaustion. Through this study, the anti-tumor effectiveness and durability of mouse SN CAR-Ts will be characterized. The findings from our investigation will extrapolate to the potential use of human SN CAR-T in the treatment of GBM patients. Determining the efficacy in immunocompetent mice will help push this cell therapy from the lab bench to the patient's bedside for the first time.

Characterization of Infection-Induced Innate Immunity in Cancer Pathogenesis

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Pooja KR* and Nathan Mortimer, *Illinois State University*

Abstract: The immune system orchestrates coordinated immune responses to protect our body from factors that appear foreign and harmful. Dysregulation of the immune response contributes to a wide range of diseases, including cancer. Tumour metastasis is a main contributor to cancer related death, and tumour immunity may influence this disease progression. Recent studies show that the innate immune system plays a crucial role in tumour metastasis, however how immune mechanisms influence metastasis are poorly understood. The cross talk between the innate immune system and tumour cells is complex as the immune response can eliminate metastatic cells but can also promote metastasis. Here, we are investigating the role of the innate immune response in tumour development and progression using a *Drosophila melanogaster* model of tumour metastasis. Based on our preliminary observation, parasitoid wasp infection modulates the accumulation of tumour cells and the extent to which they metastasize. We observed reduced tumor size and the extent of metastasis was also greatly reduced compared to the uninfected *Drosophila*. This study aims to better understand the mechanisms underlying the immune regulation of tumour progression and specifically the role of infection-induced innate immunity in tumorigenesis. Understanding the molecular details of the interactions between the innate immune system and cancer can promote tumor immunity and could have major implications for the new immunotherapeutic strategies for treating metastatic disease, which is the major cause of cancer deaths.

Using Base Editing to Investigate How Mutations in DNA Repair Proteins Drive Disease Phenotypes

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Carlos Vasquez* and Alexis Komor, *University of California, San Diego*

Abstract: It is widely accepted that DNA damage, once propagated as mutations, causes cancer. To prevent such an event, living organisms have evolved DNA damage responses (DDR) to protect the integrity of the genome. Mutations to DNA repair proteins, however, causes a dysregulation to DDR and are associated with a predisposition to several forms of cancer. The specific molecular details surrounding these processes have not been fully elucidated. The difficulty in understanding such pathways is due to the involvement of several interacting proteins. Therefore, using purified proteins to conduct experiments outside of the cellular environment may alter interaction stoichiometries or miss key protein-protein interactions that have not yet been explicitly discovered. As such, the most physiologically-relevant manner in which to study disease-relevant DNA repair protein mutants is in living cells. However, the introduction of cancer-relevant mutations into the genome using traditional genome editing methods is cost and time prohibitive due to low genome editing efficiencies and high byproduct formation. This study employs novel base editing technologies to introduce point mutations into the genome of live cells with efficiencies >1000-fold higher than traditional genome editing methods. We have initiated our studies by investigating mutations to the base-excision repair glycosylase enzyme, MUTYH, which we hypothesize contribute to developing colorectal cancer. By precisely installing MUTYH mutations into the genome of living cells, our research shows the ability to directly probe the relationship between MUTYH and oxidative stress, and thus, better understand how cancer-relevant MUTYH variants contribute to colorectal cancer in their native cellular context.

The Effects of Uranium on Human Breast Cancer Cells *in Vitro.*

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Desirae Enriquez*; Chloe Greenhalgh-Adam and Catherine Propper, *Northern Arizona University*

Abstract: Uranium is an environmental contaminant that can cause both malignant and non-malignant diseases through inhalation of air or ingestion of water. Uranium contamination in water, air and soil heavily occurs naturally in several parts of the world and especially in areas where there has been heavy mining activities such as on the tribal lands of Northern Arizona. This contamination is linked to increases in chronic kidney diseases and some cancers. However, little is known about the effect of uranium exposure on breast cancer. We hypothesize that exposure to uranium will dose-dependently influence proliferation, metabolism, and gene expression in breast cancer cells. We exposed cells from the human breast cancer cell line, MCF-7, to increasing concentrations of uranyl nitrate (0, 0.1, 1, 10 uM). All uranium doses decreased both metabolism and cell viability. To determine whether this effect of uranium is limited to the MCF-7 cell line or is more universal, future studies will evaluate the effect of uranium exposure on other breast cancer cell lines. Furthermore, we will test the effect of uranium on tumor progression and metastasis using a zebrafish xenograft model. This research may help evaluate breast cancer risk in populations exposed to uranium contamination.

Analysis of the Anti-Angiogenic Effect of Vasohibin in Breast Cancer Models

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Shirisha Desai*; Rojina Nekoonam and Jason Bush, *California State University, Fresno*

Abstract: Invasive breast cancer is an angiogenic-dependent malignancy. Angiogenesis is the formation of new blood vessels from existing vasculature that plays an important role in the progression of solid tumors. Cells that form blood vessels (endothelial cells) can produce intrinsic angiogenesis inhibitors induced by angiogenic factors. A recently discovered inhibitor called Vasohibin1 (VASH1) has potential as an anti-angiogenic agent. In this study, we are investigating the anti-angiogenic effect of VASH1 in combination with another potential anti-angiogenic agent, Zoledronic acid and an FDA-approved agent, Everolimus. We are taking a two-pronged approach by optimizing conditions using *in vitro* cell-based experiments and then transitioning into a zebrafish-based *in vivo* angiogenesis assay. The breast cancer cell line, MDA-MB-231, was used in cell viability assays for Zoledronic acid and Everolimus and the resulting IC50 values (concentration resulting 50% inhibitory effect) range between 60-70µM and 160-250nM, respectively which is consistent with concentration found in the literature. We are currently testing these agents in spheroid-based sprouting assays to monitor the spread of cancer cells in a 3D environment. Furthermore, an established transgenic zebrafish expressing fluorescent green protein during vascular development in embryos are being used for *in vivo* angiogenesis assays. Angiogenesis in zebrafish can be quantified by visualizing the extent of green glowing vessels under fluorescent microscopy. Current results demonstrate strong and consistent vascularization during the first few days after hatching. By testing the effect of combinations of potential and known anti-cancer agents, we hope to improve the therapeutic shortcomings against angiogenic growth in breast cancer.

Atrx Loss of Function Impairs Self-Renewal in Glioma Stem Cells By Sensitization to Proton Radiation Therapy

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Angel Garces* and David Grosshans, *University of Texas MD Anderson Cancer Center*

Abstract: Glioblastoma Multiforme (GBM) is the most prevalent and aggressive form of malignant glioma in the United States with a five-year survival rate of only 6.8%. Glioma stem cells (GSCs), a subpopulation of undifferentiated, self-renewable, stem-like cells in GBM tumors, have been recently implicated in promoting GBM chemoradioresistance, metastasis, and tumorigenesis. Interestingly, 70-80% of low-grade glioma (LGG) and secondary GBM patients carry the IDH1^{R132H} mutation, which has been shown to inhibit GSC aggression by impairing migration and invasion along with promoting GSC differentiation. However, the effects of alpha-thalassemia/mental retardation syndrome X-linked gene inactivating mutations (ATRX^{Loss}), which often co-present with IDH1^{R132H} in younger LGG patients, on GSC response to chemoradiotherapy are not well understood. Proton radiation therapy has been recognized as an effective treatment modality in LGG and GBM due to its superior ability to target tumors and induce more complex DNA damage than conventional X-ray therapy (XRT). Based on previous studies that associate ATRX^{Loss} with XRT sensitivity, we hypothesize that ATRX^{Loss} promotes diminished survival compared to ATRX^{WT} in GSCs treated with proton radiation.

To test this hypothesis, we treated TS543-wtATRX and puromycin activated TS543-shATRX isogenic GSCs with 1-4 Gy proton radiation. GSC self-renewal was quantified using extreme limiting dilution analysis (ELDA).[6] Our results demonstrate that ATRX^{Loss} significantly impairs GSC self-renewal compared to ATRX^{WT} in response to proton radiation based on neurosphere formation frequency. In the future, we will elucidate changes in the DNA damage repair of ATRX^{Loss} isogenic GSCs to further the development of optimal treatment regiments for IDH1^{R132H}/ATRX^{Loss} glioma patients.

Characterization of Mechanisms of Resistance to Atxii in Pediatric Cell Lines

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ivan Xavier Albino Flores*; Andrew Robles and Peter Houghton, *University of Texas Health Science Center San Antonio*

Abstract: Ewing sarcomas (EwS) are bone and soft tissue malignancies that affect children and adolescents, resulting from specific EWS-ETS gene fusions, most frequently between EWSR1 and FLI1. An unbiased, mechanism-blind screen was designed to identify compounds with selective activity against pediatric solid tumors and the fungal metabolite altertoxin II (ATXII) was found to have highly selective activity against multiple EwS cell lines. Mechanism of action studies have been conducted to determine the molecular target(s) of ATXII. It has been shown that ATXII selectively induces DNA damage and replication stress in EwS cells, but does not directly bind DNA. Therefore, ATXII will help identify a new vulnerability of EwS and may identify a new therapeutic target. Hybridization of an EwS cell line with an ATXII-resistant RMS cell line (EW8- Rh30) suggested that sensitivity to ATXII is recessive. The generation and characterization of an ATXII-resistant EwS (EW8) cell line potentially allows for identification of mutated gene(s) that confer resistance or altered gene signatures between parental and resistant cells. In addition, differences in cellular metabolism of ATXII between the different sarcoma cells that might influence their sensitivity to ATXII, have been investigated and differ among EwS vs Non-EwS cell lines. Our results provide

us with valuable insight into genes/pathways important for sensitivity in Ewing sarcoma cells, as well as the therapeutic potential of ATXII.

BRCA1 Activates the G2/M Cell Cycle Checkpoint By Regulation of PLK1 (Polo Like Kinase 1)

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Yanira Gonzalez-Rodriguez* and Samuel Bunting, *Rutgers University*

Abstract: The G2/M cell cycle checkpoint reduces the risk of chromosome mutations that drive the onset of cancer, by preventing cells with unrepaired DNA damage from entering mitosis. The tumor suppressor protein, BRCA1, is required for normal induction of the G2/M checkpoint, but it is not clear how BRCA1 activates the checkpoint. We used two cellular models to address how BRCA1 regulates the G2/M checkpoint. Mouse embryonic fibroblasts or B lymphocytes expressing mutant forms of BRCA1 were treated with ionizing radiation to induce DNA double-strand breaks. The proportion of cells entering mitosis was quantified by flow cytometry, and the activation of DNA damage responses was analyzed by Western blotting of key signal transduction components. Our results show that PLK1 (Polo-like kinase 1), a key protein that promotes the transition into mitosis, remains active after DNA damage in BRCA1-mutant cells. In contrast, PLK1 is inactivated by dephosphorylation in control cells. Measurement of mitotic cell populations revealed that PLK1 hyperactivity in BRCA1-mutant cells correlated with a failure of the G2/M cell cycle checkpoint, allowing cells to enter mitosis even after DNA damage. In addition, we find that treating BRCA1-mutant cells with a PLK1 inhibitor can rescue the G2/M checkpoint, indicating that it may be possible to restore normal responses to DNA damage in cells that lack functional BRCA1. These results demonstrate a novel mechanism for regulation of cell division by BRCA1, and offer a potential opportunity for future clinical interventions to reduce cancer susceptibility in patients with BRCA1 mutations.

Elucidating the Role of Spenito (Nito), an RNA-Binding Protein, in the Sexual Dimorphism of Drosophila Metabolism

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Arely Diaz*; Kelsey Hazegh and Tania Reis, *University of Colorado Anschutz*

Abstract: Genetic studies of obesity have revealed major hereditary contributions to variation in body weight, but the vast majority of these remain unidentified. The large number of genes that contribute to obesity means that a treatment plan that works for one individual may not work for another. In order to develop individualized treatments for obesity we need a mechanistic understanding of the pathways in which obesity-linked genes normally function. An additional complication is that males and females are fundamentally different with regards to metabolism, but the underlying molecular mechanisms are incompletely understood. The research presented here shows the role of Spenito (Nito), an RNA-binding protein in *Drosophila melanogaster,* in the regulation of fat storage, in a sex dimorphic manner. Preliminary data suggests a role for Nito in the fat body (FB, equivalent to liver and adipose) in a sex-specific manner to potentially modulate splicing and gene expression via m6A methylation, as was previously shown for sex determination. To test this molecular mechanism, I will utilize the robust genetic, cellular and molecular tools of *Drosophila* paired with metabolomics, and transcriptomic analysis. Ultimately, my work will elucidate how differences in male and female metabolism are established and regulated at the molecular and cellular level.

Defining the Role of the Adherens Junction-Actin Cytoskeletal Linker Canoe/Afadin in Morphogenesis

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Kia Z. Perez-Vale*; Kristi E. Dixon; Noah J. Gurley and Mark Peifer, *The University of North Carolina at Chapel Hill*

Abstract: Maintaining tissue architecture involves apical-basal polarity establishment and maintenance and cell-cell and cell-matrix adhesion, and both require linkage of adhesions to the actin cytoskeleton. Cell junction disruption and polarity loss help drive cancer metastasis. Embryo morphogenesis requires linking adherens junctions (AJs) with the actin cytoskeleton. An outstanding model to study this in an intact animal is the *Drosophila* embryo. Our lab determined that Afadin/Canoe links AJs to the actin cytoskeleton. Canoe is a multidomain protein and much is still unknown about how Canoe's different domains contribute to Canoe localization and function during development. Using CRISPR/Cas9, I engineered *canoe*'s locus to introduce a series of mutants, deleting Canoe's RA, PDZ or F-actin binding (FAB) domains, to define how they contribute to Canoe localization and function throughout development. My working hypothesis was that Canoe's PDZ and FAB domains link junctions to actin and play key roles in Canoe's localization and function at many stages but may not be essential for all roles. To our surprise, neither the PDZ nor FAB domains were essential for adult viability. However, a significant fraction of maternal/zygotic ΔFAB domain mutants die as embryos. Thus, the PDZ and FAB domains contribute to full function but are not essential, supporting an emerging view of a robust multiprotein AJ-actin linkage. I am analyzing in detail how the PDZ and FAB domains regulate Canoe localization and function. This research provides novel insight into how Canoe acts as a machine to link AJs with the actin cytoskeleton during key conserved developmental processes.

Determining Roles for Khnyn and ZAP in Hepatitis B Virus Pgrna Regulation

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Jorge Guerrero*[1]; Sofia Romero[1]; Chad Swanson[2] and Nathan Sherer[1], *(1)University of Wisconsin - Madison, (2)King's College London*

Abstract: Zinc-finger antiviral protein (ZAP) senses viral RNA molecules that encode high levels of CpG dinucleotides and can target them for degradation in the cytoplasm. A protein with no previously known function, KHNYN, was recently shown to interact with ZAP and be necessary for its antiviral properties (Ficarelli et al., *ELife*, 2019). Here, we test the relevance of ZAP and KHNYN to the regulation of hepatitis B virus (HBV) pre-genomic RNAs (pgRNAs) that encode high levels of CpG. Using a lentiviral mediated CRISPR/Cas9 system, we created KO cell lines for both *ZAP* and *KHNYN* in Huh7 and HepG2-NTCP liver carcinoma cells. After infecting HepG2-NTCP cells or transfecting Huh7 cells with plasmids encoding wild-type or CpG-modified derivates of HBV pgRNAs, cells and viruses are tracked using a combined FISH-IF protocol prior to unbiased computational image analysis. Long-read MinION sequencing serves as a complementary approach to measure changes to HBV and host cell gene expression in the presence or absence of ZAP and KHNYN. Taken together, this system allows us to test the hypothesis that HBV pgRNAs, having acquired a relatively high number of CpG dinucleotides, exploit ZAP and KHNYN to maintain replication at low levels in the context of chronic hepatocyte infection.

Protecting Stem Cell Derived Pancreatic Beta-like Cells from an Immune Attack

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

Roberto Castro-Gutierrez*[1]; Aimon Alkanani[2]; Aaron Michels[2] and Holger Russ[1], *(1)University of Colorado Anschutz Medical Campus, (2)Barbara Davis Center for Diabetes*

Abstract: Type 1 diabetes (T1D) results from an autoimmune attack towards pancreatic beta cells mediated by CD8$^+$ T cells. Transplantation of cadaveric beta cells has been proposed as a cure but has been hampered by donor shortage. We and others have described the generation of an abundant source of functional stem cell derived beta-like cells (sBCs) that can rescue diabetes in preclinical animal models. Now, our goal is to understand how sBCs respond to a T1D inflammatory environment and how to protect them.

In order to study the beta cell-immune cell interactions in a human context we have generated an *in vitro* stimulation assay that recapitulates critical aspects of T1D pathogenesis. Our data suggests that upon pro-inflammatory cytokine stimulation, sBCs upregulate Human Leukocyte Antigen (HLA) receptors that allow for their recognition by diabetogenic CD8+ T cells in a peptide and receptor dependent manner. Furthermore, to protect sBCs from such immune recognition, we employed genome engineering to stably and site specifically integrate an inducible Programmed Death Ligand 1 (PD-L1) overexpression system in human pluripotent stem cells (hPSCs). PD-L1 is an immune checkpoint inhibitor that can prevent immune detection. sBCs that overexpress PD-L1 receptors can reduce stimulation of diabetogenic CD8+ T cells.

In sum, my data provide critical insights into immunoreactivity of sBCs to diabetogenic immune cells. We will further test the effects of genetic modifications such as HLA KO to evade an immune attack. Taken together, we provide novel strategies for the design of cell therapy modalities for patient suffering from T1D.

CRIP2 a Novel Cu-Binding LIM Domain Protein That Contributes to Skeletal Muscle Differentiation

Discipline: Life Sciences

Subdiscipline: Cell/Molecular Biology

May Maung*, *Wesleyan University* and Teresita Padilla-Benavides, *Wesleyan Univeristy*

Abstract: Cu is an essential cofactor for cellular processes, such as respiration and oxidative stress homeostasis. Failure in Cu homeostasis leads to severe conditions, such as Wilson's and Menkes diseases. These are characterized by neurological deficiencies and defects in skeletal muscle development and function. It is assumed that muscular deficiencies result from impaired systemic metal transport. However, it is not known whether these myopathies are instead the result of dysfunctional Cu-dependent transcriptional mechanisms. In eukaryotic cells, the evidence for Cu and Cu-transcription factors (Cu-TFs) is limited to metal homeostasis, and only three Cu-TFs have been identified in mammalian cells.

Using an unbiased metalloproteomic approach of native gel electrophoresis coupled to mass spectroscopy, we identified a novel protein with potential to bind Cu, CRIP2, in differentiating primary myoblasts. CRIP2 is annotated as Zn-binding LIM domain protein that regulates NF-κB-mediated proangiogenic cytokine transcription; however, no information is available on the biological role of CRIP2 in the skeletal muscle lineage.

Sequence analyses showed that CRIP2 might bind Cu at various metal-binding sites, which were confirmed by atomic absorbance spectroscopy and affinity assays. In proliferating and differentiating myoblasts, CRIP2 presents a stable expression which is enhanced by Cu, suggesting a role for CRIP2 in myogenesis that may be associated with Cu availability. CRISPR/Cas9 deletion of CRIP2 impaired differentiation with no evident effect in myoblast proliferation. The data supports the hypothesis that proteins that are annotated as Zn-binding proteins may bind Cu with higher affinity and have essential roles in developmental processes.

Characterization of the Mechanisms of Vacuole Localization and Movement in Fission Yeast

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Emily Conrad*[1]; Mark Chan[1] and Will Chadwick[2], *(1)San Francisco State University, (2)University of California, San Francisco*

Abstract: Organelle positioning and movement within the cell are critical to cellular function and to the production of cell diversity. Fission yeast (*Schizosaccharomyces pombe*) is a unicellular eukaryote often used as a model to study basic cellular functions such as organelle positioning and movement. Positioning studies in *S. pombe* have shown that the distribution of a major organelle, the vacuole, is non-random; vacuoles cluster at high density around the nucleus, and vacuole density drops as distance from nucleus increases. This pattern is mirrored in both compartments of the cell, which are separated by a large, medially-located nucleus. It is unknown what mechanism(s) maintain the positioning pattern of these vacuoles throughout interphase in *S. pombe*. Despite the durability of vacuole distribution patterns in *S. pombe*, vacuoles have been observed to cross the nucleus from one cell compartment to the other. How vacuole distribution patterns persist despite consistent vacuole movement is also unknown. This presentation will report efforts to further characterize patterns of vacuole movement and determine the molecular mechanisms *S. pombe* uses to orchestrate vacuole localization and movement. Movements will be characterized by time lapse microscopy using fluorescently dyed vacuoles. Molecular mechanisms of movement will be determined using cytoskeletal disrupting drugs to observe vacuole localization and movement in absence of individual cytoskeletal components. The resulting knowledge will improve our understanding of the variety of mechanisms found in eukaryotes that lead to the generation of cellular diversity.

Optimizing Cell Factories: Uncovering the Role of Vacuolar Size in Biochemical Yield

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Gabriela Alvarez Azanedo* and Mark Chan, *San Francisco State University*

Abstract: The organelles of eukaryotic cells house molecules involved in specialized biochemical reactions. We focus on the vacuoles of *Saccharomyces cerevisiae* yeast since they are dynamic organelles that have been suggested to hold the potential to manufacture biochemical products that can be converted to liquid fuels such as gasoline. The aim of this study is to determine if the sizes of these organelles impact the quantity of chemical products stored within them, which can provide insights on its capacity to yield compounds. Our compound of interest is 5-Aminoimidazole ribonucleotide (AIR), which accumulates in the vacuoles of *S. cerevisiae* mutants defective in the *ADE2* gene (also involved in the DNPB pathway) when cells are grown in adenine-deprived medium. AIR emits red fluorescence naturally when exposed to oxygen, allowing us to measure the extent of its accumulation in vacuoles using fluorescent microscopy. We used spinning disk confocal microscopy to image AIR accumulation in *ade2* mutants whose vacuoles were also labeled at the limiting membrane with a *VPH1-GFP* fusion. These images were used to quantify the three-dimensional size of the vacuoles using computational shape reconstruction as well as the AIR content from integrated fluorescence intensity. Our preliminary results suggest a positive correlation between vacuolar size and the amount of AIR accumulated. Understanding how vacuolar size affects the amount of a compound accumulated within the vacuoles could shed light on finding effective ways to engineer yeast vacuoles as bioreactors to manufacture other compounds of interest in larger scales.

Reprogramming Pancreatic Cancer: Understanding How to Make an Acinar Cell

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Diane Hernandez*; Shuba Narayanan and Charles Murtaugh, *University of Utah*

Abstract: Pancreatic ductal adenocarcinoma (PDAC) arises from the reprogramming of acinar cells. We are interested in understanding how acinar specific transcription factors (TF) are able to promote acinar cell identity. Our lab has demonstrated the importance of an acinar TF, pancreas specific factor 1A (Ptf1a), in early development of PDAC. Ptf1a is part of a larger regulatory network and it is unclear whether other TFs play a role in reversing PDAC formation. We aim to determine which TFs are sufficient for fibroblast-to-acinar reprogramming. This approach will inform our larger goal of reprograming cancerous cells back to their original identities.

To reprogram fibroblasts into acinar cells, we introduced different combinations of acinar-specific TFs to fibroblasts using lentiviral infection. Our candidate TFs have been implicated in development and maintenance of acinar cells. We measured differential gene expression to determine whether these TFs are sufficient to induce an acinar-like cell fate. We also used this approach to attempt to reprogram human PDAC cell lines back into acinar cells.

Our early results suggest Ptf1a alone is not sufficient to reprogram fibroblasts into acinar cells. However, when we induce expression of Ptf1a with our candidate TFs, we observe induction of multiple acinar-specific genes. Performing similar experiments in PDAC cell lines, we find Ptf1a alone is sufficient in some lines, but not others, to inhibit growth and induce expression of acinar-specific genes. The differential effects of Ptf1a on these cell lines provides an opportunity to understand what makes a cell either amenable or resistant to reprogramming.

The Study of Organelle Structure Under Toxic Metal Stress

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ramon Rodriguez* and Mark Chan, *San Francisco State University*

Abstract: Understanding how the vacuole interacts with toxic heavy metals could further our insight into how these same toxic metals affect the human body since organelles like lysosomes have been known to be homologous to vacuoles. This study focuses on different concentrations of copper chloride and its effects on the vacuole measured in volume. To quantify these results, we studied BY4741 cell strains tagged with a green fluorescent protein on the vacuole membrane. This fluorescent protein will allow us to create a 3D model of the vacuoles to obtain its volume

Confocal microscopy was used to gather images of the vacuoles that had been exposed to various concentrations of copper chloride. These images were then analyzed using image J, an analytical imaging software program. Vacuoles exposed to higher concentrations of copper chloride demonstrated a significant increase in both size and volume, whereas vacuoles exposed to lower concentrations displayed a smaller size and volume relative to the size of the cell.

The Effects of HIV Inflammatory Mediators and Cart on Bone Mass and Bone Quality in NSG-Hupbl Humanized HIV Mouse Model.

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Arnold Olali*; Ryan Olali and Lena Al-Harthi, *Rush University Medical Center*

Abstract: People living with HIV (PLWH) have reduced bone mineral density (BMD) compared to uninfected individuals increasing their risk of osteoporosis and osteoporotic fractures. Furthermore, initiation of combined anti-retroviral therapies (cART) is linked to greater bone loss within 1-2 years of initiation. However, loss in bone mass does not fully explain the increased fracture risk in PLWH. Due to the widespread use of cART, it is difficult to detangle the individual contribution of HIV infection and cART use on bone-related pathology. In this study, we tested the effects of HIV infection and *Atripla* on bone mass and bone quality using the immunodeficient mice humanized mouse model, NSG-HuPBMCs. NSG-HuPBL were first humanized by reconstituting with human peripheral blood mononuclear cells (PBMC). Mice were then infected with HIV-Bal-1 or Injected Atripla. *Atripla* as administered every other day for three weeks via Intraperitoneal (IP) injection. Changes in bone mass was measured weekly using Dual-energy X-ray absorptiometry (DXA). Upon sacrifice, changes in bone quality was measured using micro computed tomography (μCT). We detected a statistically significant decrease in total body BMD in HIV infected mice and a reduction in femoral BMD in *Atripla* treated mice. Both HIV infected and *Atripla* treated mice also had moderate reduction in BV/TV. While there are clincal studies demonstrating bone loss in PLWH and with the initiation of several cART regimens, the relative contribution of HIV and cART is not well-established. The following findings sets the stage independently assess how HIV infection and cART contribute to BMD loss.

Exploration of the Mechanism behind Wnt Transport

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Madu Nzerem*; Lisa M. Galli and Laura W. Burrus, *San Francisco State University*

Abstract: Cells communicate by sending signals, such as Wnts, to each other to activate genes. Wnts are proteins required for embryonic development and maintenance of healthy adult cells. Interruption of Wnt signaling can result in embryonic defects and diseases like cancer. Mounting evidence suggests that filopodia play a key role in the transport of Wnts from Wnt-producing to Wnt-receiving cells. We have previously shown that the overexpression of WNT1 and WLS, a Wnt cargo transporter, in embryos and in cultured cells induces new filopodia, which are likely important for Wnt signaling. However, the mechanism by which signaling filopodia are induced is not known. Our goal is to distinguish between two competing hypotheses: 1) WNT1 and WLS induce filopodia using machinery associated with Wnt production and 2) WNT1 and WLS induce filopodia using machinery associated with Wnt reception. To distinguish between these two hypotheses, I developed a co-culture assay in which Wnt-producing L cells (stably transfected with WNT1) were co-cultured with Wnt-receiving HEK 293T cells, which were transiently transfected with a membrane marker. I then wrote Python code to analyze the filopodia data. Upon counting the filopodia in the HEK293T cells, I found that there was no significant increase in the number (or length) of filopodia, suggesting that the molecular machinery for filopodia induction is associated with Wnt production and not reception. Future experiments will assess the role of CDC42, a G-protein involved in both filopodia induction and Wnt signaling, in the transport of Wnt via filopodia.

Investigating the Induction and Growth of Wnt-Delivering Filopodia in Cell Communication for Tissue Homeostasis and Repair

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Angela Lane* and Laura W. Burrus, *San Francisco State University*

Abstract:

Wnts are secreted proteins that are vital for embryonic development and adult tissue homeostasis. Dysregulation of Wnt signaling can lead to embryonic defects and cancer. Therefore, proper Wnt signaling and transport from one cell to another is crucial. Mounting evidence suggests that filopodia are a key conduit for the transport of Wnts from Wnt-producing to Wnt-receiving cells. We have recently shown that the co-expression of WLS (a Wnt cargo transporter) along with WNT1 in HEK293T cells causes the induction of new filopodia and the redistribution of WNT1 from the endoplasmic reticulum to the filopodia. However, we do not know if the co-expression of WLS along with other Wnt family members will have the same effect. My goal is to determine the effects of WNT1, WNT3A or WNT5A on filopodia length and number in 3T3 cells. WNT3A is functionally redundant with WNT1 while WNT5A often antagonizes WNT1. Thus, I hypothesize that WNT5A will induce filopodia length and number less than WNT1 and WNT3A. To test this hypothesis, I generated expression constructs for WNT3A and WNT5A. Each construct has a fluorescent tag, which allows for visualization using live imaging. I then transfected 3T3 mouse cells with the WNT1 construct, imaged using confocal microscopy and analyzed for filopodia number and length. My preliminary data shows that the overexpression of WNT1 and WLS in 3T3 cells induces a statically significant increase in filopodia length (p-value<0.01), while filopodia number remained unaffected. I am currently evaluating whether WNT3A and WNT5A also induce filopodia length and number.

Isolation of Anthrax Toxin Lethal Factor Interacting Partners Using Human Heart T7 Phage Display cDNA Human Libraries

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Flavio Rodriguez Polanco*, *University of Puerto RIco of Mayagüez* and Carlos Ríos Velázquez, *University of Puerto Rico at Mayagüez*

Abstract: *Bacillus anthracis* is a pathogenic bacterium that causes anthrax disease that has been used as a biological weapon in bioterrorist attacks. Pulmonary anthrax is the most lethal form of anthrax due to the lethal factor (LF) component of the tripartite toxin secreted by the bacteria. It is known that LF is a metallo-protease capable of inactivating regulators such as mitogen activated protein kinase (MAPK), interfering with cell cycle, leading to cell death. However, it is not clear if MAPKs are the only target for LF; therefore, it is necessary to explore novel potential ligands for LF, using different strategies to further unravel new molecular pathogenesis pathways. LF has been also associated with cardiac dysfunction, suggesting human heart (HH) cells as potential targets. The purpose of this research is to isolate and identify LF specifics interactions peptides using premade T7 Phage Display cDNA from HH as ligands. After several biopannings rounds, using wt and active site-mutant LF as targets, a total of 3.9×10^8 and 3.4×10^8 pfu/mL were obtained for wt and mutant LF respectively. Individual plaques DNA were isolated, and the cloned HH cDNA amplified using PCR. The amplicons ranged from 200 to 300bps. Work is in progress to perform specificity test and to sequence and in silico analyze the samples in order to identify the protein family involved in the interaction. Understanding novel LF interaction ligands in the HH, have the potential of identifying targets to develop new biomarkers and therapeutics against anthrax disease in case of a bioterrorism attack.

The Role of the SOX10-DDX3X Interaction in Salivary Gland Stem Cell Self-Renewal and Differentiation

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Christina Jones*; Alex Carson; Harleen Athwal and Isabelle Lombaert, *University of Michigan School of Dentistry*

Abstract: Therapeutic irradiation (IR) is a commonly used treatment for head and neck cancer patients. IR treatment has many adverse effects, including irreversible salivary gland (SG) damage and xerostomia. Current therapies aim to alleviate xerostomia but fail to address the underlying mechanism of dysfunction, thus new strategies for tissue regeneration are needed. To this end, it is vital to understand how SG epithelial stem/progenitor cells are maintained and form complex, functional secretory units. Our group previously identified the potential of KIT+ stem/progenitor cells in rescuing hyposalivation, and demonstrated that SOX10 plays a major role in their proliferation and differentiation potential. DEAD box polypeptide 3 X-linked (DDX3X), an evolutionarily conserved member of the RNA helicase family, was recently identified by us as a binding partner of SOX10 in SG stem/progenitor cells. Emerging evidence indicates that DDX3X plays dual roles in modulating proliferation, migration, invasion, drug resistance, and/or stem cell-ness in a variety of cancers. Preliminary data show that RNAi of DDX3X in murine SG cells caused apoptosis at embryonic stage 13 (E13) but not at later stages (E16 and/or adult), suggesting DDX3X may exert different functions in stem/progenitor cells at various developmental stages. In this study, we aim to investigate the role of DDX3X in human and murine epithelial cells to provide insight in stem cell renewal and differentiation. Through various assays, the DDX3X-SOX10 interaction and function will be characterized and/or manipulated with the end goal of generating a clinical therapy that aids in the repair of SGs post-IR.

Embryonic Hyperglycemia Causes a Reduction in Photoreceptor Cells and Increased Oxidative Stress in the Developing Retina

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Kayla Titialii-Torres* and Ann Morris, *University of Kentucky*

Abstract: Poor blood glucose regulation has been linked to long-term metabolic disruptions in adults, such as tissue damage in the eye. Yet, little is known about the effects of embryonic hyperglycemia on retinal development. To address this question, our lab uses a comparative approach between Pdx1$^{-/-}$ zebrafish which does not produce insulin and a "nutritional model" established by our lab to induce hyperglycemia by submerging zebrafish embryos in fish water containing 50mM glucose +/- 10µM dexamethasone (G+D) from 10 hours post fertilization (hpf) until 120 hpf. Following treatment, larval heads were fixed, and the remaining body was used to quantify glucose concentration using a glucose assay from Biovision as well as genotyping for the Pdx1. The fixed heads were processed for sectioning and immunohistochemistry to label and quantify cell types in the retina. Pdx1$^{-/-}$ and G+D treatment reliably produced hyperglycemic larvae, with >2-fold increased whole-body glucose concentration compared to control-treated and wildtype larvae. Our results show that both models of hyperglycemic larvae had a significant reduction in rod and cone photoreceptors with abnormal morphology, aberrant Müller glia morphology, and significant increase in reactive oxygen species (ROS) production as well as abnormal expression of enzymes in metabolic pathways related to ROS in the retina. Our results suggest that embryonic hyperglycemia results in abnormal photoreceptor development via ROS production, which is accompanied by aberrant Müller glia cell development. As the rate of diabetes increases, it is imperative to pinpoint the effects of embryonic hyperglycemia via innovative models to further development of therapeutic strategies.

Preparing the Next Generation for Climate Change: Parental Effects on Larval Thermal Tolerance in the California Mussel (*Mytilus californianus*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Heidi Waite*, *University of California Irvine* and Cascade Sorte, *University of California, Irvine*

Abstract: Under changing climate conditions, marine organisms will need to cope with or adapt to increasing temperatures to persist. Parental effects, where offspring responses to environmental change are influenced by parental environments through non-genetic changes and maternal provisioning, may influence the ability of populations to cope with thermal stress. This study evaluated whether thermal environments across a natural gradient (tide height) impacted the temperature tolerance of larvae of the mussel, *Mytilus californianus.* Adult mussels were collected from the rocky intertidal of Newport Beach, CA, USA. LT_{50} (temperature lethal to 50% of individuals) was quantified for field-collected adults and their 3-day old veliger larvae raised in the laboratory. We used a generalized linear mixed model approach to examine which factors predicted larval mortality. The best-fit model indicated that LT_{50} assay temperature, adult (parent) LT_{50}, and parental environment (collection tide height) all significantly contributed to level of larval mortality. Overall, survival was lowest for larvae with parents who were collected from the warmest environment (high tide height). Egg diameter varied by tide height, with the smallest eggs occurring at high tide height. Adult gonadosomatic index, a measure of reproductive condition, varied significantly by tide height with lowest condition in high tide height mussels. These results suggest parental effects are maladaptive for thermal tolerance and indicate negative effects of stress. Stressed mussels may invest less in reproduction leading to lower larval tolerances. Thus, maladaptive parental effects could leave larvae more vulnerable to thermal stress and impact the survival of the mussel under climate change.

Evolutionary Relationships Among Bifidobacteria and Their Hosts and Environments

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Cynthia Rodriguez* and Jennifer Martiny, *University of California, Irvine*

Abstract: The assembly of animal microbiomes is influenced by environmental factors and host genetics, although the relative importance of these factors remains unclear. Bifidobacteria (genus *Bifidobacterium*, phylum Actinobacteria) are common colonizers of gut microbiomes in humans, other mammals, social insects, food, and sewages. In humans, the presence of bifidobacteria in the gut has been correlated with health-promoting benefits. Here, we compared the genome sequences of over 150 *Bifidobacterium* strains publicly available to investigate the adaptation of bifidobacteria diversity. We tested **1)** whether bifidobacteria show a phylogenetic signal with their isolation sources and **2)** whether key traits encoded by the bifidobacteria genomes depend on the host or environment from which they were isolated. We analyzed *Bifidobacterium* genomes available in the PATRIC and NCBI repositories and identified their isolation source. We conducted a phylogenetic analysis to compare the genetic relatedness the strains harbored by different hosts and environments. Furthermore, we examined differences in genomic traits and genes related to amino acid biosynthesis and degradation of carbohydrates. We found that bifidobacteria diversity appears to have evolved with their hosts as strains isolated from the same host were non-randomly associated with their phylogenetic relatedness. Moreover, bifidobacteria isolated from different sources displayed differences in genomic traits. In contrast, when analyzing diversity within human-derived bifidobacteria, we observed no phylogenetic signal or differences on specific traits. Looking into the genomic signatures of bifidobacteria from different environments can give insights into how this bacterial group adapts to their environments and what types of traits are important for these adaptations.

Individual and Ecological Consequences for an Intertidal Rockweed to Conditions Associated with Sea Level Rise

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ariel Heyman* and Jennifer L. Burnaford, *California State University, Fullerton*

Abstract: Organisms in the intertidal zone, which experience terrestrial conditions during low tide emersion and are submerged in seawater during high tide, are threatened by sea level rise (SLR) which could reduce annual emersion time by over 50% over the next 100 years. Using a manipulative field experiment, we tested the hypothesis that SLR conditions would negatively impact performance of individuals of the canopy-forming seaweed *Pelvetiopsis californica.* At two southern California sites, we established three treatments: marked in place individuals (transplant controls: MP) were not moved; middle-zone transplant individuals (MT) were relocated at the same tidal elevation; and below-zone transplant individuals (BT) were moved to a lower tidal elevation, exposing them to shorter emersion times (= SLR conditions). We assessed health through monthly measurements of size, cover of epiphytic seaweeds (which grow on the host, blocking light and nutrients), and reproductive potential. In two eight-month replications, we saw lower performance in the SLR condition treatment (BT) than in non-SLR treatments. BT individuals lost more tissue (on average, 25% of their original length) than individuals in other treatments. More than three times as many individuals in the BT treatment were infected with epiphytic seaweeds than in MT or MP treatments. While reproductive potential did not differ among treatments, BT individuals became reproductive a month before individuals in other treatments. These data indicate substantial risk of SLR to seaweed populations and may help managers develop mitigation efforts for this important intertidal producer.

Investigating the Role of Immunity in the Colonization Specificity of a Bumble Bee Gut Symbiont

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Bryan Sierra-Rivera* and Ben Sadd, *Illinois State University*

Abstract: In the past decade, the gut microbiome has gained traction as an avenue of importance across taxonomical groups to better understand its implications for host health. Bacterial species within the gut must endure harmful conditions such as lack of nutrients, attack by the host immune system and potential negative interactions with other community members leading to evolutionary pressure for local adaptation. Although studying the gut microbiota in humans is difficult due to a high species richness, many of which are uncultivable in laboratory settings, the bumble bee gut serves as a tractable system due to only being comprised of nine core bacterial species clusters. Past research has suggested host – strain specific establishment of gut microbes from honeybees to bumble bees, but no studies have been conducted on higher level specificity within bumble bees or the role of immunity as a driver of specialization. To investigate the role of colonization specificity of a bumble bee gut symbiont, native and foreign bacterial strains will be inoculated into *Bombus impatiens* to test whether native strains better colonize their hosts compared to foreign strains. I will, then focus on the role of the host's innate immune system in the relationship between the co-evolved beneficial gut microbe and its host. To address this, RNA seq will be utilized to compare host immune gene expression in response to the native and foreign inoculations.

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Finding the Right Home: Depth As a Driver of Adaptive Evolution in the Genus *Sebastes*

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Daniel Olivares-Zambrano*, *California State University Los Angeles* and Andres Aguilar, *California State University, Los Angeles*

Abstract: This project aims to identify genomic regions that have contributed to ecological differentiation among recently diverged Northern Pacific species pairs from genus *Sebastes*. Using whole exome sequences, we have identified regions within the genome that display patterns of positive selection based on a proposed significant driver of ecological speciation within this genus: depth. Furthermore, we expect depth segregated speciation to be a result of hitchhiking divergence that generates islands of genomic diversification. So far, we have sequenced exomes from *Sebastes chlorostictus-S. rosenblatti* and *S. crocotulus-S. miniatus*. The former pair is more recently diverged (0.21 Ma) while the latter pair has a deeper divergence (2.3 Ma). Species pairs that are more recently diverged should have more numerous but smaller genomic islands due to the recency of their divergence and contemporary gene flow. Species pairs that are more diverged should have larger but fewer genomic islands across their genomes. As expected, genome wide differentiation was lower for *S. chlorostictus-S. rosenblatti* and we were able to identify numerous divergence islands in this species pair. *S. crocotulus-S. miniatus*. which had a greater degree of genome-wide fixation. Future work will focus on more recently diverged species pairs to identify common genomic islands of divergence.

Frugivore Loss Leads to Decreased Investment in Fruit Traits of a Wild Tomato (*S. pimpinellifolium*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Brittany Cavazos* and Haldre Rogers, *Iowa State University*

Abstract: While we know plants can respond to abiotic factors like light and precipitation, and more recently, biotic factors like herbivore and pollinator visitation, it is unclear whether plants can respond to changes in their frugivore community. Given that fruits are costly to create and frugivores may be unreliable or inconsistent in most communities, we hypothesize that fleshy-fruited plants should respond to frugivore activity. Specifically, we hypothesized that they could shift their resource allocation towards traits more attractive to frugivores. To test this, we set up a greenhouse experiment with a wild tomato species, *Solanum pimpinellifolium*, using replicate genotypes and simulating low, medium, and high frugivore visitation. We measured fruit size, seed size, seed number, flesh:seed ratio, and ripening time and tested for differences in these traits across time under different removal treatments.

We found no effect of fruit removal on seed size, seed number per fruit, or ripening time. However, we found that with decreased frugivory, fruit size and mass were significantly smaller over time and the effect size varied based on the tomato source population. This is consistent with the hypothesis that some plants are reducing investments in fruits when not being dispersed and this varies geographically. While we do not know the natural rates of frugivory on these plants in these locations, this could indicate high plasticity under different natural levels of fruit removal. These results imply that some fleshy fruited plants can rapidly respond to changes in frugivore communities in ways that could impact their overall fitness.

Oxygen-Regulated Gene Families Evolve Via Speciation and Transfer Events

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jaime A. Cordova*[1]; Andrew O. Hasley[1]; Eric C. Neeno-Eckwall[2]; Jeremy D. Glasner[2] and Nicole T. Perna[1], *(1)Laboratory of Genetics, University of Wisconsin, Madison, (2)Center for Genomic Science Innovation, University of Wisconsin, Madison*

Abstract: Microorganisms vary in their metabolic oxygen requirements. Some are strict aerobes, unable to grow without oxygen. Others are strict anaerobes, unable to tolerate oxygen. Facultative anaerobes, in contrast, grow by adjusting their metabolic system in response to varying oxygen levels; using aerobic respiration, anaerobic respiration, or fermentation. We previously conducted comparative transcriptome experiments with three strains of *Escherichia coli* (including model organism K-12) and four additional species of enterobacteria (*Salmonella enterica, Pectobacterium atrosepticum, Dickeya dadanti*i, and *Yersinia intermedia*), revealing complex oxygen-dependent regulatory networks and extensive variation in the response to oxygen availability. Here, we follow up on the observation that several key metabolic enzymes showed copy number and regulatory variation among these organisms by examining the distribution of hydrogenases and fumarases across 110 enterobacteria. We used OrthoMCL and BLASTP to identify homologs of all genes related to these enzymatic activities, including non-homologous isofunctional equivalents. Comparisons of the genomic context of these genes revealed variation in the architecture and content of operons. We used BadiRate to map expansions and reductions of copy number of genes linked to these two key metabolic reactions onto a robust genome-scale species phylogeny constructed using RAxML, showing parallel copy number changes in multiple independent lineages. We used Ranger-DTL gene-tree reconciliation to demonstrate the events that have contributed to variation in copy number of these gene families, including speciation and transfer events. Together these analyses show that hydrogenase and fumarase genes have been repeatedly gained, lost, and rearranged in concert with divergence of their transcriptional regulatory systems.

Abundant Floral Resources Reduce Pathogen Pressure for Bees in Agroecosystems

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Laura Jones*; Ginamaría Román-Echevarría; Kristen Brochu; Rudolf Schilder and Margarita López-Uribe, *Pennsylvania State University*

Abstract: Environmental conditions and biotic interactions—including landscape composition and host availability—impact the distribution of pathogens. Some pathogens utilize multiple host species, as is the case for many bee pathogens in agroecosystems. However, the differential contribution of bee hosts to disease transmission, as well as the environmental conditions that are conducive to disease transmission, remain unknown. In this study, we propose that (1) abundant floral resources in agroecosystems will dilute bee host interactions on flowers and thus reduce disease transmission events, and (2) the most abundant bee host in *Cucurbita* agroecosystems will drive pathogen dynamics. Bee abundance was quantified using visitation rate data. Floral abundance was estimated using landscape cover data from USDA CropScape. Quantitative PCR was used to survey *Apis mellifera* (honey bees), *Bombus impatiens* (bumble bees) and *Eucera (Peponapis) pruinosa* (squash bees) populations across Pennsylvania for *Crithidia bombi*, a gut pathogen associated with bee declines that is known to elicit disease symptoms in *A. mellifera* and *B. impatiens*. Preliminary results indicate that decreasing proportion of tree cover and increasing proportion of crop cover (i.e. greater access to floral resources) reduces *C. bombi* loads in *A. mellifera* and *B. impatiens.* High *E. pruinosa* abundance was found to increase *C. bombi* prevalence, suggesting that *E. pruinosa* is the predominant host mediating pathogen dynamics in *Cucurbita* agroecosystems. These findings indicate that floral availability and wild bee host abundance mediate pathogen dynamics. For management implications, increasing the abundance of floral resources around *Cucurbita* farms may help reduce pathogen pressure on bee pollinators.

Niche Segregation between Two Species of Armadillo in the Southern Pantanal, Brazil

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Jeffrey Esparza* and Fritz Hertel, *California State University, Northridge*

Abstract: The Pantanal of Brazil is the largest tropical wetland in the world and home to one of the highest diversities of armadillos with five extant sympatric species. Among these species are the similarly sized nine-banded armadillo (*Dasypus novemcinctus*) and six-banded armadillo (*Euphractus sexcinctus*). Both species are highly specialized diggers with varying diets. I am exploring how these two armadillos partition their resources and facilitate coexistence by exploring multiple aspects of their ecology including space use and activity time through camera trapping; and substrate and habitat preference in forest and grassland habitats. I found no significant difference between burrows in both locations (forest and grassland). Preliminary data suggest temporal segregation between both species with the nine-banded armadillo exhibiting more nocturnal activity and the six-banded armadillo exhibiting more diurnal activity. Additionally, these armadillos would benefit from greater scientific scrutiny and basic ecology that should ultimately contribute to management decisions regarding their conservation efforts as some species are considered endangered and/or species of special concern.

Species and Lakeshore Development Effects on the Relationship between Fish Abundance and Angler Catch Rates

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Camille Mosley*[1]; John Caffarelli[1]; Colin Dassow[1]; Greg Sass[2]; Alex Ross[3]; Chris Solomon[4] and Stuart Jones[1], *(1)University of Notre Dame, (2)Wisconsin Department of Natural Resources, (3)McGill University, (4)Cary Institute of Ecosystem Studies*

Abstract: Recreational fisheries are important resources due to their social, economic, and ecological value. Two important links between the social and ecological components of recreational fisheries are shoreline development and the relationship between fish abundance and angler catch rates. Increases in building development may have influences on fish behavior due to the negative correlation between coarse woody habitat, which is utilized by many species of fish, and building density. Hyperstability can occur when catch rates are not proportional to abundance. Understanding this mechanism is important because as fish abundance decreases, anglers cannot sense the decline in catch rates resulting in continued angling and potential over-harvest. To determine whether hyperstability differs across species or gradients of shoreline development we completed an analysis of Wisconsin Department of Natural Resources fisheries data to observe the relationship between catch rate and abundance for popular sport fish in the region, including Bass, panfish, and Walleye populations. All species showed evidence of catch hyperstability, but the magnitude of non-linearity in the relationship between catch and relative abundance differed across species. For some species there was an effect of lakeshore development on the strength of hyperstability. Because hyperstability decreased with shoreline development, catch rates are a more reliable indicator of fish abundance in more developed lakes. Also, the observation of hyperstability across all species investigated suggests that non-angling information on population abundance is important for sustainable management management of these fisheries.

Can Butterfly Wing Patterns Signal a Novel Predator Community?

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Christiana-Jo Quinata* and Haldre Rogers, *Iowa State University*

Abstract: As we see a decline of birds throughout the world, many of which are predators of butterflies, we may find changes in prey communities. Butterfly wing morphology patterns may function as proxies of selection pressure by predators. My research aims to understand the rapid evolution of batesian mimicry in a sexually dimorphic Common

Mormon Swallowtail (*Papilio polytes)*. I hypothesize that the batesian mimic form will not be selected for in the absence of the model species and in a relaxed avifauna predator community. I will compare butterfly wing patterns of females from locations with model species present (Taiwan and Philippines), not present in a community with bird predators (Saipan and Japan), and not present in a community without bird predators (Guam). I will use digital images of museum and field collected specimens to quantify wing size and shape using geometric morphometric tools. I will compare wing color pattern by measuring the area of red pigment on each hindwing, indicative of mimetic forms. I expect to find a distinct variation in butterfly hindwing size in Guam females because of the relaxed avifauna predation selection. I expect to see less red pigmentation in butterflies in Saipan and none in Guam. The Asia Pacific region are experiencing loss of biodiversity and this research looks to inform conservation of declining species that may affect predator prey interactions.

Assessing the Survival and Post-Fire Recovery of *Pinus Montiola* Saplings to Increasing Levels of Fire Intensity

Discipline: Life Sciences
Subdiscipline: Environmental Science

Alexander Blanco* and Alistair Smith, *University of Idaho*

Abstract: Western white pine (*Pinus montiola*) has a habitat range from British Columbia to California and is an important commercial species in the Intermountain west. Within this region the frequency and intensity of wildland fires are projected to increase under climate change and thus the ability to predict mortality and growth rates following fires will improve predictions of forest recovery, growth, and yield. Past studies have demonstrated that two *Pinus* species saplings exhibited 100% probability of survival to a low intensity fire (fire radiative energy dosage 0.4 MJ m^{-2}). Thus the hypothesis we seek to answer is do *Pinus monticola* saplings also exhibit 100% survival at 0.4 MJ^{-2} or conversely, does a different threshold exist? To achieve this, 60 2-year-old saplings are being grown from seed and divided into replicates of 10 and subjected to 6 levels of fire intensity (N=50, L=6, n=10): unburned control, 0.2, 0.4, 0.6, 0.8, and 1.0 MJ m^{-2} within a climate controlled combustion laboratory. Probability of mortality and post-fire growth rates will be assesses up to 12-months post-fire using standard methods. We will also compare these data to predictions of mortality derived using the FireStem2D fire-effects mode and other models that rely only on pre-fire sapling characteristics. This data will help reduce uncertainties in estimates of carbon and timber yield in forests where known low intensity prescribed fires are been utilized to lower risk of future catastrophic wildfires.

Soil Physical Properties Under Avocado and Tropical Rainforest

Discipline: Life Sciences
Subdiscipline: Environmental Science

Patricia Marie Cordero-Irizarry* and Dr. Rattan Lal, *The Ohio State University*

Abstract: Soil organic carbon (SOC) stocks enhance soil quality which can lead to an increase in crop productivity, water-use efficiency, and natural resources conservation. Physical soil quality indicators include aggregate stability (AS) and water retention capacity (WRC). SOC stocks can fluctuate depending on land management, soil physicochemical properties and environmental conditions. In subtropical dry forest life zones, mechanisms of SOC stabilization are less known and such studies have recently gained importance for the avocado, due to its increasing popularity. The objective of this study is to quantify SOC stocks and determine their influence on AS and WRC in an avocado orchard (AO) and a natural vegetation area (NV). We hypothesize that the AO will have higher SOC stocks and better AS and WRC than the NV. The study was conducted in the Juana Díaz Agricultural Experimental Station, where the dominant soil series is San Antón (*fine-loamy, mixed, superactive, isohyperthermic Cumulic Haplustolls*). Soil samples were taken using GIS to determine tree trunk proximity. C/N will be determined with the dry combustion method, aboveground and belowground C storage with GIS and tree measurements, and quantification of SOC within aggregate size fractions will be done by the wet sieving of soil, as well as the AS test. WRC will be determined with the pressure plate extractor test. An analysis of variance (ANOVA) will be performed for statistical analysis. Data continues to be processed and preliminary results are expected by December 2020.

Nitrogen Removal Potential of Floating Wetlands; Preliminary Results from a Mesocosm Study

Discipline: Life Sciences
Subdiscipline: Environmental Science

Isabel Sanchez-Viruet*[1]; Lora Harris[1]; Jeremy Testa[1] and Allan Straughan[2], *(1)University of Maryland Center for Environmental Science, (2)Koolhof Earth*

Abstract: Nutrient enrichment of estuarine waters remains a problem globally. Mitigation of nutrient enrichment, primarily achieved through limiting the transfer of nitrogen and phosphorus from land to coastal waters, is a persistent challenge because there are strong social and economic forces that generate these nutrients and facilitate their mobility. Recently, new efforts have sought to promote conditions for nutrient removal within the streams and estuaries themselves by constructing habitats that may support enhanced nitrogen removal. These include the construction of restored oyster reefs, stream wetlands, and more recently, floating estuarine wetlands. While each of these habitats have been suggested to be “hotspots” for nitrogen removal, the quantification of their impact is difficult due to the variety of other processes that influence nitrogen transformation and loss within tidal estuarine waters. Here, we report preliminary results from

mesocosm experiments to estimate the nutrient uptake potential of floating wetlands under estuarine conditions typical within the mesohaline Chesapeake Bay, USA through mass-balance approaches and in-situ incubation experiments.

Bruno **and** ***P*****-element Transposition: Positive Regulator or Cellular Responder?**

Discipline: Life Sciences
Subdiscipline: Genetics

Lorissa Saiz*, *University of Houston - Main Campus* and Erin Kelleher, *University of Houston*

Abstract: Transposable elements (TEs) are genetic parasites that guarantee transmission to offspring by replicating in germline cells. TE replication harms hosts by causing DNA damage that prevents the production of viable gametes. In response, hosts can employ two different strategies to minimize these effects: resistance and tolerance. Resistance mechanisms prevent TE replication, while tolerance mechanisms allow host cells to withstand the damaging effects of TE activity. However, the cellular mechanisms of tolerance remain largely unknown.

P-elements are a family of TEs in *Drosophila* which are causative agents of hybrid dysgenesis. We identified *bruno* as a possible source of natural variation in tolerance of *D. melanogaster* to *P*-element transposition. *bruno* loss of function (LOF) alleles are strong suppressors of *P*-element-induced germline loss, but *bruno* has no known function in TE regulation. To determine whether *bruno* regulates *P*-element transposition or represents a tolerance factor, we compared *P*-element expression and excision rates between *bruno* mutants and wild-type, as well as between natural tolerant and sensitive alleles of *bruno*. If *P*-element transposition is independent of *bruno*, expression and excision should not differ between *bruno* genotypes. Our data suggest that *P*-element transcription does not differ between tolerant and sensitive alleles, consistent with *bruno*'s proposed role in tolerance. However, excision rates in *bruno* LOF mutants are greatly reduced, suggesting that *bruno* might influence germline loss by facilitating *P*-element excision. This function does not clearly align with established models of resistance and tolerance, but rather suggests *bruno* determines the permissivity of host cells to *P*-element transposition.

Genome-Wide Association Study: Initial Pilot Longitudinal Study in Hispanic Population of the Lower Rio Grande Valley

Discipline: Life Sciences
Subdiscipline: Genetics

Kimberly Moreno*; Victoria Padilla; Chun Xu; Gladys Maestre; Mario Gill and Priscila Acevedo, *University of Texas Rio Grande Valley*

Abstract: Life expectancy has incremented in the last couple of decades and according to CDC Data (National Vital Statistics Report ,2017), Hispanics of both genders have the highest life expectancy in the USA. Yet, CDC data also shows that life expectancy for Hispanics between 2016 to 2017 has decreased slightly due to the incrementation of health issues such as Alzheimer disease (AD).

This study focuses on genes that have been previously associated with longevity or the onset of AD in Caucasian populations and replicated in minority populations, such as the Hispanic population, due to limited studies associated to them. Would Hispanic subjects share the same genes and susceptible alleles that are linked with healthy ageing and/or AD in previous studies conducted in non-Hispanic populations? We hypothesize that genetic, environmental factors and their interactions can contribute to longevity (e.g., delaying the onset of age-related diseases), AD and expect to observe similar results as previous studies.

The methodology of the study is as followed: Hispanic families with octogenarians/ nonagenarians are incorporated into a case control/ family study design to assess how lifestyle factors with genetic input can result in healthy ageing, and/or AD. De novo genotyping of eight SNP's: ApoE (ε2 and ε4), TOMM40, SIRT6, APOC1, IGF1R, CETP and FOXO-3A and statistically analyzed with t-test, c2 test in the SPSS v25 and others. The SNP's will be tested on their interactions between lifestyle factors to observe the impact in healthy ageing or development of AD in Hispanic population.

Involucrin Knockout Mice Exhibit Reduced Vitamin D Agonist Induced Skin Inflammation and Reduced Vitamin D Receptor Expression

Discipline: Life Sciences
Subdiscipline: Genetics

Alina Schmidt*; Mary Elizabeth Mathyer; Erin Brettmann and Cristina de Guzman Strong, *Washington University in St. Louis*

Abstract: Involucrin (*IVL*) dosage may benefit cutaneous health as we previously discovered recent evolution for relatively lower *IVL* levels in African populations in contrast to higher levels in European populations. In barrier house conditions *Ivl* -/- mice show no defect in epidermal barrier development. However, we have a poor understanding of the role of *IVL* for epidermal barrier maintenance in response to an inflammatory trigger. We induced inflammation in ears of *Ivl* -/- and control wild-type mice with vitamin D agonist (MC903) topical treatment. Wild-type mice exhibited notable skin inflammation and hyperkeratosis in the MC903-treated ears as expected in comparison to ethanol-treated controls ($P<.001$). However, *Ivl* -/- mice revealed a surprising reduction in skin inflammation compared to wild-type mice. The dampened inflammatory response coincides with reduced expression of *Tslp*, a known mediator of MC903-induced inflammation, in *Ivl -/-* compared to wild-type mice. We next examined the potential mechanism by which MC903-induced inflammation was reduced in *Ivl -/-* mice and found reduced Vitamin D receptor (*Vdr*) expression in *Ivl -/-* skin that was not observed in wild-type mice. The data suggests a positive correlation for *Ivl* dosage to *Vdr* expressions. Together, our findings identify functional significance for *IVL* in the epidermis revealing an emerging paradigm for *IVL* dosage that has recently evolved in human adaptation to potentially regulate *VDR* expression in the epidermis.

A Comparison of the Safety and Pharmacogenetics of Potential Therapeutic Candidates and Adeno-Associated Virus (AAV) Mediated Gene Transfer for the Treatment of RPE65 Gene Inherited Retinal Dystrophies (IRD)

Discipline: Life Sciences
Subdiscipline: Genetics

Natalí Chávez* and Guy diSibio, *California Northstate University*

Abstract: The RPE65 gene is essential for the vision cycle. Mutations of this gene can cause one of the leading causes of childhood blindness known as Leber's congenital amaurosis (LCA). LCA is a rare inherited genetic ocular disorder caused by mutations in both copies of the RPE65 gene. Approximately 1,000 to 2,000 people in the U.S. have RPE65 mutations associated with inherited retinal dystrophy (IRD). Luxturna is the first FDA approved targeted gene therapy of the inherited retinal disease LCA. This study discusses the safety, efficacy and pharmacogenetics of Adeno-Associated Virus (AAV) gene transfer treatment in comparison to current potential therapeutic candidates. To investigate this, a combination analysis of current gene therapy models will be examined and compared. This protocol includes a collection of U.S. published longitudinal LCA therapeutic data meeting the eligibility criteria for data collection process, study selection, unbiased studies, and informational sources. Preliminary results suggest utilizing the AAV-mediated gene transfer model is most effective in the restoration of cone and rod photoreceptors in patients with LCA. The significance of this study illustrates the novel Luxturna AAV-mediated gene transfer for the restoration of the function of cone and rod photoreceptors in patients with LCA. This study shows important implications resulting from treating human patients with RPE65-mutated IRD. This analysis models the understanding of the pharmacogenetics of current and potential gene therapies for LCA. Assessing the successful pharmacogenetics and safety among Luxturna treated patients shows remarkable promise in the field of gene therapy.

Glucose Acts through the Insulin Signaling Pathway to Induce a Developmental Delay in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Genetics

Saifun Nahar* and Pamela Padilla, *University of North Texas*

Abstract:

A significant amount of research has shown that type 1 diabetes in children causes a delay in puberty. However, it is unclear if hyperglycemia is associated with this delay in puberty. Hyperglycemia, which is associated with diabetes, refers to elevated blood glucose levels. To model hyperglycemia at molecular level, we use genetic model system *C. elegans* fed a glucose-supplemented diet and study the physiological and molecular impacts. We found that *C. elegans* fed a glucose-supplemented diet induces a developmental delay in comparison to the control food (OP50 *E. coli* diet). Use of the ΔPTS *E. coli* OP50 bacteria strain, which lacks a glucose transporter, confirmed that the developmental delay is likely not due to metabolites produced by the *E. coli* OP50 bacteria. A genetic approach was used to examine the glucose-induced developmental delay phenotype. Specifically, we examined mutants known to have a slight developmental delay and were dysfunctional in either ceramide biosynthesis, electron transport chain activity or insulin signaling (*hyl-2(tm2031)*, *isp-1(qm150)* and *daf-2(e1370*), respectively). A glucose-supplemented diet further exacerbates the developmental delay of the *hyl-2(tm2031)* and *isp-1(qm150)* mutants but did not induce a developmental delay in the *daf-2(e1370)* animal. However, a glucose-induced developmental delay was observed in the *daf-2(e1370)* animal if the downstream transcription factor DAF-16 was disrupted (*daf-16(mu86)*). Our next step is to use RNA sequencing and genetic analysis to understand how modulating insulin signaling alters developmental progression and to identify the DAF-16 regulated genes associated with such.

Identification of Transcriptional Regulators Impacted By a Glucose-Supplemented Diet in *C. Elegans*

Discipline: Life Sciences
Subdiscipline: Genetics

Jose Robledo*; Pamela Padilla; David Burks and Rajeev Azad, *University of North Texas*

Abstract: T2D patients display various metabolic abnormalities (e.g. hyperglycemia, insulin resistance, increase free fatty acids) that contribute to severe and detrimental human health issues. There is still little understanding of how hyperglycemia or a sugar-supplemented diet impacts gene expression and physiology. We use the genetic model system *Caenorhabditis elegans* to study the impact a glucose-supplemented diet has on physiology and gene expression. Previously, we showed that a glucose-supplemented diet impacts the expression of 2,370 genes, increases lipid composition, and increases the sensitivity to stress responses. To further understand glucose induced gene expression changes and the consequences to stress survival, we sought to further examine gene regulators from our transcriptomic analysis. We determined the *acs-2* gene as a glucose-responsive gene; this was shown by RNA-sequencing analysis, the *acs-2::GFP* reporter strain, and quantitative RT-PCR. To identify the transcriptional regulators that respond to a glucose diet we used the *acs-2::GFP* reporter strain and performed a targeted RNA interference screen. We targeted transcriptional regulators, many of which are known to be differentially expressed by a glucose diet, to identify those that modulate *acs-2* expression in a glucose diet dependent manner. We screened 130 genes and identified ~20 GRs that significantly impact the expression of *acs-2* transcript in a glucose diet dependent manner. The screen identified the NHR family as the most abundant class of gene regulators impacting *acs-2* gene expression and identified some novel gene regulators. Together, these studies add to our understanding of the physiological, transcriptional that occur due to a glucose supplemented diet.

Hanging By a Thread: Investigating the Effect of Low Tide Temperature on Mussel Attachment Strength.

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Georget Oraha* and Jennifer L. Burnaford, *California State University, Fullerton*

Abstract: *Mytilus californianus*, the California mussel, is a foundation species and dominant space-holder in the rocky intertidal zone, an environment that goes through extreme temperature shifts on a daily basis as organisms are submerged in seawater during high tide and exposed to terrestrial conditions during low tide. Mussels create protein 'anchors' called byssal threads that allow them to attach to rocks and each other. Previous work has examined how wave action negatively affects mussel attachment. Yet to date, few studies have addressed the role of temperature during low tide on attachment strength of mussels, despite the clear importance of this topic in the context of the rising temperatures predicted with a changing climate. We used laboratory manipulations to investigate how temperature during low-tide affects three components of mussel attachment: byssal thread production, individual mussel attachment strength, and single byssal thread strength. We collected mussels from two southern California field sites and set up a fully factorial seven-day experiment with two types of treatments: number of low tide exposures (exposure on the first day followed by six days of submersion or exposure each day for seven days) and temperature during low tide exposure (ambient or elevated temperature). In the elevated temperature treatment, we used small heaters to individually raise body temperatures by XoC. We predicted and have found that mussels exposed to natural ambient treatments generally have greater individual mussel attachment strength and single byssal thread strength than mussels exposed to elevated temperatures.

Surviving Marginalized Reefs: Assessing the Implications of the Microbiome on Survivorship

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Sofia Roitman*[1]; Tomás López-Londoño[1]; F. Joseph Pollock[1]; Kim B. Ritchie[2]; Claudia T. Galindo-Martínez[1]; Kelly Gómez-Campo[1]; Luis A. González-Guerrero[1]; Valeria Pizarro[3]; Mateo López-Victoria[4]; Roberto Iglesias-Prieto[1] and Mónica Medina[1], *(1)The Pennsylvania State University, (2)The University of South Carolina Beaufort, (3)Fundación Ecomares, (4)Pontificia Universidad Javeriana*

Abstract: Coral reefs are undergoing degradation due to overexploitation, pollution, and climate change. Management and restoration efforts require that we gain a better understanding of the complex interactions between corals, their microbiomes, and their environment. For this purpose, Varadero reef in Cartagena, Colombia, serves as an informative study system. Varadero is located in the Bay of Cartagena adjacent to the Canal del Dique, which carries turbid and polluted water into the bay. Varadero's survival under poor environmental conditions makes it a great study site for investigating the relationship between the microbiome and coral resiliency. To determine whether the microbiomes of Varadero corals differ from those in less impacted sites, we conducted a reciprocal transplant experiment by relocating coral fragments from Varadero as well as a geographically proximate reef that is less affected by plume dynamics (Rosario) across a gradient of turbidity (low, medium, and high). After 6 months of acclimatization, transplanted corals developed site-specific microbiomes that differed significantly from pre-transplant microbiomes, and corals transplanted to the highly impacted site from both Varadero and Rosario site saw higher mortality and an increase in overall microbial diversity. In combination with survivorship results, our results indicate that, rather than surviving, Varadero reef is experiencing a slow decline, and its corals are likely on the brink of dysbiosis. With continued anthropogenic interference in marine environments, sites such as Varadero will become increasingly common, and it is imperative that we understand how corals and their microbial symbionts are changing in response to these new environmental conditions.

Evaluating Chemical Changes in a Culturally Significant Intertidal Marine Calcifier throughout the Holocene

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Veronica Padilla Vriesman*[1]; Hannah M. Palmer[1]; Jessica R. Bean[2]; Tessa Hill[1]; Sandra J Carlson[1] and Roxanne Banker[3], *(1)University of California, Davis, (2)University of California Museum of Paleontology at UC Berkeley, (3)California Academy of Sciences*

Abstract: Marine bivalve shells can serve as records of oceanographic change, seasonal cycles, and human impacts over the Holocene. In particular, the California mussel (*Mytilus californianus*) presents the opportunity to examine environmental and biological changes recorded in its shell chemistry. Given that *M. californianus* has been well studied by archaeologists to track human migration patterns, there is an abundance of stable isotope data from radiocarbon-dated southern California midden specimens. Here, we synthesize oxygen and carbon isotope data generated from *M. californianus* specimens from 13 archaeological sites south of Point Conception (~35°N) spanning the mid to late Holocene (7550 BP through 500 BP). We compare both average values and extreme values through time and across locations in order to identify site-specific changes to *M. californianus* shell chemistry. A ~7000-year-long record provides the opportunity to (1) characterize isotopic variability, (2) assess the frequency, magnitude, and rate of both past and recent changes, and (3) identify departures from normal baseline variability. Specifically, we aim to determine whether or not there are rapid or severe changes in shell stable isotope values and whether these values have appeared previously in the ~7000-year-long archive. While *M. californianus* can potentially be used to track changes in upwelling intensity and nearshore sea surface conditions among and within coastal sites, it is critical to deepen our understanding of shell chemistry to discern biological factors from environmental conditions. Through the synthesis of isotope data, we document spatial and temporal changes in *M. californianus* shell chemistry in southern California nearshore environments.

Understanding the Diversity and Function of the Mangrove Forest Root Microbiome

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Natalia Erazo* and Jeff Bowman, *Scripps Institution of Oceanography, UC San Diego*

Abstract: Mangrove forests are a key tropical coastal ecosystem and provide many ecosystem services. These forests serve as a buffer for storm surge, facilitate nutrients exchange with marine ecosystems, provide habitat for marine species, and play a role in mitigating climate change. Despite the ecological role of mangroves, they are disappearing worldwide by 1 to 2% per year, a rate greater than or equal to declines in adjacent coral reefs or tropical rain forests. The long-term survival of this ecosystem is at great risk; thus, it is crucial to develop a better understanding of the health and functioning of mangrove forests. Mangroves support a high diversity of microorganisms present in water, sediments, and mangrove roots.The roots provide a growth surface for microbes responsible for nitrogen fixation, carbon remineralization, and defense mechanisms against pathogens. Here we examined the differences in the microbial community associated with the rhizosphere in non-perturbed and perturbed *Rhizophora mangle* trees exposed to aquaculture effluent. The rhizosphere was characterized by lower diversity dominated by *Deltaproteobacteria*, *Plantomycetes*, and *Bacteroidetes* suggesting for a more specialized community associated to methane, sulfur, and nitrogen transformations. We saw a shift in the community composition in the perturbed sites to a more opportunistic and pathogenic community associated to plant-pathogen pest (*Candidatus* Carosnella ruddii). The results of this study provide a deeper understanding of plant-microbe co-dependence, and of the functions of the root microbiome. This is necessary for further developing rhizoremediation approaches to improve mangroves resilience in the face of changing climate and other anthropogenic stressors.

Fibrin Shifts Macrophages Towards Anti-Inflammatory Response during Catheter-Associated Urinary Tract Infections

Discipline: Life Sciences
Subdiscipline: Microbiology

Armando Marrufo*; Felipe H. Santiago-Tirado and Ana Lidia Flores-Mireles, *University of Notre Dame*

Abstract: Urinary catheterization is a common procedure used in healthcare facilities to safely drain urine from patients with dysfunctional bladders. However, catheterization predispose patients to developing catheter-associated urinary tract infections (CAUTIs). Upon catheterization, fibrinogen is released into the bladder where it is converted into fibrin in order to heal damaged tissue. Deposition of fibrinogen and fibrin on catheters promote colonization of prevalent CAUTI pathogens, such as *Enterococcus faecalis*. Despite recruitment of immune cells, *E. faecalis* is still able to persist and disseminate. Previous *in vitro* studies have shown that macrophages can switch between pro- or anti-inflammatory behavior when interacting with either fibrinogen or fibrin by production of inducible nitric oxide synthase (iNOS) and arginase-1, respectively. Therefore, we hypothesize that fibrin in the bladder is shifting the macrophage response from pro- (M1) to anti-inflammatory activity (M2), which impairs its bactericidal activity during CAUTI. Using the CAUTI mouse model, *in vivo* temporal studies were performed from 1-hour to 14 days post-catheterization in the absence or presence of *E. faecalis*. Our *in vivo* studies, using western blot and immunostaining, demonstrated prevalent iNOS production in acute CAUTI and increased arginase-1 production in prolonged CAUTI. Furthermore, we observed elevated production of arginase-1 in catheterized plasmin-deficient mice bladders where there was a higher accumulation of fibrin. This suggests that fibrin contributed to the shift of M1 to M2 macrophages' anti-inflammatory phenotype where macrophages can no longer

eradicate *E. faecalis*. Understanding this macrophage response will provide crucial information for the development of efficient intervention strategies for treating CAUTIs.

Bacterial Antagonism Can Provide a Fitness Benefit for *Pseudomonas Syringae* in Plant Leaves

Discipline: Life Sciences
Subdiscipline: Microbiology

Hanareia Ehau-Taumaunu* and Kevin Hockett, *The Pennsylvania State University*

Abstract: To antagonize closely related bacterial strains, most bacteria can produce and release bacteriocins, a class of narrow-spectrum toxins. This mechanism of antagonism is viewed as a potential biological control for plant diseases, yet little research has explored the dynamics of bacteriocin production in plants. A series of *in planta* co-infiltrations tested whether bacteriocin production by *Pseudomonas syringae* pv. *syringae* (*Psy*) provide a fitness benefit when competing with *P. syringae* pv. *phaseolicola* (*Pph*) in common bean leaves. Populations of each strain were measured for 8 dpi. In 1:1 co-infiltration, *Psy* reduced *Pph* populations by 100-fold at 4 dpi, whereas a *Psy* bacteriocin-deficient mutant (*Psy* Dbac) reduced *Pph* by 10-fold. Surprisingly, there was no detectable fitness benefit for *Psy*. In 1:9 co-infiltration, *Psy* at a low cell density (*Psy* 1: *Pph* 9) achieved a 2-fold population increase at 6 dpi compared to *Psy* Dbac, indicating a bacteriocin-mediated benefit. *Psy* also reduced *Pph* to a larger extent for all dpi especially when *Pph* is at low cell density. Additionally, to assess host plant effects on bacteriocin interactions, avirulent *Psy* Type III Secretion System (T3SS) mutants were 1:1 co-infiltrated with *Pph*. This resulted in no reduction of *Pph* at all dpi. *Psy* T3SS mutant populations also significantly increased when co-colonized with a virulent strain. These results highlight the plant-microbe dynamics between competing *P. syringae* in which bacteriocin production can be beneficial. As competition often forms the basis for biocontrol strategies, understanding the ecological factors that contribute to strong competition will help develop robust strategies.

Population Structure and Virulence Gene Distribution Among *B. Cereus* group Isolates from Diverse Sources

Discipline: Life Sciences
Subdiscipline: Microbiology

Naomi Niyah*[1]; Jasna Kovac[1]; Cassidy Prince[1]; Taejung Chung[1] and Sophia Johler[2], *(1)The Pennsylvania State University, (2)University of Zurich*

Abstract: The *Bacillus cereus* group is a diverse group of closely related species distributed across 7 phylogenetic clades. *B. cereus* group isolates have been associated with diseases in animals and humans, as well as insecticidal and probiotic properties. Molecular methods such as 16S rRNA sequencing lack the ability to differentiate between species of the *B. cereus* group. In addition, the pathogenic potential of a particular isolate is not species-dependent. Whole-genome sequencing (WGS) can address these challenges and aid in taxonomic classification and virulence potential predictions. The goals of this project were to utilize WGS to characterize the population structure of isolates from diverse sources, and evaluate the distribution of virulence genes across different phylogenetic clades and species.

A total of 165 isolates from various sources underwent WGS using Illumina platform and 101 sequences were retrieved from NCBI. Sequences were checked for quality, trimmed, assembled *de novo* using SPAdes, and analyzed using BTyper. The phylogenetic clade was determined based on the *panC* gene sequence. Afterwards, single nucleotide polymorphisms (SNPs) were identified using kSNP3. A maximum-likelihood tree was generated based on identified core SNPs using RAxML and visualized using FigTree.

Of the 266 isolates, 249 had information on the isolation source, which included food (n=210), clinical (n=7), environment (n=16), biopesticides (n=11), and animals (n=1). These isolates were distributed across the 7 phylogenetic clades (clade I=5, clade II=32, clade III=77, clade IV=67, clade V=44, clade VI=30, and clade VII=10). Overall, *B. cereus* virulence genes are broadly distributed, but not consistent across species and/or clades.

Characterizing the Biochemistry of the Ammonia Oxidation Pathway in Archaea.

Discipline: Life Sciences
Subdiscipline: Microbiology

Andres Rivero Gamez* and José de la Torre, *San Francisco State University*

Abstract: Ammonia Oxidizing Archaea (AOA) produce energy by aerobically oxidizing ammonia (NH_3) into nitrite (NO_2^-). This reaction is a critical, rate limiting step in the global nitrogen cycle, but it can also give rise to nitrous oxide (N_2O), a powerful greenhouse gas. Unlike the pathway in Ammonia Oxidizing Bacteria (AOB), the biochemistry in AOA is poorly understood. Genomic analyses show that homologs of the AOB enzyme catalyzing the oxidation of key intermediate hydroxylamine to nitrite are not found in AOA genomes. Our hypothesis is that AOA possess a different enzyme catalyzing this oxidation. Indeed, we have shown that the thermophilic AOA *Nitrosocaldus yellowstonensis* encodes an enzymatic activity capable of oxidizing hydroxylamine to nitrite. We have developed a semi-continuous culture system to generate sufficient biomass for a biochemical purification. Using ultracentrifugation of whole cell lysates, we have found that the hydroxylamine-oxidizing activity (HAx) is associated with the membrane when cells are lysed at pH 7.5, but appears to be in the cytosol fraction at pH 9.3. Using different chromatographic techniques coupled to HPLC tandem mass spectrometry, we have designed a

biochemical approach to purifying the HAx enzyme. Comparisons of the proteins in our fractions to genes sets conserved in all AOA have revealed several potential candidates for the HAx activity. Results of this research will allow further understanding of AOA's metabolism and improve our knowledge of the nitrogen cycle, ultimately helping with climate change scenario modeling and decision making.

Plasmid Conjugation from Bacterial Cooperators into Cheaters Stabilizes Cooperation

Discipline: Life Sciences
Subdiscipline: Microbiology

Priscila Guzman*; Reilly Jensen and Thomas Platt, *Kansas State University*

Abstract: Bacterial cooperation often involves individuals contributing toward the production of a public good at a cost to themselves. Cheaters, individuals who benefit from public goods but do not pay the costs of cooperation, threaten the stability of cooperative systems due to their innate advantage over cooperators. However, cooperators can act to limit cheating behaviors. The cooperative pathogenesis of *Agrobacterium tumefaciens* is encoded by the tumor inducing virulence plasmid (pTi). Cooperative agrobacteria can genetically transform plant cells; however, this requires the costly expression of pTi-encoded *vir*-genes. Infected plants produce opines, a public good that agrobacteria use as an energy source. Availability of opines provides an opportunity for the spread of cheaters that use opines but cannot infect plants. These cheaters do not pay the costs of infection and can outcompete cooperators. Cheaters have been observed in natural systems and greenhouse experiments show that cheaters are able to outcompete cooperative agrobacteria under some conditions. We are investigating mechanisms promoting the evolutionary stability of agrobacterial cooperation using *in vitro* experiments as well as a theoretical model. Our model supports the hypothesis that Ti plasmid conjugation from cooperators into cheaters can stabilize cooperation in this system by transforming cheaters into cooperators. Further, our model predicts that this mechanism of stabilization is only effective when cooperative populations are dense, and cheaters are rare. Our work aims to evaluate if conjugation enhances the evolutionary stability of agrobacterial cooperation. This mechanism may be important to cooperative bacterial systems in which genes encoding for cooperation are plasmid encoded.

Isolation of Specific Bacteriophages for *Pseudomonas Aeruginosa* from Wastewater from a Treatment Plant in Mayagüez, Puerto Rico.

Discipline: Life Sciences
Subdiscipline: Microbiology

Angélica González Martínez*, *University of Puerto Rico, Mayagüez* and Carlos Ríos Velázquez, *University of Puerto Rico at Mayagüez*

Abstract: *Pseudomonas aeruginosa* is a multidrug resistant pathogenic bacterium considered by the CDC as a serious threat with urgent treatment needs. Carbapenems are last resort broad-spectrum antibiotics used to treat resistant bacteria. However, resistant strains produce carbapenemases to evade antibiotics making them difficult to treat. An alternative treatment that has been revisited experimentally involve the use of phage therapy (PD), which employs the specificity and bactericidal properties of bacteriophages to target specific strains. This research seeks to isolate *P. aeruginosa* bacteriophages. Given that *Pseudomonas* is found in wastewaters and bacteriophages can survive with their host, samples from a wastewater treatment plant in Mayagüez, Puerto Rico were collected and used as sampling sites. To increase the bacteriophages concentration, an enrichment was performed by inoculating wastewaters filtrate with *P. aeruginosa (ATCC 19660) as host*, and after amplification, the presence of the phages was confirmed using bacterial lawn-spotted test and plaque assays. Bacteriophages were successfully isolated, being necessary to dilute the sample to 10^{-7}-10^{-12} to avoid concurrent lysis in the plaque assay. The estimate bacteriophages in the lysate was 2.5×10^{12} pfu.mL. The average diameter of the plaques ranged from 0.8 to 1.0 mm. The isolated bacteriophages uniqueness will be determined by performing specificity tests, morphological analysis using TEM, and their genetic material isolated for molecular analysis, including genome sequencing and in silico analysis. These findings confirm the presence of bacteriophages in the environment tested, allowing their use potentially as bioprospect in phage therapy to antibiotic resistance strains of *P. aeruginosa*.

A *Chlamydia Trachomatis* Effector Interacts with the Host Ubiquitin Ligase TRAF7 to Regulate Infection

Discipline: Life Sciences
Subdiscipline: Microbiology

Clara Herrera*; Cherilyn Elwell; Eleanor McMahon; Khavong Pha; Jessica Sherry and Joanne Engel, *University of California, San Francisco*

Abstract: *Chlamydia trachomatis* is an obligate intracellular pathogen for which no effective vaccine exists. After entering host cells, *Chlamydia* species replicate within a protective membrane-bound compartment, termed the inclusion. *Chlamydia* species employ a specialized protein export system to deliver secreted effectors into either the host cell cytoplasm or the inclusion membrane. The latter group represents inclusion membrane proteins (Incs), which are thought to interact with host proteins to modulate infection. An extensive affinity purification-mass spectrometry (AP-MS) screen conducted by the Engel lab identified potential host binding partners for approximately two-thirds of the *C. trachomatis* Incs. This screen predicts a high confidence interaction between the early-expressed Inc CT224 and human tumor necrosis factor receptor associated factor 7 (TRAF7), a ubiquitin ligase that is part of a family of proteins (TRAFs) that stimulates diverse cellular pathways such as proliferation, apoptosis, and cytokine production. Using co-affinity purification and immunofluorescence microscopy, we demonstrate that CT224 and TRAF7 interact in the context of infection, that TRAF7 recruitment to the inclusion membrane is CT224-dependent, and that CT224 may modulate post-translation modification of TRAF7. We define the protein regions of CT224 and TRAF7 that are necessary and sufficient for their interaction. Finally, we demonstrate that CT224 interferes with native TRAF7 protein-protein interactions. These studies will illuminate the cellular and molecular mechanisms that contribute to *C. trachomatis* pathogenesis.

Nanodisc Based Targeted Antiretroviral Drug Delivery to the Brain for the Treatment of HIV-1

Discipline: Life Sciences
Subdiscipline: Neurosciences

Caroline Garcia*[1]; Upal Roy[1]; Armin Tahmasbi Rad[2]; Farnoosh Saeedinejad[2] and Mu-Ping Nieh[2], *(1)The University of Texas Rio Grande Valley, (2)University of Connecticut*

Abstract: The Human Immunodeficiency Virus (HIV) is a deadly virus that, as of 2018, affects over 37.9 million people worldwide. While HIV-1 treatment has been revolutionized by antiretroviral therapy since its discovery, HIV-1 still remains persistent in organs that do not allow easy penetration of anti-HIV drugs, such as the central nervous system (CNS). Inaccessibility of the blood-brain barrier allows for the persistent CNS HIV-1 infections and inflammation to contribute to the progression of HIV-1 associated neurological disorders. To combat this challenge, researchers have turned towards nanotechnology-based drug carriers, such as the nanodisc. The nanodisc, a lipid bicelle, preserves the drug in its nanoformulation until metabolized by the body thus allowing a drug to be released in a controlled, long-lasting dosage. This proposed study will look into the nanodisc to encapsulate an anti-HIV drug within its structure that will be safe and effectively perform extended drug release for long term inhibition of HIV-1 within infected cells in the brain. Methods such as ROS assay and MTS assay have been conducted using the nanodisc at varying concentrations on microglial and neuroblastoma cells to determine its viability for *in-vivo* studies. Observed results indicate that the nanodisc at low dosages would be effective in targeting HIV-1 while also reducing oxidative stress on the brain and not inducing cytotoxicity in cells. A nanodisc based drug delivery system offers an attractive solution to the low permeability of the CNS to access HIV-1 within the brain to reduce viral load and prevent further neurodegeneration.

Sugar Binge Drinking during Adolescence Alters Oxycodone Hedonic Effects in Adult Rats

Discipline: Life Sciences
Subdiscipline: Neurosciences

Zinar Simsek*[1]; Alejandro Torres[2]; Kathleen Curtis[2] and Dolores Sanroman[1], *(1)Oklahoma State University College for Health Sciences Anatomy and Cell Biology, (2)Oklahoma State University Center for Health Sciences*

Abstract: **Introduction:** Illicit use of opioid analgesics represents a problem among American high-school students. An overlooked potential contributor to the epidemic of prescription opioids such as oxycodone is food choices. Sweet tastes produce a sensation of intense reward that, in certain circumstances, exceeds those associated with drugs of abuse. However, the effect of this diet on the brain reward and motivational systems has rarely been addressed in adolescents. Moreover, it is unknown if ingestion of or preference for sucrose during adolescence may act as a predisposing factor for drug use/abuse by adults. **Aims:** We 1) determined whether adolescent rats engage in a sucrose binge-drinking (SBD) behavior and whether SBD depends upon different sucrose concentrations, 2) investigated the effects of SBD and preference during adolescence on oxycodone's rewarding properties in adults using a Conditioned Place Preference (CPP) method. **Methods:** 1) An SBD model was used to determine sucrose taste preferences and intake in adolescent rats. 2) Subsequently, rats were trained in oxycodone CPP to evaluate changes in oxycodone seeking behavior. **Results:** Adolescent rats showed significantly higher levels of SBD at 5% over 15% sucrose concentration, and, 82% of the rats developed oxycodone-induced CPP as adults. Interestingly, the SBD group also showed significantly more rats that were 'high' seekers compared to the control group. Moreover, SBD group developed greater sensitization to the locomotor-activating effects of oxycodone than controls. Thus, differences in oxycodone CPP and greater locomotor sensitization due to previous SBD may indicate excess sucrose intake is a contributing factor in oxycodone abuse.

The Cerebellum and Oxycodone Reward, Is BDNF the Answer?

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alejandro Torres* and Dolores Vazquez Sanromán, *Oklahoma State University Center for Health Sciences*

Abstract: **Introduction:** In 2018, over 33,000 Americans died of a drug overdose involving opioids. Abuse and addiction to prescription opioids such as oxycodone, a Mu opioid receptor (MOP-r) agonist, is pressing a public health issue, as being one of the most commonly abused opioids in the United States. Some data have supported the involvement of the cerebellum in the functional alterations observed after prolonged drug use, but this brain structure has been traditionally overlooked from studies of the circuitry affected by addictive drugs. Although MOP-r is expressed in cerebellar granular layer, Purkinje cells, and within the deep cerebellar nuclei, little information exist on oxycodone effects in the cerebellum. One of the main systems believed to be involved in triggering opioid reward is brain-derived neurotrophic factor (BDNF). However, oxycodone effects on BDNF and its precursor protein, proBDNF, in the cerebellum is unknown. The conditioned

place preference (CPP) paradigm is a standard preclinical behavioral model used to study the rewarding and aversive effects of drugs. **Aim** Here, we determine the effects of oxycodone rewarding properties on the cerebellum BDNF levels. **Methods:** Rats were trained using an oxycodone CPP protocol to evaluate changes in oxycodone seeking behavior as an index of the rewarding properties of oxycodone. After the preference test, the cerebellar vermis was dissected and prepared for immunoassay analysis (ELISA) for identifying Pro-BDNF and Mature BDNF levels. **Results:** Rats exhibit oxycodone conditioned preference and sensitization to the locomotor-activating effects of oxycodone. BDNF and proBDNF levels results are underway.

Molecular Characterization of a Hemichordate Nervous System (*Saccoglossus kowalevskii*)

Discipline: Life Sciences
Subdiscipline: Neurosciences

Jose Miguel Andrade Lopez* and Christopher Lowe, *Stanford University*

Abstract: Hemichordates are a key deuterostome phylum for understanding the evolution of the vertebrate central Nervous System (NS). Their NS is organized around a pervasive nerve plexus concentrated anteriorly and two nerve cords, one dorsal and one ventral. Despite the major organizational differences between the NS of hemichordates and vertebrates, they share a well-conserved gene regulatory network for anterior-posterior patterning. It is still unclear whether this conserved pattern regulates similarities in neural cell type specification. Here, we present expression data of neural markers by *in situ* hybridization and immunohistochemistry, including the pan-neural markers *elav* and synaptotagmin and genes involved in the synthesis and transport of neuro-transmitters/peptides, to determine the level of regionalization of the neural plexus and nerve cords in 3 gill slit *S. kowalevskii* juveniles. We show that *S. kowalevskii* has: one, a regionalized NS with bouton-like structures within the plexus; two, a condensed multi-layered plexus at the proboscis base populated with diverse neural cell types; three, the serotonergic, GABAergic, and FMRFamidergic NS show differences in both cell body location and projection directionality. I will also present preliminary data where we generated transgenic animals expressing GFP in a subset of neurons using pan-neural constructs (*synapsin*, *elav*), cell-type-specific markers for GABAergic (GAT) and dopaminergic (TH) neurons, and an endogenous synaptic vesicle fusion protein, synaptotagmin-GFP, to label synapses. These data facilitate more direct neural comparisons with vertebrates and impacts our understanding of the comparative relevance of the hemichordate NS to broader questions of NS evolution including the origins of the vertebrate brain.

Neuroprotective Effects of Estrogen in a 6-OHDA Mouse Model of Parkinson’s Disease

Discipline: Life Sciences
Subdiscipline: Neurosciences

Sara Zarate* and Rahul Srinivasan, *Texas A&M Health Science Center College of Medicine*

Abstract: Parkinson's disease (PD) is caused by the loss of midbrain dopaminergic (DA) neurons and is predicted to affect over 12 million people worldwide by 2040. Currently treatments for PD do not alter disease progression. Therefore, there is an urgent need to develop neuroprotective drugs for PD. Hyperactive endoplasmic reticulum (ER) stress is an apoptotic process observed in the DA neurons PD patients. Hyperactive ER stress is characterized by the translocation of three key proteins, ATF6, XBP1, and CHOP into the nucleus of DA neurons. We tested if cytisine, a partial nicotinic acetylcholine receptor agonist, attenuates hyperactive ER stress in mice injected with 6-hydroxydopamine (6-OHDA), a neurotoxin known to cause PD in rodents. Our data show that alternate day injections of 0.2 mg/kg cytisine improves PD related motor deficits only in female mice. To test if cytisine attenuates PD related motor deficits by reducing hyperactive ER stress in DA neurons, we exposed primary DA neurons to 6-OHDA which resulted in the nuclear translocation and hyperactivation of all three key ER stress proteins, ATF6, XBP1, and CHOP. We found that 200 nM cytisine inhibited the activation of two key ER stress proteins, ATF6 and XBP1. We also found that 200 nM cytisine in conjunction with 10 nM 17-β-estradiol, type of estrogen, inhibited the activation of CHOP, which is the third key ER stress protein. Thus, we conclude that cytisine along with estrogen prevents hyperactive ER stress in DA neurons providing a potential target for drug development.

Maternal Microbiome Modulates Fetal Neurodevelopment

Discipline: Life Sciences
Subdiscipline: Neurosciences

Austin Qiu*, *California Northstate University* and Elaine Hsiao, *University of California, Los Angeles*

Abstract: The gut microbiome is emerging as an important modulator of central nervous system development and function. Recent findings demonstrate that absence of an early life microbiome can affect brain neurochemistry and behavior. However, despite several studies correlating changes in the microbiome to behavioral phenotypes, there is a lack of clear mechanistic studies demonstrating that alterations in the microbiome lead to changes in brain development, function, and behavior. In this study, we focus on the maternal microbiome and its role in fetal neurodevelopment. Fetal brains were acquired from dams that were specific pathogen free (SPF), germ-free (GF), and antibiotic-treated (ABX). In GF and ABX groups, the absence of the maternal microbiome resulted in changes in fetal brain gene expression and disruption of axon development. In addition, postnatal day 8 brains isolated from ABX and GF mice showed differences in cytochrome oxidase staining in secondary somatosensory cortex compared to SPF mice. These anatomical changes correlated with changes in

paw tactile sensation. Gnotobiotic colonization of the maternal microbiome with a consortium of spore-forming bacteria was able to prevent disruption in thalamocortical axons and behavioral abnormalities. These results suggest the maternal microbiome can modulate fetal brain development and offspring behavior by altering fetal brain gene expression and axon growth.

Retrieval-Extinction Using Novel Information

Discipline: Life Sciences
Subdiscipline: Neurosciences

Angela Gonzalez*, *Washington State University, Vancouver* and Barb Sorg, *Legacy Research Institute*

Abstract: Established memories can be modified during the reconsolidation time window by incorporating new and relevant information into an existing memory. Current studies have targeted maladaptive memories using reconsolidation-based mechanisms like retrieval-extinction, a paradigm that incorporates extinction learning during the reconsolidation vulnerability window. We attempted to update a cocaine-associated memory by presenting novel information during a retrieval session followed by extinction. Male rats were trained for 2 hr sessions for 14 days on a fixed-ratio 1 (FR1) schedule and then given a 30 min memory retrieval during which cocaine was received on an FR1 or variable ratio 5 (VR5) schedule- the latter was given to induce a prediction error. One hour later, rats underwent a 190 min extinction session during which lever pressing had no consequences and the next day were tested for cue reinstatement. Three additional control groups received either no retrieval (No Retrieval) or an FR1 or VR5 retrieval but no extinction (No Extinction groups). We hypothesized that a VR5 *vs*. FR1 retrieval would be required to incorporate extinction learning and subsequently diminish cue reinstatement. Contrary to our hypothesis, VR5 retrieval did not reduce lever pressing during cue reinstatement compared with FR1 retrieval and No Retrieval groups and responding was similar to both No Extinction groups. These findings suggest that memory retrieval using a predictable (FR1) but not an unpredictable (VR5) contingency allows for integration of extinction learning into the original memory and that the VR5 retrieval may have protected the original “FR1 memory” from extinction.

Implementation of Prechtl’s General Movement Assessment and Capute Scales in Children with Congenital Heart Disease.

Discipline: Life Sciences
Subdiscipline: Neurosciences

Alexa Escapita*[1]; Namarta Kapil[1]; Heather Raiees-Dana[2]; Diana Escalona-Vargas[2] and Tara Johnson[2], *(1)University of Arkansas for Medical Sciences, (2)Arkansas Children's Hospital*

Abstract: Congenital heart disease (CHD) is the most common birth defect affecting 1% of children in the United States. Seventy-five percent of children with CHD have Neurodevelopmental Disabilities (NDD), which are usually diagnosed between 4 to 5 years of age. Early diagnosis is crucial in providing early access to therapies and treatments. One method to diagnose a child with NDD at an early age is Prechtl’s General Movement Assessment (GMA). GMA is a qualitative video assessment that is highly predictive of future motor and cognitive dysfunction. Capute Scales are used to identify infants and toddlers with cognitive and language delays. We hypothesize that GMA and Capute Scales will identify NDD at an earlier age in infants with CHD. The patient cohort consisted of 10 infants with Hypoplastic Left Heart Syndrome who were first evaluated between ages 1-24 months. A pediatric neurologist (TJ) conducted Neurodevelopmental assessments in the Cardiovascular Intensive Care Unit and the Cardiac-Neurodevelopmental Program clinic at Arkansas Children’s Hospital. Four of the children were evaluated using GMA and their results indicated a normal GMA. All 10 children were assessed using Capute Scales, which showed typical language and cognition developmental quotients. The developmental quotients for language and cognition were of 105±15 and 99±10, respectively. Future studies will track the neurodevelopmental outcomes of each participant as they mature. The combination of GMA and Capute Scales in the evaluation of infants with CHD will provide early identification and intervention for these high-risk children, allowing access to proven treatments and therapies.

Vitamin D Supplementation Positively Affects Activity and Memory but Impairs Stimulus Response Behavior in an Age and Sex Specific Manner in C57BL/6 Mice

Discipline: Life Sciences
Subdiscipline: Neurosciences

David Narvaiz* and Joaquin Lugo, *Baylor University*

Abstract: Vitamin D deficiency (VDD) is a prevalent condition that has been associated with cognitive decline and negative effects on neurological development. In the present study, we examined the effects of a high dose vitamin D (HDVD) diet administered during the peripubertal period in C57BL/6 mice. Dietary treatment began at either postnatal day (PD) 28 or PD 56 to investigate the effects of vitamin D on cognitive development, and the diet was continued throughout behavioral testing into adulthood. After four weeks on the diet, C57BL/6 vitamin D treated and control groups underwent a battery of behavioral tests. We found that a HDVD diet affected behavior in both an age- and sex-specific manner. When vitamin D was administered to juveniles (PD 28), behavior was altered in both sexes, with treated females having impaired prepulse

inhibition compared to female controls, and both sexes displaying impaired habituation to a loud tone and increased cued fear memory. For adults (PD 56), HDVD affected only male behavior, who expressed an increase in exploratory and locomotive behavior compared to female mice. Overall, our results suggest that in C57BL/6 mice, behavioral sex differences do not appear to occur when a supplemented diet is first administered during adolescence and continued into adulthood.

Modeling Effector-Host Interactions in the Context of the Barley Protein Interactome

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Valeria Velasquez Zapata*[1]; Sagnik Banerjee[1]; Mitch Elmore[1] and Roger Wise[2], *(1)Iowa State University, (2)ARS-USDA/Iowa State University*

Abstract: Pathogen effectors are excellent tools to explore dynamic regulation of plant resistance and susceptibility. To discover novel mechanisms of effector action, we exploited the biotrophic powdery mildew fungus, *Blumeria graminis* f. sp. *hordei* (*Bgh*), and its host, barley (*Hordeum vulgare*). We used next-generation sequencing to identify interacting partners from high-throughput yeast two-hybrid assays, using *Bgh* effectors as baits, and as preys, a time-course cDNA library from infected barley and isogenic immune mutants. Interacting partners were scored using a robust informatics and statistics pipeline, including mapping reads to barley and *Bgh* genomes, reconstruction of prey fragments and fusions with GAL4-AD, and processing of count data. We used this information to develop a ranking system for the preys, comprising: **1)** significant enrichment under selection for positive interactions, **2)** in-frame with GAL4-AD, and **3)** degree of enrichment in pairwise comparisons of baits under selection. Outputs from this pipeline facilitated sorting and validation by binary Y2H. We integrated the top ranked effector targets with a predicted barley protein-interactome to identify barley-*Bgh* interaction hubs. Additionally, we filtered the interactions based on co-expression to detect tightly regulated genes during the immune response. The identified immune modules exhibited an enrichment for genes with molecular functions associated with transcription, phosphorylation and intracellular transport

Impact of Renal Lymphatic Density on the Inflammatory Response to Acute Kidney Injury

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Heidi Creed*; Gaurav Baranwal and Joseph Rutkowski, *Texas A&M University College of Medicine*

Acute Kidney injury (AKI) reduces kidney function and increases the risk of Chronic Kidney Disease (CKD). The mechanisms of AKI-to-CKD transition remain unclear, preventing accurate identification of patients at risk of developing CKD. Lymphatic vessels and inflammation-associated lymphangiogenesis (LAG) have been observed restoring tissue homeostasis following injury. Understanding the initial inflammatory LAG response of AKI may improve mechanistic understanding of progression to CKD. We investigated whether increasing LAG in the kidney reduces the inflammatory response in AKI, acting as a protective mechanism against transition to CKD. Transgenic mice with inducible overexpression of the LAG factor Vascular Endothelial Growth Factor-D (VEGF-D), 'KidVD' mice, were crossed with a model of isolated glomerular injury through targeted podocyte apoptosis, the 'POD-ATTAC' mouse. LAG was induced in KidVD mice prior to podocyte ablation and mice were assessed at seven- and 28-days post-injury. Renal injury response was determined by measuring glomerular filtration rate (GFR), proteinuria resolution, renal fibrosis, and inflammatory gene expression. KidVD mice demonstrate preserved renal function by GFR and urinary protein measurement following initial podocyte loss at day 7 and during the AKI-to-CKD transition period at 28 days post-injury. No significant differences were identified for measured inflammatory genes and while not significant there was an observed trend of reduced fibrosis quantified fibrotic markers and Picrosirus red staining. Data indicates increased LAG prior to renal injury improves renal function and elucidates a potential mechanism through which renal lymphatics may regulate the AKI-to-CKD transition.

Optimization of *In Planta* transformation Methods in Rice (*Oryza sativa*) Using Nanoparticles

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Tia Dunbar* and Michael Thomson, *Texas A&M University*

Abstract: CRISPR/Cas gene editing technologies offer the potential to precisely modify crops, however their efficient *in planta* delivery remains a challenge. Existing tissue culture methods are time- and labor-intensive, hence, bypassing them could facilitate gene editing and expand its broader usage. Our research investigates diverse transformation approaches that could directly alter germline cells to eliminate the challenge of plant regeneration. Recent studies have demonstrated that carbon nanotubes (CNTs) loaded with plasmid DNA are able to penetrate plant cell walls, facilitating transient expression of foreign genetic elements. Therefore, we predict that CNTs delivering Cas9 and single-guide RNA plasmids into mature embryos will create heritable genetic edits. To test this hypothesis, the phytoene desaturase (*PDS*) gene in rice was targeted for knockout. It is well-documented that biallelic *PDS* knockouts result in an albino phenotype due to inhibition of pigment biosynthesis. Rice seeds and excised embryos were imbibed in 1:3 (CRISPR/Cas DNA to CNT ratio) solutions varying in concentrations from 1.5 ng/uL to 5.0 ng/uL of plasmid DNA and were grown to determine if *PDS* had been knocked out. Successful DNA-CNT delivery and gene editing can be observed visually and by sequencing potential *PDS* knockout seedlings. Preliminary data indicate that CNTs transporting gene editing machinery are capable of passive diffusion through the seed coat. Efforts are now aimed at increasing transformation rates to more efficiently achieve heritable genetic modifications. If successful, our optimized gene editing protocol will enable accelerated improvement of rice to meet the challenges of future global production.

Climate Change and Recovery for Endangered Plants

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Amy Wrobleski*[1]; Rebecca Bliege Bird[1]; Douglas Bird[1]; Jennie Miller[2] and Aimee Delach[2], *(1)The Pennsylvania State University, (2)Defenders of Wildlife*

Abstract: In the United States, the policy and recovery strategies surrounding endangered species largely center around the Endangered Species Act (1973). The Endangered Species Act requires that each species has recovery plan, which addresses the key concerns for the species and how the species can be protected in the future. For some species, it is likely that climate change is a component of the population’s decline. This analysis has already been undertaken to examine animals on the endangered species list. However, we do not know if climate change is being considered in creating these action plans for endangered plants in the United States.

To address this gap in knowledge, I will evaluate each endangered plant species in the United States using publicly available sources on the species. Each plant species will be evaluated on its sensitivity to climate change, using criteria such as: temperature threshold, disturbance regime dependence, geographic range, invasive species threats, chemical sensitivity, life history triggers (such as temperature for flowering events), and dependence on other species. Then, we will examine the recovery plans for the same plant species to see if they mention these climate change factors in managing the recovery of the species. Using this method, we will be able to determine if species that appear to be highly sensitive to climate change have these factors addressed in their recovery plans. Better understanding this potential gap will allow the creation of management plans that incorporate climate change sensitivity and better protect the flora of the United States.

Impact of Rhizobia on Growth and Productivity of the Newly Introduced Tropical Legume, *Crotalaria Juncea* in Massachusetts

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Jedaidah Chilufya*; Avery Dunn and Dong Wang, *University of Massachusetts Amherst*

Abstract: The importance of legumes in providing sustainable ways to increase crop productivity through symbiotic nitrogen-fixation with rhizobia bacteria has allowed them to be grown and established outside their native regions. One example is sunn hemp (*Crotalaria juncea* L.), a tropical legume native to India. Today, sunn hemp is extensively cultivated in the Southern United States as green manure, cover crop, and forage plant. When it was introduced to our cooler region in Massachusetts, we wanted to help our local farmers attain high productivity with this new crop. As such, we tested which rhizobia would establish successful symbioses with sunn hemp in Massachusetts farmland by assessing their nodulation and determining the impact of the rhizobia on crop growth and productivity. Our results show that rhizobia native in Massachusetts induced nodules on sunn hemp but these nodules did not fix nitrogen or provide growth benefits to the crop. Instead, sunn hemp formed successful symbioses with rhizobia in commercial inocula intended for other legumes including soybean, peas, vetch, lentil, dry bean, and peanut. Successful symbiosis with these rhizobia resulted in the formation of pink nitrogen-fixing nodules and plant-growth benefits; comparatively higher chlorophyll content, shoot height and shoot biomass. Further, when compared to the Massachusetts-native rhizobia, the successful rhizobial-partners in commercial inocula persisted in the Massachusetts farmland as effective nitrogen-fixers providing growth benefits to sunn hemp for up to three years. Together these results help provide guidelines to our local farmers on how to sustainably achieve high productivity for this newly introduced crop.

A Genomic Pipeline for Developing Genome Edited Rice for Shortened Days to Flowering

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Karina Morales*[1]; Christopher Polo[1]; Benjamin Rogers[1]; Haley Sloan[1]; Blake Pope[1]; Emily Chao[1]; Rodante Tabien[2] and Michael Thomson[1], *(1)Texas A&M University, (2)Texas A&M University AgriLife Research*

Abstract: Rice is an essential food crop providing the daily caloric intake of over 50% of the world's population. Flowering is one of the most sensitive stages of rice growth and is highly variable among varieties and across environments. In Texas, early maturing varieties are desired as they can avoid flowering in the hottest part of the summer and allow the ratoon crop to mature before cold temperatures set in. In order to develop shorter flowering rice varieties, a diversity panel was genotyped using both the 7K Cornell IR-LD Rice Array and AgSeq, a skim sequencing method. A genome wide association study (GWAS) was performed using phenotypic data from the diversity panel grown in Beaumont, TX in 2017 and 2018. Candidate genes identified from our GWAS will be validated using CRISPR/Cas9 genome editing in an elite variety from Texas in a multiplexed fashion to identify how they act individually and in combination with each other. Finally, a custom

multiplex amplicon sequencing panel is being developed for characterizing diversity of flowering time candidate genes and validation of target genes in the genome edited progeny.

Evaluating the Effect of Chalcogen Composition on Proton Stabilization in Chevrel-Phase Chalcogenides

Discipline: Materials Research
Subdiscipline: Materials Research

Jessica C Ortiz-Rodríguez*[1]; Nicholas R. Singstock[2]; Joseph T. Perryman[1]; Charles B. Musgrave[2] and Jesús M. Velázquez[3], *(1)University of California Davis, (2)University of Colorado at Boulder, (3)University of California, Davis*

Abstract: The successful use of electrolysis processes at an industrial scale such as aluminum electrorefining, brine electrolysis and water splitting has increased the interest of using electrochemistry to promote other promising reactions such as hydrogen evolution, CO_2 reduction and ammonia synthesis. To design electrocatalyst that are able to selectively produce fuel from aqueous media, the tuning of local surface coordination and electronic structure becomes an imperative. In this work, we evaluate the effect of increasing chalcogen electronegativity in binary Chevrel Phase chalcogenides (Mo_6X_8; X= S, Se, Te) on their ability to stabilize proton adsorption under relevant conditions for hydrogen production. Binary chalcogenides were synthesized successfully via microwave-assisted synthesis. Density functional theory predictions indicate favorable electronic structure for proton reduction upon increasing chalcogen electron affinity. This was confirmed experimentally via X-ray absorption spectroscopy as well as electrochemical analysis. We have identified that increasing the electronegativity of the X in Mo_6X_8 increases the hydrogen adsorption strength owing to a favorable shift in p-band position as well as an increase in the Lewis basicity of the chalcogen, thereby improving hydrogen evolution reaction energetics. Bulk Mo_6S_8 exhibits the highest hydrogen evolution activity of the catalysts evaluated, requiring an overpotential of 321 mV to achieve a current density of 10 mA cm^{-2} ECSA and a Tafel slope of 74 mV per decade. Agreement between theory and experiment in this work indicates that the compositionally tunable Chevrel-Phase chalcogenide family is a promising framework for which electronic structure can be predictably modified to improve catalytic small-molecule reduction reactivity.

P-Adic Tropicalizations of Toric Varieties

Discipline: Mathematics
Subdiscipline: Algebra/Number Theory/Combinatorics

Jose Ortiz* and Gabe Kerr, *Kansas State University*

Abstract: Tropical geometry is a newly developing branch in the field of algebraic geometry, which is concerned with translating questions about geometry and algebra into combinatorial questions, namely, counting intersections of spaces or other structures. Tropical geometry can be viewed as a convex, piecewise linear approximation of algebraic geometry, where one takes a system of algebraic structures—namely, geometric spaces constructed from solution sets to equations which are called varieties—and tropicalizes them to obtain a discrete version of the former system. Surprisingly, tropicalized varieties retain much more geometric information than one would initially guess, and this allows us to pass information between settings. The benefit of this approach to studying these types of spaces is that we are effectively trading a difficult algebra problem for an easier combinatorial problem about polyhedral complexes. Furthermore, the tropicalization of a variety can be viewed as a sort of approximation to a type of analytic space similar to the field of p-adic numbers—called a Berkovich space—which is used extensively in complex and arithmetic dynamics. Classically, toric varieties have been studied for their deep connections to polyhedral geometry and combinatorics; this combined with the connections between p-adic analysis and Berkovich spaces, motivated this avenue of research since tropicalization methods serve as an intermediary between these fields. Our goal is that this approach will lead to further insights into the interplay between toric varieties and p-adic analysis.

Discourse Analysis of Pairwise Twitter Hashtags

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Maia Powell* and Arnold Kim, *University of California, Merced*

Abstract: Viral hashtags frequently emerge on Twitter to discuss political topics and bring attention to acts of injustice. Response hashtags are often created subsequently to express divergent stances (e.g. #AllLivesMatter in response to #BlackLivesMatter). Understanding the nature of online disagreement can provide insight into how individuals debate and navigate sensitive topics. We evaluate the potential for classification between hashtag pairs by characterizing discourse surrounding opposing hashtags using Linguistic Inquiry and Word Count (LIWC), Bidirectional Encoder Representations (BERT) word embeddings, and measures of entropy and divergence. Analyses found uniformity in topic, diction, and syntax, but observed distinctions in sentiment and psychological processes.

Image Classification in Synthetic Aperture Radar Using Reconstruction from Learned Inverse Scattering

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Jacqueline Alvarez*; Omar DeGuchy and Roummel Marcia, *University of California, Merced*

Abstract: Synthetic aperture radar (SAR) is a remote sensing technique used to obtain high-resolution images, where image classification is a primary application. However, reconstructing SAR data is difficult which makes the classification of these images even more challenging. We present a study that investigates techniques for classifying SAR images using machine learning. In particular, we compare the classification accuracy using three different training data: raw SAR observation data, reconstructions using Kirchoff migration, and reconstructions by learning an approximation to the inverse of the SAR sensing operator. We consider two different architectures, namely a multi-layer perceptron and a convolutional neural network. The training set is composed of 50,000 images from the CIFAR-10 dataset. We find that the images reconstructed using the learned approximate inverse have a higher classification accuracy than that from the SAR measurement and the Kirchoff migration approach. Furthermore, combined with a more sophisticated machine learning architecture, such as convolutional neural networks, the proposed methods can improve classification accuracy over standard multi-layer perceptron architectures.

Super Resolution Using Variational Autoencoders

Discipline: Mathematics
Subdiscipline: Applied Mathematics

A. Ali Heydari*, *University of California, Merced* and Asif Mehmood, *United States Air Force Research Laboratory*

Abstract: The emergence of Generative Adversarial Network (GAN)-based single-image super-resolution (SISR) has allowed for finer textures in the super-resolved images, thus making them seem realistic to humans. However, GAN-based models may depend on extensive high-quality data and are known to be very costly and unstable to train. On the other hand, Variational Autoencoders (VAE) have inherent mathematical properties, and they are relatively cheap and stable to train; but VAEs produce blurry images that prevent them from being used for super-resolution. In this paper, we propose a first of its kind SISR method that takes advantage of a self-evaluating VAE (IntroVAE). IntroVAEs judge the quality of generated high-resolution (HR) images with the target images in an adversarial manner, which allows for high perceptual image generation. First, the encoder and the decoder of our introVAE-based method learn the manifold of HR images. In parallel, another encoder and decoder are simultaneously learning the reconstruction of the low-resolution (LR) images. Next, reconstructed LR images are fed to the encoder of the HR network to learn a mapping from LR images to corresponding HR versions. Using the encoder as a discriminator allows SRVAE to be a fast single-stream framework that performs super-resolution through generating photo-realistic images. Moreover, SRVAE has the same “nice” latent manifold structure of VAEs and stable training while playing a max-min adversarial game between the generator and the encoder like GANs. Our experiments show that our super-resolved images are comparable to the state-of-the-art GAN-based super-resolution.

Aerosols and Sky Brightness: A Lidar-Based Investigation

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Sabrina DeSoto* and Robert Stencel, *University of Denver*

Abstract: We hypothesized and began testing a correlation between nighttime urban sky brightness and air pollution, given that higher particulate loads in the atmosphere can scatter more photons from light sources. Wavelength dependent Lidar scans of the low atmosphere compared with Sky Quality Meter readings showed overlapping areas of higher aerosol readings and brighter nighttime sky measurements. These initial findings based off one experimental run (cut short by the COVID-19 outbreak) exhibit promising results for a new technique in mapping localized sky glow using well-monitored aerosols as a proxy, and potentially using nighttime skyglow as a proxy for air quality.

All Atom 200-Ns Simulations of Loop Transitions in a Lipocalin

Discipline: Physics & Astronomy
Subdiscipline: Physics

Kiara Fenner* and Lorenzo Brancaleon, *University of Texas at San Antonio*

Abstract: Loop mobility in proteins has been associated with many fundamental properties such as catalysis, gating, ligands access, etc.. Conformational changes of loops can be triggered by many events. In several lipocalin a loop at the entrance of the internal pocket appears to be triggered by an unusual protonation/deprotonation of an acidic residue. In bovine b-lactoglobulin (BLG) this residue is a Glu at position 89 position at the beginning of a loop (EF loop).

A survey of available BLG structures reveals that the side chain of Glu 89 is parallel to the opening of the internal pocket but in some structures the protonatable amino group is under the loop while in others is on the outside of the loop. We have tested this event using 200 ns all atoms molecular dynamic simulations. We have demonstrated that only in structures where the Glu side chain is directly under the EF loop, the deprotonation of the residue prompts a conformational transition of the loop. These changes were not previously detected by MD simulations.`

Assessing Trauma in Latinx Adolescents Using Socioculturally Adapted Measures

Discipline: Psychology & Social Sciences
Subdiscipline: Clinical Psychology

Benjamin Juarez*; Jailene Mazariegos and Tomas Martinez, *Pepperdine University*

Abstract: Culture, family dynamics, and acculturation contribute to how a person from the Latinx community is able to internalize and externalize a traumatic experience. Current trauma measures do not take into account these sociocultural parameters which may result in the inaccurate assessment of trauma in Latinx individuals. This study adapts the Child Revised Impact of Event Scale (CRIES) measure by adding sociocultural parameters, such as, country of origin, familial generation, cultural upbringing, to assess trauma in Latinx children and adolescents. The study utilizes the Complex Trauma Inventory (CTI), to validate the CRIES measure. The measures are applied to the traumas the sample population (n~30) experienced, through individual interviews with students currently going through psychotherapy, in middle and high schools, ages ranging 11 to 18 years of age, provided by non-profit Luminarias Institute. Data were drawn from a sample of youth considered at risk for Post-Traumatic Stress Disorder (PTSD) based on the experienced risk factors reported by their psychotherapist in the students' charts. The study utilizes multiple regression and multivariate analysis to process data provided from previously administered anxiety, depression, and adverse childhood experiences (ACE) measures to assess PTSD susceptibility in the Latinx child and adolescent population. Personal, interpersonal and community traumas will be investigated. We hypothesize that the CRIES measure will show that Latinx adolescents with anxiety and elevated ACE scores will be more susceptible to PTSD. Expected findings show above-average anxiety scores in relation to the average adolescent with family violence being a strong predictor of interpersonal trauma.

Early-Life Low-Level Chronic Lead Exposure Increases Anxiety-like Behaviors and Alcohol Consumption Using a Two-Bottle Choice Preference Test in Male and Female C57BL/6 Mice

Discipline: Psychology & Social Sciences
Subdiscipline: Other Psychology & Social Sciences

Maribel Hernández*; Gabriel Filippelli and Stephen Boehm, *Indiana University - Purdue University Indianapolis*

Abstract: Despite extensive progress made to eradicate toxic levels of Pb in the environment, children, predominately in lower socioeconomic areas, are still exposed to varying levels. Human studies suggest that childhood Pb exposure results in altered drug consumption in adults; however, there is limited research at translational Pb levels (<10 µg/dL). To model how early-life low-level Pb exposure effects alcohol consumption in adulthood, we used C57BL/6J mice. Litters were weaned at PND 21 and assigned to either a three-week exposure period of 30ppm Lead (IV) Acetate or a control condition (0ppm) in DI drinking water. After the Pb exposure period, mice were switched to regular tap water until they reached adulthood. Then, alcohol consumption was tested using a three-week Drinking-in-the-Dark (DID) (20% v/v) or 24-hr two-bottle choice preference test (10% v/v) in two separate groups. Prior to or following the alcohol access phase, anxiety-like behaviors were assessed via elevated plus maze. We predicted that mice with early-life Pb exposure would consume higher levels of alcohol and exhibit higher preference for alcohol than the control group in both paradigms. There was no difference in binge-like consumption between exposure groups; however, mice with a prior Pb exposure history displayed significantly higher alcohol intake and preference scores than control mice. Further, we predicted that Pb-exposed mice would exhibit greater anxiety-like behaviors, which was confirmed in experiments conducted prior to an alcohol history. Future studies will assess the expression of several key proteins to further probe how early Pb exposure alters a developing brain.

The Influence of Relationship Values on Women's Perpetration of Violence in Friends with Benefits Relationships

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Angela Hart* and Rebecca Weston, *University of Texas at San Antonio*

Abstract: This study seeks to investigate the way in which relationship values influence women's perpetration of physical and psychological violence in friends with benefits relationships (FWBRs). To do so, we will examine online survey data collected from (N = 914) female students attending a southwestern university. The data will be analyzed using structural equational modeling, with three latent variables. Relationship value will be comprised of four indicators: investment, commitment, alternatives, and satisfaction. Perpetration of physical violence will be comprised of three indicators: physical abuse, sexual abuse, and threatening behavior. Perpetration of psychological violence will be comprised of two indicators: relational aggression and emotional and/or verbal abuse. Preliminary results suggest a negative association between relationship values and perpetration of physical violence ($\beta = -0.13$, $p < .05$), such that, as relationship values decreased, women's perpetration of physical violence against their friends with benefits partner(s) increased. We expect to also find a negative association between relationship values and psychological violence. This study is the first in the literature to examine these associations in FWBRs.

Individual Acoustic Differences in Female Black-Capped Chickadee (*Poecile atricapillus*) *Fee-Bee* Songs

Discipline: Psychology & Social Sciences

Subdiscipline: Psychology (general)

Carolina Montenergro* and Christopher Sturdy, *University of Alberta*

Abstract: Birdsong has traditionally been considered a vocalization produced by males. However, recent research suggests that both sexes produce song. While the function and structure of male black-capped chickadee (*Poecile atricapillus*) *fee-bee* song has been well-studied, research on female song is limited. Past operant go/no-go discrimination experiments show that male chickadees can discriminate between individual males via *fee-bee* song. Recently we have shown that both sexes can identify individual females via their *fee-bee* song, and can do so even when presented with only the *bee* position of the song. Therefore, we predicted that a difference between female black-capped chickadee song would most likely be found in the *bee* note portion of their *fee-bee* songs. Here we used a discriminant function analysis (DFA) and an Artificial Neural Network (ANN) to investigate the acoustic features of female song that are individually distinctive. DFAs correctly classified songs (90%) to the individual based on several acoustic features including, but not limited to, *bee*-note length and *fee*-note frequency. ANNs were trained to identify individuals based on the features identified by DFAs and achieved 96% accuracy. Our results provide a quantitative understanding of the acoustic structure of female song but the perception and function of female song in chickadees requires further study.

Work Patterns and College Financing: A Descriptive Regional Report Regarding Students at Hispanic-Serving Institutions in New Mexico and Texas

Discipline: Psychology & Social Sciences
Subdiscipline: Psychology (general)

Jorje Ramos*, *West Texas A & M University* and Michael Preuss, *WTAMU*

Abstract: As part of an NSF-funded project, college students (n=463) at 14 Hispanic-Serving Institutions (HSIs) in New Mexico and Texas were surveyed about their experiences in and perceptions of higher education. Three primary foci were students' employment status, work commitments, and means of financing college. Most of the informants, 95.2%, reported having worked during college or that they were working while in college. Actively employed students were 69.4% of the sample which is similar to reported national averages. Over three-quarters of the working students (75.7%) reported part-time employment with 24.3% working full-time. There were no significance differences in these areas between females and males, Hispanics and non-Hispanics, or even when broken out as Latinas, Latinos, non-Hispanic females and non-Hispanic males but students of non-traditional age reported a work commitment at significantly higher levels than traditional aged students. In respect to funding college, Hispanic/Latinx individuals were more likely to be using Pell Grants and work study positions to pay for college, while comparisons by age of the student followed a predictable pattern. When broken out as Latinas, Latinos, and female and male non-Hispanics there were significant differences regarding paying for college with money the individual earned, with Pell Grants, and with work study positions. The survey results demonstrate that students at the HSIs were not working more than their peers across the nation, although nearly 70% were actively employed, and that work commitment was related to age, relational status, and state of residence but not gender and ethnicity.

Mediating Roles in the Relationship between Mentorship and STEM Interest

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Tabitha Black* and Dr. Kristin Conover, *Alliant International University, Los Angeles*

Abstract: Based on current academic and vocational interests, the United States is predicting a future economic crisis due to a lack of STEM educated individuals (Castleman, Long, & Mabel, 2014). There is an established positive relationship between mentorship and vocational development in the area of STEM (Hund, 2018; Long & McGinnis 1985; Lyons, Scroggins, & Rule, 1990; Marciniak, 2019; Robnett et al, 2018). Identification of possible factors that mediate this relationship will offer mentorship program developers firm objectives in curriculum criteria to mitigate the impending STEM-driven economic crisis in America. The current study seeks to investigate if there is an indirect effect of Locus of Control and Self Efficacy on the relationship between mentorship and STEM. Gender differences will also be analyzed. One hundred twenty-eight participants, recruited via social media platforms, will indicate their mentorship history and quality, locus of control, self-efficacy, and STEM interest using self-report measures. The data will be analyzed to control for the effects of their intrinsic differences (locus of control and self-efficacy) to determine if the relationship between mentorship and STEM interest remains. If not, it will be arguable that these mediators are in fact indirectly affecting the a priori relationship. As such, training programs aimed at mentorship development can design programs that increase the mentors' ability to affect their mentees' locus of control and self-efficacy in the direction that is most related to the positive results in STEM development. Significant differences found among gender and socio-economic factors also discussed.

Which Factors Influence Scientific Argumentation Skills about Biodiversity Conservation?

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Iresha Jayasinghe*, *Illinois State University, Normal* and Rebekka Darner, *Illinois State University*

Abstract: Understanding individuals' relationships with nature provides insight into how we might mitigate human-induced environmental issues. This study examines how individuals' relationships with nature (NR), emotions experienced during evidence evaluation, and conservation concern drive evaluation of claims made about biodiversity conservation. The participants were 236 undergraduate students from a large, Midwestern institution recruited via a university mass email. NR was measured using the short NR scale. Scientific argumentation skills were measured using the Uncertainty-Infused Scientific Argumentation Test (USAT), focused on biodiversity conservation argumentation, in which participants were asked to evaluate claims made about biodiversity conservation across two scenarios: a scenario in which an anti-conservation claim was made and a scenario in which a pro-conservation claim was made. A multiple linear regression with bootstrapping was performed for each scenario to predict argument evaluation skills, where NR and emotion were independent variables. Conservation concern score was removed from the model due to having a nonlinear relationship with argumentation skills in both scenarios. Although it was predicted that participants with strong NR would exhibit motivated reasoning, resulting in strong argument-evaluation skills as they evaluated an anti-conservation claim, we found that participants' emotions during evidence evaluation were more predictive of their argument-evaluation skills. These findings suggest the importance of addressing negative emotions experienced when evaluating evidence. This indicates that math anxiety, usually thought to be unrelated to one's decision-making about environmental issues, may be especially important when empirical data is a basis for that decision-making.

A Pilot Study: Investigating Science Discourse Practices in STEM Undergraduate Classes Using Decibel Analysis for Research in Teaching (DART)

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Lara Charles-Kuhlman* and Molly Weinburgh, *Texas Christian University*

Abstract: This exploratory study investigates the use of the Decibel Analysis for Research in Teaching (DART) to analyze classroom audio recordings, the use of productive discourse practices, and student learning gains. DART has the potential to help faculty analyze and assess the ratio of lecture to non-lecture, and thereby assess their use of innovative practices such as productive discourse.

Undergraduate STEM teaching in the U.S. continues to be primarily lecture-based. Research indicates learning is enhanced when students are more actively engaged through the use of innovative teaching practices such as productive discourse. Productive discourse provides students with opportunities to talk about ideas, form arguments based on evidence, and engage in higher-level thinking. Current methods of analyzing teaching practices include time- and resource-intensive approaches such as classroom observations and video analyses.

The purpose of our study is to investigate the relationship between the DART analysis of classroom audio recordings, observations of productive discourse practices, and student learning gains. We used DART to analyze audio recordings from large-enrollment undergraduate biology classrooms. We then analyzed relationships between the DART results and classroom observations of productive discourse practices, and correlated these with student performance and learning gains. In this session, we will share results from our pilot study. It is our hope that this work will help us understand how productive discourse practices lead to enhanced learning, and also equip faculty with knowledge and tools to critically reflect on their teaching practices and their use of productive discourse.

First Year Students' Confidence in Pursuit of Biology Careers Correlates to Content Interest and Career Self-Efficacy

Discipline: STEM Education & Learning
Subdiscipline: Science Education

Krista Donis*[1]; Christina Rjeili[1]; Lisa Corwin[2] and Sarah Eddy[1], *(1)Florida International University, (2)University of Colorado, Boulder*

Abstract: As a powerful motivational process, *career interest* guides students' academic persistence and career choices. According to Social Cognitive Career Theory, *career interest* is strengthened through a network of personal qualities,experiences and beliefs. Chief among these beliefs are self-efficacy and outcome expectations: students who believe they can succeed in a career will anticipate positive career outcomes, and develop more robust professional interests. However, within students (person inputs) and educational experiences will regulate their occupationally-relevant self-efficacy and outcome expectations. This work explores the career interest of White and Hispanic first-year biology students (n=396) at two R1 institutions. Students completed a survey with items on (1) **person inputs and background**(demographics,goal orientation) ; (2) **learning experiences** (previous biology enrollment, and a tally of influences that built their biology interest); (3) **motivations and beliefs** (career self-efficacy, biology interest, career outcome expectations) and (4) **career goal confidence (a measure of career interest).** We employed a three-step hierarchical linear regression analysis by adding blocks of predictor variables to a model with career goal confidence as the outcome. Results indicate that among person inputs, race and goal orientation predicted 7.0% of the variation (F (2,213) = 8.041, p<0.01). When adding learning experiences, our influences tally predicted an additional 3.4% of variation(F (5,278) = 2.4277, p<0.01). Introducing motivations/beliefs, reflected that biology interest and career self-efficacy (F (5,273) = 13.9601,

p<0.00) explained an additional 10.3% of variation, for a total total R^2 of .207. We suggest that variables beyond person inputs contribute to first-year biology students' career goal confidence.

Graduate Oral Presentations

Chemistry: Organic Chemistry & Other

Synthesis and Characterization of Ferrocenyl Derivatives As Photosensitizers for Dye Sensitized Solar Cells

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Alejandro Burgos-Suazo* and Ingrid Montes-González, *University of Puerto Rico, Rio Piedras Campus*

Abstract: Energy is utilized exhaustively every day and its non-renewable resources are becoming scarce. Seeking a renewable source is imperative; solar to electrical energy transformation presents a viable alternative through the construction of energy devices. Dye Sensitized Solar Cells (DSSC) present an energy path via a redox reaction in the dye to generate electricity. Our project's main goal is to synthesize novel ferrocenyl derivatives as dyes that will have improved energy conversion efficiency. Synthesized dye's general structure will be of Donor-π-Acceptor type including various linkers to extend conjugation and test efficiency (alkenes, alkynes, enones). Ferrocene's electrochemical properties, photosensitizer conjugation, and electronic communication are expected to improve conversion efficiency. Another plausible modification is to include into the solar cell perovskite moieties to compare efficiency changes. All dyes will be synthesized using organic reagents via condensation or coupling reactions. Once the dyes are synthesized and characterized, they are adsorbed and integrated into a small test cell, to perform energy conversion experiments. Six bromine substituted ferrocenyl chalcones (which are dye precursors) have been synthesized, and one dye's synthesis was completed to perform tests. In this presentation, synthetic methodology, analyses, and experimental results will be elaborated.

Photoacid Catalyzed C-C Bond-Formation: Synthesis of Triarylmethanes and 3,3'-Diarylindolin-2-Ones

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Jason Saway* and Prof. Joseph Badillo, *Seton Hall University*

Abstract: The development of new catalytic processes is essential for organic synthesis. In this presentation, we will discuss a visible-light-induced, thiourea catalyzed C–C bond-forming reaction. Specifically, Schreiner's thiourea [(*N*,*N*'-bis[3,5-bis(trifluoromethyl)phenyl]-thiourea] functions as a photoacid to facilitate the double Friedel-Crafts addition of indoles to aldehydes and isatins to form the corresponding triarylmethanes and 3,3'-diarylindolin-2-ones. We demonstrate that this protocol applies to a variety of aldehyde and isatin electrophiles and a range of electronically diverse indoles. Furthermore, this mild light-facilitated reaction is chemoselective for 1,2-addition to aldehydes over ketones and 1,4-conjugated systems. Mechanistic studies show that light is required for the reaction to be initiated. This presentation will also discuss the synthesis and optimization of a variety of triazole containing triarylmethanes and 3,3'-diaryloxindoles using copper-catalyzed azide-alkyne cycloaddition (CuAAC) chemistry in order to evaluate their anti-cancer properties.

Highly Regioselective Catalytic Electrophilc Alkylation of Benzenes By Trifluoromethylated α-Methylstyrenes

Discipline: Chemistry
Subdiscipline: Organic Chemistry

Jose Alvarenga*; Amir Keshavarz and Benjamin Stokes, *University of California, Merced*

Abstract: Small molecules possessing quaternary carbons, including geminal dialkyl and geminal diaryl ones, are abundant in biologically relevant natural products, but such motifs are often difficult to synthesize due to their sterically congested nature. Many catalytic electrophilic aromatic alkylations are known, but few of them efficiently afford quaternary carbons from 1,1-disubstituted alkenes. An additional challenge is achieving good selectivity of alkylation regioselectivity. We hypothesized that a Brønsted acid with a highly non-coordinating counteranion might be the best-suited catalyst to accomplish this challenging transformation by minimizing competing styrene dimerization. Herein, we report a highly regioselective method to form new intermolecular carbon–carbon bonds by engaging trifluoromethylated and other electron-deficient *α*-methyl styrenes with a variety of aromatic compounds through the action of the Bronsted acid catalyst, hydrogen tetrakis(pentafluorophenyl)borate (putatively generated in situ from the corresponding tritylium salt). The reaction optimization (including solvent effects) is described and accompanied by a detailed reaction scope (specifically yield and regioselectivity outcomes due to substituent variation). This method gives access to a wide range of interesting new quaternary carbon-containing trifluoromethylated compounds. The presence of a trifluoromethylated arene can significantly improve the reactivity and physical properties of a small molecule drug candidate, including its lipophilicity.

Smart Bubbles: Stimuli Responsive Materials for Ultrasound Molecular Imaging

Discipline: Chemistry
Subdiscipline: Other Chemistry

Gabriela Ibarra* and Jefferson Chan, *University of Illinois Urbana-Champaign*

Abstract: Ultrasound imaging is one of the safest and most accessible clinical imaging modalities. While ultrasound can characterize large anatomical features, there are limited strategies for ultrasound molecular imaging. Molecular imaging is the visualization of biological processes *in vivo* at the cellular, organ, or organism level. The most common strategy for ultrasound molecular imaging is the addition of targeting groups (e.g. peptides, antibodies) to the membrane of lipid shell microbubbles which act as ultrasound contrast agents. However, this method only allows for the intravascular accumulation of microbubbles, as due to their size, these microbubbles cannot extravasate. Therefore, despite its deep tissue capabilities, current ultrasound technology cannot be utilized to study extravascular or intracellular events. We are working on the development of novel nanobubbles that can report on biochemical events by undergoing a size change from the nano to micron scale after interaction with an analyte of interest. This would leverage the extravasation capabilities of nano sized bubbles, but favorable ultrasound properties of micron sized bubbles. The present work will outline the chemical synthesis as well as material (dynamic light scattering, microscopy, zeta-potential) and ultrasound characterization of nanobubbles developed for studying reactive oxygen species and other biological analytes. Preliminary dynamic light scattering data has demonstrated a small size increase occurs with our current platform. However, we are currently tuning our nanobubbles to drive a size change to the micron scale while balancing stability and reactivity. This work would enable ultrasound to be utilized for studying complex biological processes *in vivo*.

Chemistry: Physical Chemistry

Femtosecond Pump Probe Spectroscopy of Neutral Ti, Fe, and Ni Oxide Clusters

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Jacob Garcia*; Ryan Shaffer and Scott Sayres, *Arizona State University*

Abstract: Ti, Fe, and Ni oxides are widely used industrial catalytic materials and common interstellar media. Typically observed in the bulk phase, atomically precise surface reactivity and formation is currently lacking in experimental detail. The dissociative electron dynamics of transition metal oxide clusters provide information about the stability and reactivity of their bulk material counterparts such as molecular conformations and fragmentation patterns. In our experiments, neutral Ti_nO_m, Fe_nO_m, and Ni_nO_m oxide clusters are produced under low oxygen using laser ablation. I will present the mass spectra showing a primary stable stoichiometry of $m = n$ for Fe clusters, $m = n - 1$ for Ni clusters, and $m = 2n - 1$ for Ti clusters. Here, the ultrafast pump-probe spectroscopy of each cluster extending up to $n = 10$ shows the unique ionization, dissociation, formation, and excitation-relaxation properties. The data presented will show that the femtosecond dynamics observed for these clusters depend strongly on their metal composition, size, and oxidation state. Understanding the energy and time-resolved fragmentation patterns of large molecules may prove to produce more targeted catalysts of increased reactivity and a deeper understanding of the formation of molecules in the cosmos.

Adiabatic Connection Approaches to Thermal Density Functional Theory

Discipline: Chemistry
Subdiscipline: Physical Chemistry

Brittany Harding*; Zachary Mauri and Aurora Pribram-Jones, *University of California, Merced*

Abstract: Density functional theory (DFT) is a formally exact approach to quantum mechanics used to investigate the electronic structure of many-body systems, particularly the ground states of atoms, molecules, and condensed phases. DFT lets us examine properties that are quantum mechanically based in a computationally efficient, but still usefully accurate, manner. It is an especially useful tool for examining warm dense matter, which is too hot to be described by traditional quantum mechanical methods, but too dense to be described by plasma physics. Currently, numerous approximations exist for the exchange-correlation (XC) energy component of the total energy in DFT at zero temperature, and these approximations are often erroneously used for finite-temperature DFT. The adiabatic connection is a useful tool for analyzing and constraining approximations of the XC energy in zero-temperature theory. Here, its temperature-dependent extension is demonstrated and analyzed using a well-known parametrization of the uniform electron gas free energy. Our results indicate that, even within what is in some ways one of the simplest electronic systems, the uniform gas, not all zero-temperature constraints are satisfied. A new approximation to the XC free energy, the Generalized Thermal Adiabatic Connection (GTAC), has been proposed and tested in the uniform gas, generating new ideas about the connections between methods in ensemble DFT and thermal DFT.

Computer & Information Sciences and Civil Engineering

Detecting Cyberbullying: Two-Step Classification of Topic-Based Youtube Comments

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Christopher Gomez*; Dr. Rachel Trana and Rachel Adler, *Northeastern Illinois University*

Abstract: Cyberbullying is a form of harassment that occurs through online communication, such as messaging and posting via social networking platforms, with the intention of threatening, abusing, or causing emotional distress to the intended targets. To address the issue of cyberbullying on social networking sites, our goal is to develop a machine learning classification schema to minimize incidents specifically involving text extracted from image memes. We collected approximately 19,000 text comments from YouTube that spanned a broad spectrum of topics to be used for classifying text found in images. We first report on the efficacy of three machine learning classifiers, naive Bayes, Support Vector Machine (SVM), and a convolutional neural network (CNN) to detect cyberbullying on the entire YouTube dataset. Due to the poor classification accuracy on the full YouTube dataset, we investigated a subset of the data that was grouped based on five topics (Race/Ethnicity, Body Image, Gender Equality, Politics, and a non-specific General topic), with an equal balance of bullying and non-bullying comments. Applying the above classifiers to this smaller balanced subset of data yielded higher classification accuracy as compared to the entire dataset. We then grouped the full YouTube dataset into the same five topics and tested the classification accuracy using just the SVM classifier. We also investigated whether topic grouping via an unsupervised machine learning method, Latent Dirichlet Allocation (LDA), produced an improvement in bullying classification relative to using predetermined topic assignments when classifying using SVM. We present the classification performance for the different datasets.

Distributed Consent and Its Impact on Privacy and Observability in Social Networks

Discipline: Computer & Information Sciences
Subdiscipline: Computer & Information Sciences

Juniper Lovato*[1]; Antoine Allard[2]; Randall Harp[1] and Laurent Hébert-Dufresne[1], *(1)University of Vermont, (2)University of Laval*

Abstract: Personal data is not discrete in socially-networked digital environments. A single user who consents to allow access to their own profile can thereby expose the personal data of their network connections to non-consented access. The traditional (informed individual) consent model is therefore not appropriate in online social networks where informed consent may not be possible for all users affected by data processing and where information is shared and distributed across many nodes. Here, we introduce a model of "distributed consent" where individuals and groups can coordinate by giving consent conditional on that of their network connections. We model the impact of distributed consent on the observability of social networks and find that relatively low adoption of even the simplest formulation of distributed consent would allow macroscopic subsets of online networks to preserve their connectivity and privacy. Distributed consent is of course not a silver bullet, since it does not follow data as it flows in and out of the system, but it is one of the most straightforward non-traditional models to implement and it better accommodates the fuzzy, distributed nature of online data.

Water Sustainability Using Pond-in-Pond Wastewater Treatment System

Discipline: Engineering
Subdiscipline: Civil Engineering

Kushal Adhikari* and Clifford B. Fedler, *Texas Tech University*

Abstract: Wastewater is an easily accessible but highly underutilized resource that could meet irrigation needs while conserving freshwater for future generations and is increasingly recognized as an essential and economical strategy in areas with water scarcity. However, only 6% in the US and less than 3% globally is reclaimed for beneficial use. The goal of this study is to explore the use of the Pond-In-Pond (PIP) system as an alternative for municipal wastewater treatment for reuse in irrigation. The PIP is a treatment technology where two types of ponds --anaerobic and aerobic-- are combined into a single pond and consists of a deeper inner section entirely submerged within the outer pond. This paper presents case studies on the PIP configuration and performance data from the PIP systems investigated resulted in an average BOD removal of over 80% with a deviation of less than 10%. Consequently, the PIP unit alone ensured a level of treatment required for effluent reuse in crop irrigation for typical municipal wastewater with influent BOD in the range of 200 to 300 mgL^{-1}. Moreover, the combination of PIP with other processes in a treatment system has the capability of treating high-strength wastewater for other uses such as aquaculture, fishery, and others--including stream discharge. Thus, the PIP is a potentially viable and sustainable technology for low-cost wastewater treatment especially for reuse purposes due to the savings in capital costs, operations and maintenance costs, and revenue from reclamation of the effluent.

Ecology/Evolutionary Biology, Public Health, STEM Education & Learning and Traditional Knowledge

Grand Canyon University Tobacco Free Generation Campus Initiative

Discipline: Health
Subdiscipline: Public Health

Carolina Regalado Murillo* and Veronica Perez, *Grand Canyon University*

Abstract: Nationwide, educational institutions are protecting students from exposure to second-hand smoke through campus-free tobacco policy adoption. This study aimed to understand student behaviors and perceptions of tobacco use and tobacco-free policy adoption. Students from a private university in Arizona completed a survey (N=2,407) to assess patterns of e-cigarette and tobacco use; cessation attempts; secondhand smoke exposure; and knowledge, attitudes, and beliefs about tobacco policies. Focus groups/semi-structured interviews (SSIs) were conducted to understand student perceptions of smoking/vaping; knowledge of tobacco policies; and barriers and facilitators to implementing tobacco-free policies (N=20). Survey results revealed 6% of students were current smokers (N=140), and 26% (N=583) had used e-cigarettes. Regarding cessation, 35% of current smokers had made a quit attempt (N=40) in the past 12 months, and 37% of current smokers were thinking about quitting in the next 12 months (N=43). Among students exposed to secondhand smoke, 48% (N=730) indicated secondhand smoke on campus was a concern or annoyance. Overall, 78% (N=1,585) of students agreed that colleges have a responsibility to adopt policies that ensure people have smoke-free air to breathe. Consistent themes included 1) perception of high e-cigarette use, 2) lack of understanding of existing campus tobacco-free policies, 3) enforcement as a barrier, and 4) education, awareness, and cessation support as facilitators to implementing tobacco-free policies. Findings indicate student support for campus tobacco-free policies and highlight e-cigarette use as a significant issue. Colleges adopting tobacco-free policies must address e-cigarette use, provide education and cessation support, and develop a comprehensive policy enforcement plan.

Priorities and Barriers for Undergraduate Students Participating in Field Experiences: Attracting Diverse Talent Requires Adequate Pay and Flexibility

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Alex Jensen*[1]; Sara Bombaci[2]; Laura Gigliotti[1]; Stephen Harris[1]; Courtney Marneweck[1]; Mike Muthersbaugh[1]; Blaise Newman[1]; Elizabeth Saldo[1]; Kyle Shute[1]; Anna Siegfried[1]; Keifer Titus[1]; Amanda Williams[1]; Sze Wing Yu[1] and David Jachowski[1], *(1)Clemson University, (2)Colorado State University*

Abstract: Field experiences and internships provide undergraduate students with valuable exposure to potential career pathways in environmental science, ecology, and conservation. When done well, these high impact learning experiences link college to careers and connect students to valuable professional networks. Despite these benefits and a growing interest among the environmental science community to attract and retain diverse talent, minimal data exists on what factors undergraduate students across diverse demographic groups prioritize when applying to field experiences. We used a nationwide survey of undergraduate students across the US to understand students' motivations and barriers to participation in field experiences. We found that pay and skill development are among the top factors prioritized by students when considering internships, and ethnic or racial minorities, males, non-heterosexuals, disabled, and first-generation students desired higher pay. Forty-seven percent of students indicated that their level of income has been a barrier in their academic career, while twenty-five percent of respondents indicated there were other factors that affected their willingness to participate in internships, including the timing of the internship, conflicts with work, school, extracurricular, cultural or religious activities, a lack of transportation or housing, conflicts with family care responsibilities, difficult or hostile working conditions, a lack of safe and inclusive spaces, and mental and physical health limitations. By highlighting major priorities and limitations for students participating in field experiences, our findings provide important insights for attracting a diverse workforce to this often critical stage in career advancement.

Internships Foster Academic Advancement and Achievement in Marine/Environmental Science for Pacific Island Students

Discipline: STEM Education & Learning
Subdiscipline: Education Research/Administration

Lauren Wetzell* and Robert Richmond, *University of Hawaiʻi at Mānoa*

Abstract: Pacific Islanders (PI) are dependent upon the natural resources their islands provide for food, water, and indigenous way of life. Impacts such as overfishing and land-base sources of pollution are exacerbated by the extreme effects of climate change. In order to adapt and be resilient to these impacts, indigenous expertise in science, technology, engineering and/or mathematics (STEM) is critically needed. However, of the four minority populations recognized by the US, PIs are the most underrepresented in pursuing STEM career fields (Hadfield et al., 2016). For over ten years, the

Partnership for Advanced Marine and Environmental Science for PI grant project, funded by the National Science Foundation (NSF), provided paid internships to PI students with the intent to increase STEM-related careers specifically in marine/environmental science upon graduation to the following five community colleges: American Samoa Community College (ASCC), College of the Marshall Islands (CMI), College of Micronesia-Federated States of Micronesia (COM-FSM), Northern Marianas College (NMC), and Palau Community College (PCC). The results indicate nearly all interns graduated from their 2-year college and, rather than accepting employment, 90% of graduates pursued advanced degrees at a 4-year University. This study is part of a larger effort to identify and remove barriers for PI in their academic pursuits in marine/environmental science.

Thinking about the Integration of Indigenous Science and Western Science Knowledge Systems

Discipline: Traditional Knowledge
Subdiscipline: Traditional Knowledge

Cheri Johnson* and Barbara Allen Allen, *Virginia Polytechnic Institute and State University*

Abstract: The US and Canada convened the Costal Expert Monitoring Group (CEMG) in 2014 as a co-led series of workshops to define criteria for coastal plan effectiveness in response to rapidly changing conditions in the Arctic (Behe et al., 2016). The process used by CEMG to create the effectiveness criteria for the coastal plan had as its goal the integration of both western science and local indigenous knowledge (ibid.). This exploratory paper will examine how the CEMG members originally thought about and applied an integration of western and indigenous knowledge systems in the development of the Coastal Plan. Through an examination of CEMG literature, I will discuss how the CEMG could expand their approach and understanding of integration using the theoretical frameworks of the following theories. First, I will discuss how Standpoint Theory and Strong Objectivity (Harding, 2015) can be used to help decide on equalization or privileging of knowledge within the two knowledge systems. Second, I will discuss the differences between the CEMG workshop conceptual models created independently by the experts from each of the knowledge systems. I will discuss how Civic Epistemology (Jasanoff, 2005) and Boundary Work (Gieryn, 1983) provide insight into why the experts of these two knowledge systems draw different scientific conclusions. The conclusions of this research suggest that future efforts to integrate Western and Indigenous knowledge systems must both understand the polysemous nature of these knowledge systems and acknowledge how expertise and experts are derived from value-based perspectives.

Bioengineering/Biomedical Engineering & Other

Cellular and Biophysical Optimization of Temperature-Dependent Dynamin-ELP Fusions to Modulate Endocytosis

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Hugo Avila* and Andrew MacKay, *University of Southern California*

Abstract: Endocytosis is a highly regulated process that requires an ensemble of cell components to facilitate vesicle formation and internalization. Dynamin (**DNM**) is a GTPase canonically known to scission vesicles entering a cell. Its role in clathrin-mediated endocytosis (**CME**) is well-understood, but its role in other pathways such as caveolin-mediated endocytosis, or flotillin-mediated endocytosis are less defined. Elucidating the mechanism of endocytic pathways dependent of DNM has relied on the use of small molecule inhibitors like dynasore. However, they suffer from disadvantages like irreversibility and off-target effects. Dominant-negative DNM2-K44A and siRNA genetic knockdown have also been used but are slow and can result in upregulation of alternative pathways. To overcome these limitations, we have developed a novel tool to quickly, directly, and reversibly modulate ubiquitously expressed DNM2 using elastin-like polypeptide (**ELP**) technology. ELPs are a class of thermo-responsive biopolymers that self-assemble into coacervates above a transition-temperature (T_t). When fused to effector proteins like DNM2, ELPs can modulate their spatial distribution above its T_t but remain functionally unaffected below T_t. Here, we report the formation of vesicular structures that sequester DNM2 above T_t. We characterized their morphologies and dimensions by super-resolution microscopy in 2- and 3-dimensions in fixed-cells as well as its dynamics in live-cells. Additionally, we demonstrate rapid, direct, and reversible spatial rearrangement of a panel of endogenous proteins above DNM2-ELP T_t, but not below. Taken together, we demonstrate feasibility of DNM2-ELP as a new inhibitor-tool to explore the dependence of different endocytic pathways on DNM2.

Self-Healing Hydrogel Coatings for Improving Brain Implant Biocompatibility

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Erika Davidoff* and Jay Sy, *Rutgers University*

Abstract: Many treatments for neurodegenerative diseases involve implanted electrodes. Foreign body response (FBR) to these electrodes is a major cause of treatment failure. FBR is exacerbated by oscillatory micromotion at the tissue-implant interface due to respiration and blood circulation, which generates shear strain that activates inflammatory cytokines and induces development of glial scar tissue around the implant.

To minimize FBR, we are developing shear-thinning, self-healing hydrogel coatings for neural implants. The gel featured here is a two-polymer system characterized by hydrogen bonding between β-cyclodextrin “host” moieties on one polymer and adamantane “guests” on the other. UV crosslinking provides structural stability while guest-host interactions repeatedly dissociate to absorb micromotion-induced kinetic energy that would otherwise trigger FBR.

We built a custom bioreactor to simulate micromotion by oscillating probes through agarose brain tissue phantoms at biologically relevant velocities (~0.1-0.5 mm/s). During micromotion of a 250μm-diameter probe coated with self-healing hydrogels varying from 0.1-0.25mm, the displacement of the tissue phantom within 3mm of the probe is reduced by an average of 36% compared to an uncoated probe ($p < 0.001$). We observed dramatically reduced tissue velocity within 0-1mm of the probe and more moderate reductions in the 1-3mm range. Thin coatings (~0.1mm) seem to be as effective at displacement reduction as coatings up to 0.25mm, which is advantageous for minimizing total implant diameter, a critical factor in preventing tissue damage and reducing FBR. Planned future work includes *in vitro* experimentation with 3D glial cell culture followed by an *in vivo* study in rodents.

Temporal Characterization of Blood-Brain-Barrier Disruption with High Frequency Electroporation

Discipline: Engineering
Subdiscipline: Bioengineering/Biomedical Engineering

Melvin F. Lorenzo*[1]; Sean C. Thomas[1]; John L. Robertson[1]; John H. Rossmeisl Jr.[2] and Rafael V. Davalos[1], *(1)Virginia Tech, (2)Virginia-Maryland College of Veterinary Medicine*

Abstract: The blood-brain-barrier (BBB) is a highly selective biological barrier lining blood vessels within the central nervous system. While primarily acting to maintain homeostasis, the BBB hinders transport of therapeutic molecules, thereby impeding treatment of intracranial disorders. In this study, we investigate the temporal aspect of high frequency electroporation (HFE)-mediated BBB disruption (BBBD) in an *in vivo* healthy rodent brain model. 36 male Fischer rats were anesthetized with isofluorane anesthesia. A craniectomy was implemented and two blunt-tipped stainless steel electrodes were inserted. HFE was applied as 200 bursts of bipolar pulses at 400 V and energized time 100 μs per burst. BBBD was evaluated using a 5:1 Gadolinium:Evans blue solution at time points of 1, 24, 48, 72, and 96 hours post-HFE. A 1.5T MRI was used to quantify BBBD volumes with Gadolinium enhancement and verified in histological sections via Evans blue staining. Thereafter, a numerical model was constructed to attain the electric field threshold for BBBD by matching the experimentally determined volumes with those from the model. T1W scans demonstrated significant BBBD (0.077 ± 0.004 cm^3) 1-hour post-HFE with an exponential decay in the following days. Numerical analysis demonstrated BBBD threshold as 113.1 V/cm, with tissues experiencing high field strengths undergoing longer BBBD. Western blotting indicated decreased tight junction protein expression with gradual recovery. We conclude BBBD is achieved at low electric fields with minimal cell death attributed to HFE therapy. These data further suggest HFE induces long-lived BBBD (~3 days) of tissue exposed to higher electric fields (529.3 V/cm).

Cytotoxicity Induced By Two-Dimensional (2D) Engineered Nanomaterials

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Roxana Coreas* and Wenwan Zhong, *University of California, Riverside*

Abstract: Two-dimensional (2D) engineered nanomaterials (ENMs) are promising in biomedical research and electronic devices due to planar topographies and unique physiochemical properties. Despite wide production and use, there are limited studies that address the possible impacts they may have on biological systems, justifying demands for intensive research efforts to study these interactions. This study investigated the cytotoxicity of a series of 2D ENMs, including graphene (G), graphene oxide (GO) with varied reduction treatments, hexagonal boron nitride (hBN), and molybdenum disulfide (MoS_2). Two tumor cell lines, HeLa and MDA-MB-231, and one non-tumor cell line, MCF-10A, were studied. Cells were incubated with ENMs at 5, 20, and 50 μg/mL for 1 hr or 3 hrs. Additionally, ENMs were concentrated and/or a protein corona was formed to mitigate interactions between cells and surfactants. The toxic impacts observed were dependent on cell type and ENM surface property. For all cell lines, there was significant toxicity after incubation with rGO and prGO, but not GO. Pristine MoS_2, hBN, and G did not show significant toxic effects on MCF10A or MDA-MB-231, but slightly reduced HeLa viability. The effects were far more drastic with the concentrated ENMs. By far, the protein corona on the concentrated ENMs was most toxic to the cells. This may be related to the level of cell uptake, which is under investigation. This work compared the behaviors of diverse ENMs, and sheds light on potential impacts to cytotoxicity from the chemical and surface properties of ENMs, which can be tuned for future biomedical applications.

Bioengineering/Biomedical Engineering & Chemistry

In Silico Screening of Chiral Compounds in Amino Acid-Based Molecular Micelle Systems Using Molecular Dynamics Simulations

Discipline: Chemistry

Subdiscipline: Other Chemistry

Mauro Garcia*[1]; Eugene Billiot[1]; Fereshteh Billiot[1]; Kevin Morris[2] and Yayin Fang[3], *(1)Texas A&M University - Corpus Christi, (2)Carthage College, (3)Howard University College of Medicine*

Abstract: Synthesized pharmaceutical drugs often yield in racemic mixtures. The enantiomers produced are similar in atomic connectivity, but their spatial orientations differ. This directly affects their functionality and interactions with biologically active molecules. Furthermore, one enantiomer may produce the desired medicinal effect, whereas the other may be detrimental. This calls for the establishment and optimization of enantiomeric separation processes.

Previous studies have shown that Micellar Electrokinetic Chromatography (MEKC) can be utilized to separate enantiomeric compounds using Amino Acid-Based Molecular Micelles (AABMMs) as the pseudo-stationary phase. Further investigation reveals that the alteration of the AABMM dipeptide polar head constituent largely affects its formation and effectiveness as a chiral recognition medium.

To holistically understand, compare, and predict the effectiveness of different AAMBBs, the creation of a quantitative structure-enantioselective retention relationships (QSERR) database must be established. In working towards the development of this database, this research is focused on using molecular dynamics simulations of AABMMs, in conjunction with chiral compounds, to gain insight into the factors responsible for enantiomeric separation. The AABMMs being investigated are composed of the undecyl form of all dipeptide combinations using L- alanine, valine, and leucine, as well as achiral glycine. Experimental MEKC results were compared to the computational binding free energy calculations to validate this model. The QSERR database, which will be developed from this study, will allow for the comparison and screening of chiral compounds in AAMBB systems.

Microenvironmental Engineering for the Elucidation of Circulating Tumor Cell Dormancy Via Extracellular Vesicles

Discipline: Engineering

Subdiscipline: Bioengineering/Biomedical Engineering

Xilal Y. Rima*; Nicole Walters; Jingjing Zhang; Luong T. H. Nguyen and Eduardo Reátegui, *The Ohio State University*

Abstract: Tumor-derived extracellular vesicles (EVs) have been implicated in adapting the microenvironment for the onset of metastasis, the leading cause of cancer-related deaths. These distant microenvironments harbor circulating tumor cells (CTCs) in a quiescent state, allowing them to evade immune responses, resist chemotherapeutics, and persist for timeframes extending to decades. We present cell patterning as a high-throughput method to visualize the cellular response to hypoxia-mimetic agents as well as characterize the EVs released due to hypoxic stress. Employing the non-biofouling properties of poly(ethylene glycol) (PEG) and UV lithography for rapid fabrication, we have developed different dimensions of *in vitro* cell patterning to control the microenvironment. By taking advantage of different functional groups, we used UV light to either photodegrade or photopolymerize PEG in distinct surface locations. Through photodegradation, breast cancer cells were patterned in 2D culture. Through photopolymerization, 3D microwells were elaborated in which the breast cancer cells aggregated into spheroids. After subjecting the breast cancer cells to the hypoxia-mimetic agents, the EVs were collected and characterized for surface proteins and enveloped RNA through fluorescent microscopy. While 3D patterning was more indicative of the *in vivo* microenvironment, 2D patterning allowed for precise control ranging from organized populations of cells to single-cell patterning. The anticipated results for this study are to find whether the EV-enclosed micro-RNA can regulate the cell cycle of naïve breast cancer cells. Understanding the role of EVs in CTC dormancy is essential for comprehending the progression of metastasis, which is a window for novel therapeutics.

In Situ Force Sensors for Measuring Microenvironmental Forces during Mesenchymal Condensation

Discipline: Engineering

Subdiscipline: Bioengineering/Biomedical Engineering

Robert A. Gutierrez*; Mohammad M. Rahaman; Wenqiang Fang; Haneesh Kesari and Eric M. Darling, *Brown University*

Abstract: Mechanical forces are an essential element to early tissue formation, regeneration, and disease systems. Investigating these forces remains a significant challenge but is critical for understanding how the mechanical microenvironment shapes cell behavior, in accordance with their mechanosensitivity. We describe a versatile approach to quantify microscale forces during mesenchymal condensation by using our developed hyper-compliant microparticles (HCMPs). Uniform HCMPs deform in response to cell-generated stresses surrounding them, thus providing the necessary information to extract multi-directional pressure measurements. The objective of this study was to incorporate HCMPs into cell-only spheroids to investigate how cellular forces varied during formation. Experiments showed that spheroids self-assembled within approximately five hours, with only minor morphological changes to the packed spheroid microtissue over the remainder of the testing session. HCMPs revealed that microenvironmental forces varied widely during the initial five hours but settled as spheroids became more cohesive and adopted more uniform geometries. Analysis of HCMPs

revealed the average surface pressure to be between -100 Pa and 50 Pa. Results suggest that cell-dense tissues exerted significant forces on HCMP probes during the early stages of tissue formation. The highly compliant nature of our force sensors allowed for increased sensitivity and greater accuracy compared to stiffer microparticles used in previous works. This technique introduces real-time tracking of force measurements in an arrayed, 3D system using our novel HCMPs as force sensors to measure local traction forces applied by cells within microtissues. HCMPs can potentially serve in any number of systems with minimal disruption of the larger structure.

Reverse Engineering of a Fatty Acid-Tolerant E. coli Strain Identifies Rpoc Mutation Conferring Increased Tolerance to Industrially Relevant Inhibitors

Discipline: Engineering
Subdiscipline: Chemical Engineering

Efrain Rodriguez-Ocasio*; Yingxi Chen and Laura Jarboe, *Iowa State University*

Abstract: The *rpoC* gene, which encodes for the RNA polymerase β' subunit, was discovered to have a single point mutation in an evolved strain of *E. coli* tolerant to octanoic acid. Tolerance tests showed that the mutation was crucial for octanoic acid tolerance and therefore expression. Understanding how the evolved organism mutated to adapt and how the mutation may translate to tolerance to other compounds of interest may aid the development of tools for the industrial production of biorenewable chemicals. In this project, the spectrum of tolerance conferred by the identified *rpoC* mutation was investigated by challenging the strain with the mutant *rpoC* gene with several industrially relevant inhibitors. The inhibitors ranged from feedstock and industrial conditions to bio-products. The specific growth rates under these conditions were measured and compared to a control strain to determine how the mutation affects the organism's tolerance. The *rpoC* mutation was shown to confer increased tolerance to a variety of bio-products, such as short-chain fatty acids, alcohols and organic acids. Interestingly, the organism adapted to grow in octanoic acid and other bio-products at the cost of slower growth at higher temperatures. It was also hypothesized that the mutation under investigation may impact binding of the stringent response alarmone ppGpp to its binding site in *rpoC*. These findings may be relevant for future design strategies for robust microbial cell factories.

Geoscience, Environmental Science & Other

A Preliminary Kinematic Model of Afar Triple Junction from Initiation Onward

Discipline: Geoscience
Subdiscipline: Geology

Ryley Collins*, *University of Southern California* and Vincent Cronin, *Baylor University*

Abstract: The Afar Triple Junction is a relatively young ridge-ridge-ridge (RRR) triple junction that divides the Arabian, Nubian, and Somalian tectonic plates. Each of the triple junction's limbs - the East African Rift System, the Red Sea Rift, and the Aden Ridge – are transitioning from continental rift systems to oceanic spreading ridges, providing geoscientists with a unique locality to study an extensional region in which both early continental breakup processes and active oceanic ridge emplacement are preserved within the same system. Here, I present a preliminary kinematic model of the Afar Triple Junction from its initiation to its current position 600 km eastward and its projected future location in 5 My, 120 km northeastward. By determining velocity vectors for the Arabian, Nubian, and Somalian tectonic plates using the most accurate available dataset of individual plate motions in a no-net-rotation reference frame (Kreemer et al 2014) recast in a hot spot reference frame (Wang et al 2017), I establish the initiation of the Afar Triple Junction at 22 Ma by closing the East African Rift using control points adjacent to each plate boundary in a reverse-time cycloid rotation model (Cronin 2017). The current and future projected locations of Afar Triple Junction are then determined by running the cycloidal model forward in time from 22 Ma. Modeling the finite motion of points associated with the Afar Triple Junction allows for evaluation of the continued extensional nature of each rift system surrounding the triple junction.

Applying Solar Spectroscopy to Estimate Methane Emissions from California Dairies

Discipline: Geoscience
Subdiscipline: Other Geoscience

Isis Frausto-Vicencio*[1]; Sajjan Heerah[2]; Yifan Ding[1]; Ranga Rajan Thiruvenkatachari[1]; Alison Marklein[1]; Harrison Parker[3]; Seongeun Jeong[4]; Marc L. Fischer[4]; Akula Venkatram[1]; Manvendra Dubey[2] and Francesca Hopkins[1], *(1)University of California, Riverside, (2)Los Alamos National Laboratory, (3)California Institute of Technology, (4)Lawrence Berkeley National Laboratory*

Abstract: Methane (CH_4) is a potent greenhouse gas with a short lifetime that allows for focused reductions to quickly and significantly mitigate climate change. The dairy industry in California is an important source of CH_4 and contributes about 50% of total statewide emissions. State-based efforts for emission reduction are underway, however, CH_4 emissions from dairies are highly uncertain by up to 80%. To reduce the uncertainty in emissions, we measured atmospheric CH_4 enhancement (ΔX_{CH4}) over a concentrated region of dairy farms in the San Joaquin Valley (SJV) of California with 30 dairy farms housing >30,500 cows (~20x20 km^2). We used two portable EM27/SUN solar-viewing Fourier-transform infrared (FTIR) spectrometers, analog to satellite measurements, placed at an upwind location measuring clean background and at a downwind location capturing emissions from dairies. We deployed the FTIR instruments during four seasons and performed atmospheric flux inversions using the back-trajectory transport model, WRF-STILT. We find the observed ΔXCH_4 range from 10 to 60 ppb, illustrating the size and importance of the SJV dairy CH_4 source. Preliminary analysis suggests a seasonal variation dependent on meteorological factors such as wind speeds, and a diurnal cycle driven by wind directional shifts. This study will help constrain CH_4 emissions from California dairies, examine how seasonal variability should be handled in these emissions estimates, and demonstrate new modeling approaches for analyzing XCH_4 data.

Drill Holes and Bite Marks Shed Light on the Role of Predation in the Evolution of Echinoids

Discipline: Geoscience
Subdiscipline: Other Geoscience

Shamindri Tennakoon[*1]; Elizabeth Petsios[2]; Roger W. Portell[1]; Lyndsey Farrar[3]; Tobias B. Grun[1]; Michal Kowalewski[1] and Carrie L. Tyler[3], *(1)University of Florida, (2)Baylor University, (3)Miami University*

Abstract: Ancient traces on fossilized prey provide key evidence for the rise of predation during the Mesozoic Marine Revolution (MMR), an event thought to have led to the development of modern marine ecosystems. The Echinoid Associated Traces project is developing the first comprehensive database using the fossil record of echinoids to analyze and disseminate paleobiological data on biotic interactions affecting this important class of marine animals. The project aims to assess the evolutionary history of predation on echinoids and delineate robust criteria for interpreting trace-maker ecology. We postulate three hypotheses regarding the initial rise in predation on echinoids: (H1) a Late Jurassic radiation of burrowing echinoids; (H2) Cretaceous reorganization of marine ecosystems during the MMR; and (H3) Eocene diversification of cassid gastropods (the only known drilling predators of modern echinoids). Fossil and Recent echinoids from museums and field collections were surveyed for predation traces including drill holes and marginal traces. Diagnostic characteristics such as trace morphology, size, and location on specimens were recorded.

Time series models of trends in drilling predation suggest predatory interactions intensified during the Eocene (consistent with H3) but postdated notably the radiation of burrowing echinoids (H1) and the MMR, when mollusk-targeted drilling predation first intensified (H2). A high frequency of marginal traces, likely recording sublethal predation by crabs and/or fish, was observed in post-Miocene specimens, suggesting another, more recent, upsurge in biotic interactions late in the evolutionary history of echinoids. These results support the asynchronous intensification of predator-prey interactions through the evolutionary history of marine benthic animals.

Background Gamma Radiation and Soil Activity Measurements in the Northern Marshall Islands

Discipline: Life Sciences
Subdiscipline: Environmental Science

Maveric Abella[*], *University of Hawaii John A. Burns School of Medicine* and Ivana Hughes, *Columbia University*

Abstract: We report on external gamma radiation on 9 islands in 4 atolls in the northern Marshall Islands, all of which were affected by the US nuclear testing program from 1946 to 1958 (Enjebi, Ikuren, and Japtan in Enewetak Atoll; Bikini and Enyu in Bikini Atoll; Naen in Rongelap Atoll; and Aon, Elluk, and Utirik in Utirik Atoll). We also report americium-241, cesium-137, plutonium-238, and plutonium-239,240 activity concentrations in the soil samples for 11 islands in 4 northern atolls (Enewetak, Japtan, Medren, and Runit in Enewetak Atoll; Bikini and Enyu in Bikini Atoll; Naen and Rongelap in Rongelap Atoll; and Aon, Elluk, and Utirik in Utirik Atoll) and from Majuro Island, Majuro Atoll in the southern Marshall Islands. Our results show low external gamma radiation levels on some islands in the Enewetak Atoll and Utirik Atoll, and elevated levels on Enjebi Island in the Enewetak Atoll, on Bikini Atoll, and on Naen Island in the Rongelap Atoll. We perform ordinary kriging on external gamma radiation measurements to provide interpolated maps. Radionuclides are absent from all Majuro soil samples, and they are present at highest concentrations in samples from Runit and Enjebi islands (Enewetak Atoll), Bikini Island (Bikini Atoll), and Naen Island (Rongelap Atoll). We contextualize all results by making comparisons between islands and to various standards, as well as to regions of the world affected by nuclear accidents. We also discuss implications for informed decision-making by the Marshallese and local atoll governments and their people on issues pertaining to island resettlement.

Life Sciences: Physiology/Pathology, Pharmacology, Cancer Biology & Medicine

Expansion of Monocytic Myeloid-Derived Suppressor Cells in Infants with Severe Respiratory Syncytial Virus (RSV) Infection

Discipline: Health
Subdiscipline: Medicine

Santiago Acero Bedoya[*]; Victoria Best; Cristina Garcia-Mauriño; Fang Ye; Sara Mertz; Octavio Ramilo and Asuncion Mejias, *Nationwide Childrens Hospital*

Abstract: Respiratory syncytial virus (RSV) remains the leading cause of hospitalization of infants under the age of 5, attributed to RSV related lower tract respiratory infection (LTRI). To date, there is no vaccine; though some have shown promise in clinical trials, RSV's ability to suppress an adequate immune response has proven to be a great barrier. A mechanism of immune response suppression has yet to be elucidated. The presence and expansion of myeloid derived suppressor cells (MDSCs) have been shown to suppress CD8+ T Cells through different mechanisms, while monocytic MDSCs (M-MDSCs) have been shown to play a role in acute infection and stress response. We evaluated the MDSC population in our prospective study enrolling previously healthy young children and infants < 2 years of age born full term. Examination of MDSC populations in our patient samples at day of enrollment and at 30 and 180 days post-hospitalization show an expansion of M-MDSCs during infection that resolve to levels of age-matched healthy controls (HC). Furthermore, there is a significantly lower number of CD8+ T Cells at time of infection compared to HC, which increase to levels of HC post-hospitalization. Patients with higher levels of M-MDSCs and lower levels of CD8+ T Cells compared to HC show increase in supplemental oxygen, hospitalization, and clinical disease severity score (CDSS). These findings suggest that an expansion of M-MDSCs may play a role in T Cell suppression, leading to more severe RSV disease. To develop new vaccines, elucidation of RSV immune suppression mechanisms is paramount.

Combined Effect of the Akt Inhibitor Miransertib (MK-7075/ARQ 092) and mTOR Inhibitor Sirolimus Is Effective Against Viral and Non-Viral Non-Hodgkin Lymphomas.

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ricardo Rivera-Soto[*1]; Yi Yu[2]; Ronald Savage[2]; Brian Schwartz[2]; Dirk Dittmer[1] and Blossom Damania[1], *(1)University of North Carolina at Chapel Hill, (2)ArQule, Inc., a wholly-owned subsidiary of Merck & Co., Inc.*

Abstract: Virus-associated Non-Hodgkin lymphomas (NHL) tend to be more aggressive and chemoresistant than non-viral NHL. A possible therapeutic target that contributes to cell survival and proliferation and usually constitutively active in these lymphomas is the PI3K/Akt/mTOR pathway. Thus, using several *in vitro* and *in vivo* models of NHL, we assessed the therapeutic effect of targeting the kinase Akt with a novel allosteric inhibitor (miransertib) alone or in combination with an mTOR inhibitor, sirolimus. We found the inhibitors to be effective in silencing the activation of the signaling pathway, but their anti-proliferative effect is dependent on the NHL type. For example, the miransertib inhibitory concentration $(IC)_{50}$ for the non-viral associated follicular lymphoma (FL) cells was 0.1-0.2 μM, whereas the virus-associated primary effusion lymphoma (PEL) was 1.0-2.0 μM. We found that the combination of miransertib and sirolimus significantly reduced cell proliferation in a strongly synergistic manner. To test the feasibility of this approach, we used several xenograft models and found the results to be consistent with the *in vitro* studies. For instance, the FL xenograft model was sensitive to the inhibition of Akt alone, and the effect was enhanced when combined with the mTOR inhibitor. However, the tumor burden of PEL xenografts was only significantly reduced when both Akt and mTOR were targeted, showing a more resistant phenotype. In conclusion, our data suggest that targeting the PI3K/Akt/mTOR pathway with miransertib could be considered as a possible therapeutic approach for certain types of NHL, but a combinatorial treatment is necessary for aggressive virus-associated PEL.

Early Adolescent Subchronic Low Dose Nicotine Exposure Increases Subsequent Opioid Self-Administration in Sprague Dawley Rats

Discipline: Life Sciences
Subdiscipline: Pharmacology

Anjelica Cardenas[*] and Shahrdad Lotfipour, *University of California, Irvine*

Abstract: Initiation of nicotine products typically occurs in adolescence. Recent escalation of e-cigarette use among teens highlights the necessity to understand adolescent nicotine exposure effects on substance use. Adolescence is a critical period in development (12-18 years in humans, postnatal days (PN) 28-42 in rodents) where the maturation of brain neurocircuitry is vulnerable to nicotine. Rodent studies have shown that nicotine exposure in early adolescence consistently increases subsequent drug intake and reward. However, very few studies have assessed adolescent nicotine exposure effects on opioids such as fentanyl. We hypothesize that early adolescent, but not adult, nicotine exposure will enhance fentanyl intake. Prior to testing our hypothesis, we replicated previous studies using a 4-day nicotine paradigm. Rats were pretreated with a low dose of nicotine (2x, 30 μg/kg/0.1 mL, intravenous) or saline for 4 consecutive days during early adolescence (PN 28-31) or adulthood (PN 86-89). Following nicotine exposure, animals underwent operant self-administration for the psychostimulant, cocaine, (500 μg/kg/infusion (inf)) or fentanyl (2.5 μg/kg/inf). We successfully show that adolescent, but not adult, nicotine exposure enhances cocaine reinforcement in male rats. Similarly, we illustrate adolescent nicotine exposure enhances fentanyl self-administration, independent of sex. Overall our data have important clinical implications, identifying factors that may underlie the opioid epidemic and inform policy makers and clinicians when prescribing opioids to adolescent nicotine users.

Biliary Apical Sodium Bile Acid Transporter Expression Is Regulated Via Mast Cell Farnesoid X Receptor during Cholestatic Liver Damage

Discipline: Life Sciences
Subdiscipline: Physiology/Pathology

Vik Meadows*; Lindsey Kennedy and Heather Francis, *Indiana University School of Medicine*

Abstract: Cholangiopathies are diagnosed at advanced stages leading to poor prognosis. Mast cells (MCs) infiltrate the liver during damage release histamine (HA) and act via H1-H4 HA receptors (HRs). Cholangiocytes and MCs express apical sodium bile acid transporter (ASBT); farnesoid X receptor (FXR) and H2HR. Introduction of MCs into WT and MC deficient ($Kit^{W\text{-}sh}$) mice increases liver damage, biliary proliferation/liver fibrosis, and total bile acid(TBA) levels. We **aimed** to determine if loss of MC FXR signaling alters biliary FXR and ASBT, injury and hepatic fibrosis via HA/H2HR signaling. WT or $Kit^{W\text{-}sh}$ mice were subjected to tail vein injection of cultured MCs pretreated with PBS (PBS-MCs) to induce liver damage or the FXR inhibitor, Z-guggulsterone (10μM, FXR-MCs) and sacrificed 3 days later. Hepatic damage, ductular reaction, biliary senescence, ASBT expression and liver fibrosis were induced in WT and $Kit^{W\text{-}sh}$ mice injected with PBS-MCs; whereas, these parameters were reversed in mice injected with FXR-MCs. HA secretion and H2HR expression increased in serum and cholangiocytes, in WT and $Kit^{W\text{-}sh}$ mice injected with PBS-MCs, but were reduced in with FXR-MC group. Hepatic and serum TBA increased in WT and $Kit^{W\text{-}sh}$ mice injected with PBS-MCs and were reduced in FXR-MCs groups. Inhibition of MC FXR decreases biliary ASBT expression, liver injury and hepatic fibrosis via downregulation of HA signaling. Manipulation of BA transporters, receptors and MC mediators may be a therapeutic route for patients with cholestatic liver damage.

Life Sciences: Biochemistry

Elucidating the Role of Enolase 2 during HCMV Infection

Discipline: Life Sciences
Subdiscipline: Biochemistry

Isreal Moreno* and Joshua Munger, *University of Rochester*

Abstract: Human cytomegalovirus (HCMV) is a leading cause of birth defects and causes severe illness in immunocompromised individuals. Understanding how the virus manipulates cellular metabolism provides insight into an emerging host-pathogen interaction that can potentially lead to novel therapeutic targets, an important goal as many current HCMV therapies have poor bioavailability and elevated toxicity profiles. HCMV induces numerous metabolic activities and modulates the expression and activity of a variety of host metabolic genes. For many of these changes, it is unclear how they contribute to successful infection. One gene that we find to be induced during infection is the neuron-specific Enolase 2. My data show that targeting Enolase 2 with shRNA results in a decreased activation of glycolysis as well an approximate 8-fold reduction in the production of infectious virus. However, knockdown of Enolase 2 has little impact on the accumulation of genes representative of the various HCMV life cycle stages, which suggests a defect late in the viral life cycle, for example, assembly, trafficking, or secretion. Consistent with this, loss of Enolase 2 results in less infectious particles per packaged genomes. It remains unknown how viral infection induces the expression of neuronal specific genes and how the expression of such genes affects viral life cycle. Future experiments will address these issues, and elucidate how Enolase 2 contributes to HCMV infection and HCMV-induced metabolic reprogramming.

Discovery and Development of Novel Natural Products with Antibiotic Function

Discipline: Life Sciences
Subdiscipline: Biochemistry

Diego Trujillo*, *University of California, San Diego* and Mark Walker, *The University of New Mexico*

Abstract: Natural products (NPs) are chemical compounds produced by living organisms. Historically, NPs have been used for a wide variety of applications. The broad range of NP applications reflects the incredible diversity of NPs that exists in nature. One key application of NPs has been antibiotics. Many antibiotics currently in use are either NPs or NP-derivatives. However, because of the emergence of antibiotic resistance, it is crucial to develop new approaches to discovering NP antibiotics. We hypothesize that yeast display coupled with directed evolution can be used to create libraries of novel NPs that can be screened for antibiotic activity. To test this hypothesis, we study Ribosomally Synthesized and Post-Translationally Modified Polypeptides (RiPPs). Because RiPPs are genetically encoded, they are a well-suited system for building and screening large libraries of NPs.

Select RiPP biosynthetic gene clusters were cloned such that upon expression, the NP would be anchored to the cell wall of yeast. After expression, immunostaining and flow cytometry can be used to detect the presence and extent of modification of these surface displayed peptides. Preliminary results show we can successfully display our unmodified peptide of interest on yeast cell surfaces. The next step in this project is to induce expression of the enzyme that modifies the precursor peptide. With conformation of modification of the displayed peptide, we will generate and screen libraries of these NPs these novel compounds for antibiotic activity.

Amyloid β Receptor-Mediated Cellular Internalization: New Alternatives for Treating Alzheimer's Disease.

Discipline: Life Sciences
Subdiscipline: Biochemistry

Luis Rodriguez[*] and Jevgenij Raskatov, *University of California, Santa Cruz*

Abstract: Although Alzheimer's disease (AD) was first diagnosed over a hundred years ago, 47 million people worldwide are still losing their lifetime memories, and no therapies are currently available to prevent AD.

Amyloid beta (Aβ) is a 42-residue aggregation-prone protein implicated in the pathology of AD. Evidence linking Aβ cellular uptake and toxicity has burgeoned, and mechanisms underlying this association are subject of active research. Two major, interconnected questions are whether Aβ uptake is aggregation-dependent and whether it is sequence-specific. We recently reported that the neuronal uptake of Aβ depends on peptide chirality, suggesting that the process is predominantly receptor-mediated. Over the past decade, the cellular prion protein (PrP^{C}) has emerged as an important mediator of Aβ-induced toxicity and of neuronal Aβ internalization. We observed by flow cytometry and confocal microscopy that the soluble, non-fibrillizing Aβ(1-30) peptide recapitulates full-length Aβ stereoselective cellular uptake, allowing us to decouple aggregation from cellular receptor-mediated internalization. Moreover, we found that Aβ(1-30) uptake also depends on PrP^{C} expression. NMR characterization allowed us to identify the docking site on PrP^{C} where Aβ(1-30) binds. Our findings therefore identify a specific sequence within Aβ that is responsible for the recognition of the peptide by PrP^{C}, as well as PrP^{C}-dependent cellular uptake. Further uptake stereodifferentiation in PrP^{C}-free cells points towards additional receptor-mediated interactions as likely contributors for Aβ cellular internalization.

Taken together, our results highlight the potential of targeting cellular surface receptors to inhibit Aβ cellular uptake as an alternative route for future therapeutic development for AD.

RNA Polymerase II Interactome Analysis for the Characterization of Transcriptional Stress

Discipline: Life Sciences
Subdiscipline: Biochemistry

Dominique Baldwin[*] and Amber Mosley, *Indiana University School of Medicine*

Abstract: Messenger RNAs (mRNAs) are produced from specific target DNA regions by RNA polymerase II (RNAPII) in eukaryotes. RNAPII regulation is dependent on its dynamic phosphorylation throughout transcription. Though much is understood about RNAPII transcription, the cellular mechanisms to compensate for perturbations to essential genes are not characterized. Through interrogation of the RNAPII protein-protein interaction network using quantitative proteomics, differential interactions can be identified which may reveal novel insights into the function of each mutant of interest. Previous work in our group utilized a mutant variant of the RNAPII phosphatase Ssu72 that led to improper transcription termination due to RNAPII hyperphosphorylation. This study utilizes a hyperactive Ssu72 mutant variant that perturbs transcription termination and causes hypophosphorylation of RNAPII. The differential protein-protein interactions with RNAPII were analyzed via affinity purification (AP) quantitative mass spectrometry (MS) using tandem mass tag (TMT) labeled S. cerevisiae samples in which a core RNAPII subunit, Rpb3, was used as a purification bait. These results were compared to a system with the wild-type enzyme as well as to the results previously obtained from cells with loss of function mutations in Ssu72. Protein-protein interaction analysis shows increased interactions between RNAPII and many transcription regulatory factors in cells containing hypophosphorylated RNAPII. These findings provide evidence of general transcription regulators that may also play a role in transcriptional stress mitigation. Protein-protein interaction networks provide new insight into essential regulatory protein functions that pair with other systems approaches such as transcriptomics.

Life Sciences: Biology & Animal Sciences/Zoology

Diverse Climatic Condition of Beef Cattle Production in Hawaii

Discipline: Life Sciences
Subdiscipline: Animal Sciences/Zoology

Mandeep Adhikari[*1]; C.N. Lee[2]; Jared McLean[3]; Ryan J. Longman[4]; Matthew P. Lucas[5]; Melelani A. Oshiro[2]; Sean B. Cleveland[3]; Thomas W. Giambelluca[5] and Yanghua He[1], *(1)Department of Molecular Biosciences and Bioengineering, University of Hawaii at Mānoa, (2)Department of Human Nutrition, Food and Animal Sciences, University of Hawaii at Mānoa, (3)Hawaii Data Science Institute, University of Hawaii at Mānoa, (4)East West Center, (5)Department of Geography and Environment, University of Hawaii at Mānoa*

Abstract: Hawaii is known for its unique land topography, climate, and environment. Hawaii differs from other states in the mainland of the United States in terms of connectivity and accessibility. Hence, it faces diverse challenges to grow foods to feed its population. Beef is Hawaii's third important agriculture commodity and it contributes significantly to the state's economy. Diverse micro-climatic variations and landscape make Hawaii most favorable for cattle production. Despite plentiful resources, the state relies heavily on the import of meat and meat products from the mainland. Primary data on the beef production including ranch location, ranch size, cow number, market weight and age, carcass percentage, and price will be collected from farm-gates and slaughterhouses. Secondary data on climate variables like temperature and rainfall will be used to map the ranches. Broad datasets from the research will be analyzed to attain the following goals:

1. Micro-climatic zones of Hawaii will be explored and will be mapped with ranching practices, which comprises production system, feeding, breeding and management.
2. Prevalent adaptation practices and interventions being implemented by ranchers from different climatic zones will be investigated to acclimatize with climate extremities and global climate change.
3. Local demand and supply, and key climatic belt that drives major volume of beef supply and consumer preference towards local beef in local market will be inquired.

Research outcomes can be efficient tools in developing strategies to cope up with global climate change impact in beef production, food security and over all development of beef sub-sector in Hawaii

The Systematics of North American *Rhizopogon* Using Modern Molecular Techniques

Discipline: Life Sciences
Subdiscipline: Biology (general)

Thelmalyn Montenegro* and Alija Mujic, *California State University, Fresno*

Abstract: *Rhizopogon* is a genus of truffle-forming fungi that form mutualistic relationships with Pinaceae trees, the family of pine trees, which are critical to the healthy function of coniferous forests. *Rhizopogon* species possess reduced morphology compared with other fungi, and traditional identification methods based upon morphology have failed to accurately describe the true species diversity of the genus. The purpose of this study is to investigate the diversity of *Rhizopogon* species at the subgeneric level, and how different they are across various geographic regions of North America, with a particular focus upon the Pacific Northwest. Previous work has failed to address subgeneric level systematic relationships in *Rhizopogon* species, and the taxonomic delimitation of species is in need of refinement. To answer these research questions, modern phylogenetic experimental techniques will be used to analyze DNA sequence datasets of *Rhizopogon* species, including the historical type material from which species were originally described. The approach that will be used includes molecular genetic and systematic techniques, specifically Sanger sequencing, maximum likelihood, and Bayesian phylogenetic analyses of multilocus DNA sequence datasets. Overall, the results and conclusions of this research will have implications for future systematic studies of many fungal genera and provide valuable information for federal land use managers where sensitive species of *Rhizopogon* are found.

Developmental Impacts of Arsenic and Uranium Mixture Exposure in Zebrafish

Discipline: Life Sciences
Subdiscipline: Biology (general)

Oscar Lujan* and Matthew Salanga, *Northern Arizona University*

Abstract: Arsenic (As) and Uranium (U) are naturally occurring elements found in the earth's crust with levels varying between locations, which can contaminate ground water, and impact drinking water sources. The Navajo reservation for example contains unregulated wells that are used daily and may exceed current EPA maximum contaminant levels (MCL) of 10 µg/L As and 30 µg/L U (EPA 2001, 2000). Research has elucidated some of the effects of ingesting either As or U contaminated water using translational models such as zebrafish and rats. These models have demonstrated developmental effects including a decrease in kidney tubular function, induction of specific cancers, and an impairment in progeny development, however, these experiments generally employ doses that are much higher than what is commonly encountered (Homma-Tekeda 2013, Tokar 2010, Rodriguez 2002). Furthermore, literature is extensive when investigating As and U effects individually, there is currently no research that analyzes As and U in combination and its impacts on general human development. The fish embryo toxicity test (FET), developed by the Organization for Economic Cooperation and Development (Scheil 2009) was utilized to test the hypothesis that low-dose uranium and arsenic mixture exposure induces negative developmental outcomes. Embryonic zebrafish are raised in 24-well plates, one embryo per well containing 2-mLs of varying concentrations of sodium arsenite (NaAsO2) and uranyl nitrate ($UO_2(NO_3)_2$). Zebrafish will be scored based on general morphology development every 24-hours after exposure for a total duration of 96-hours. We predict a dose dependent increase in abnormal development and mortality with increasing metal concentrations.

Evidence of Evolution in American Alligators (*Alligator mississippiensis*) Affected By Endocrine Disrupting Chemicals

Discipline: Life Sciences
Subdiscipline: Biology (general)

Yeraldi Loera* and Shane Campbell-Staton, *University of California, Los Angeles*

Abstract: In an increasingly polluted world, contaminants are disrupting biological function and may be eliciting evolutionary responses. The wildlife at Lake Apopka, Florida could possibly be experiencing this evolutionary pressure from a pesticide spill in the 1980s. The released organochlorine pesticides are persistent organic contaminants that function as endocrine disrupting chemicals. These endocrine disruptors are known to affect steroidal hormone levels, resulting in the dysregulation of reproductive development. Exposed populations of American alligators (*Alligator mississippiensis*) at Lake Apopka consequently display widespread aberrant sexual development and maturation. Recent work has also highlighted

abnormal changes in gene expression in this population. Specifically, exposed alligators exhibit an incomplete recapitulation to normal transcriptional profiles by follicle stimulating hormone (FSH), an essential signalling molecule for sexual maturity and reproductive function. Whether selection has acted on this response to FSH rescue remains unexplored. This study will investigate the role of endocrine disrupting chemicals on the evolution of adaptive resistance via changes to FSH responses in the exposed alligator population of Lake Apopka, Florida. Towards this end, I will quantify changes in gene expression and describe the affected genetic regulatory networks associated with responses to FSH to identify the potential mechanisms of adaptation for resistance in the population. Uncovering the signatures of selection on the variation in plasticity for these transcriptional traits can ultimately aid in understanding the nature of adaptive responses to contaminants and their impacts on evolutionary trajectories.

Life Sciences: Cancer Biology

Delineating the Mechanism Adenylate Kinase 4 Exerts on Nucleotide Metabolism in Lung Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ivan Salladay-Perez* and Nathan Lanning, *California State University, Los Angeles*

Abstract: In a variety of human cancers, it is well observed that altered bioenergetics must be sustained in order to maintain the cancer cell phenotype. In Brief, there are known genes that play a role in sustaining energy flux; however, recent events show that without the expression of an Adenylate Kinase 4 (AK4), an isoenzyme localized in the mitochondrial matrix, intracellular adenine nucleotide concentrations are significantly altered. Under normal conditions, this protein has a phosphotransferase function which transfers a phosphate anion to and from adenine nucleotides (2ADP >> ATP + AMP). AK4 can also catalyze the reaction GTP + AMP $\boxed{\leftrightarrow}$ GDP + ADP and sustain critical energy flux of nucleotides in the cell. However, knocking down the expression of AK4 resulted in an even increase in all adenine nucleotides (ATP, ADP, and AMP's) suggesting that there are other nucleotide governing mechanisms that is influenced by AK4 activity. Therefore, a metabolomic profile is necessary to highlight the global impact AK4 exerts on all the metabolites in the cancer cell system. To do this, cell lines will be transfected with siRNA targeting the AK4 protein translation in human lung adenocarcinoma cells. It is hypothesized that without the expression of an AK4 protein there will be indirect or direct disruptions in the global nucleotide pools by interacting with other nucleotide regulating mechanisms; such as, *de-novo* nucleotide biosynthesis, nucleotide salvage pathways, or by using guanine nucleotides as phosphate donors. The outcome of this study will add to the small library of AK4 biology.

Arginase 1 Alters the Tumor Microenvironment in Pancreatic Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Rosa Menjivar*; Wenting Du; Christopher Halbrook; Camille Hollins; Carlos Espinoza; Fatima Lima; Ashley velez; Stefanie Galban; Yaqing Zhang; Costas Lyssiotis and Marina Pasca di Magliano, *University of Michigan*

Abstract: Pancreatic ductal adenocarcinoma (PDA) is characterized by an abundant fibroinflammatory stroma, composed of fibroblasts and immune cells, mostly myeloid cells. Myeloid cells are required for PDA tumor growth. Pancreatic cancer myeloid cells express high levels of Arginase 1 (Arg1). Arg1 is an enzyme that metabolizes and depletes L-arginine from the tumor microenvironment and it is a signature marker of immunosuppressive macrophages. L-arginine is an amino acid required for CD8$^+$ T cell function. CD8$^+$ T cells are important for killing tumor cells and are scarce in PDA. Based on these observations, I test the hypothesis that myeloid cell polarization in the tumor microenvironment mediates immune suppression in PDA through expression of Arg1. Here, I used a genetically engineered mouse model (LysM-Cre;Arg1$^{f/f}$) to delete Arg1 from myeloid cells. I implanted primary mouse pancreatic cancer cell lines into the pancreas of C57BL/6 LysM-Cre;Arg1$^{f/f}$ and wild type (WT) mice. I then evaluated tumor volume and growth by MRI imaging and investigated changes in immune cell infiltration by co-immunofluorescence, RT-qPCR, and mass cytometry analysis. Preliminary results show a (1) decreasing trend in tumor growth and volume in LysM-Cre;Arg1$^{f/f}$mice, an (2) increase in extracellular L-arginine, and (3) significant changes in immune cell infiltration. Among these changes is an increase in iNOS expression (a marker of inflammatory macrophages), and an increase in CD8$^+$ T cell infiltration and activation in the pancreatic tumor microenvironment compared to WT. These results support the notion that Arg1 might be a moderator of immune suppression in pancreatic cancer.

Exploiting Glutamine Dependencies in Pancreatic Cancers

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Mr. Joel Encarnacion-Rosado* and Alec Kimmelman, *Department of Radiation Oncology, Perlmutter Cancer Center, New York University School of Medicine, New York, NY, USA.*

Abstract: Pancreatic ductal adenocarcinoma (PDAC) is a highly aggressive disease with a 5-year survival rate less than 10%. PDAC cells activate a non-canonical glutamine metabolic pathway essential to increase the level of NADPH, an important metabolite for redox balance, promoting tumor growth. Targeting glutamine metabolism using CB-839, a small molecule that target glutaminase, the first step of glutaminolysis failed in PDAC. CB839 treatment only blocks the carbon utilization of glutamine and not the nitrogen portion which is critical for anabolic processes. We have previously shown that PDAC cells can rewire their metabolism and overcome GLS inhibition within days. We hypothesize that using a glutamine analogue, such as 6-Diazo-5-oxo-L-norleucine (DON), will provide a new therapeutic avenue for PDAC.Here, we used a recently develop prodrug of DON (DRP-104), which has better pharmacological properties and less toxicity compared to DON. Glutamine blockage using this compound lead to a profound decrease in proliferation, TCA cycle metabolites and mitochondrial basal respiration in a panel of PDAC cells. In vivo studies using a syngeneic orthotopically transplantation model in pancreas demonstrated a significant decrease in tumor growth. Bulk RNA-seq studies demonstrated a decrease in transcriptional signature of ECM and hypoxia, which was confirm by histology, suggesting the role of the TME in the response to glutamine blockage. Currently, we are testing the role of this drug using an autochthonous PDAC mouse model.

PP2A Inhibition Overcomes TRAIL Resistance in Triple-Negative Breast Cancer Cells

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Julio Pimentel* and Gen Sheng Wu, *Wayne State University School of Medicine*

Abstract: Triple-negative breast cancer (TNBC) is an aggressive disease that does not respond to widely used targeted/endocrine therapies because of the absence of progesterone, estrogen and HER2 receptors. Previous studies indicate the majority of TNBC cells are highly sensitive to TRAIL-induced apoptosis, but the development of TRAIL resistance limits its efficacy. In this study, we evaluated the effects of protein phosphatase 2A (PP2A) inhibition on TRAIL-induced cell death in TRAIL-resistant TNBC cells. We generated two TRAIL-resistant cell lines from TRAIL-sensitive parental cells (MDA-MB-231 and SUM159). We found that both TRAIL resistant cell lines are sensitive to the PP2A inhibitor LB-100 as compared to their corresponding TRAIL-sensitive counterparts. Similar results are confirmed in a panel of TNBC cell lines that are intrinsically resistant to TRAIL. Mechanistically, we found that TRAIL-resistant TNBC cells express higher basal levels of AMP-activated protein kinase (AMPK) than TRAIL-sensitive cell lines. We also observed that acute treatment with LB-100 increases PD-L1 expression in TNBC. Collectively, these data suggest that the inhibition of PP2A activity could be a novel therapeutic strategy for overcoming TRAIL resistance in TNBC.

The JAK/STAT3 Pathway Drives Myeloid Cell-Mediated Immunosuppression in Pancreatic Cancer

Discipline: Life Sciences
Subdiscipline: Cancer Biology

Ashley Velez*; Kristee Brown and Marina Pasca di Magliano, *University of Michigan*

Abstract: Pancreatic Ductal Adenocarcinoma (PDAC) is a lethal malignancy with a 5-year survival rate of 10%. PDAC is characterized by a dense stroma with a heterogeneous population of fibroblasts and infiltrating immune cells. While the immune infiltration is abundant, it is mostly composed of immunosuppressive cells, such as tumor associated macrophages and myeloid derived suppressive cells (MDSCs). Hence, effective anti-tumor $CD8^+$ T cell responses are not elicited in PDAC. My preliminary data shows that the JAK/STAT3 signaling pathway is active in the stroma, specifically in fibroblasts and myeloid cells. My main goal is to investigate the role of JAK/STAT3 signaling pathway in driving immunosuppression in myeloid cells. **I hypothesize that targeting JAK/STAT3 pathway in myeloid cells will lead to reversion of the immunosuppressive phenotype aiding in the treatment of pancreatic cancer.** To understand the role of JAK/STAT3 signaling in the polarization of myeloid cells and consequently in tumor growth, I used a genetically engineered mouse model (LysMCre;$Stat3^{f/f}$) that depletes *Stat3* specifically in myeloid cells. Using this mouse model, I implanted syngeneic tumor cells orthotopically in the pancreas. After two weeks, I weighed the tumor, and assessed the immune infiltration by Mass Cytometry (CyTOF). Deleting *Stat3* from myeloid cells resulted in a significant decrease in tumor mass compared to controls. Analysis showed a decrease in macrophages and increase in memory $CD8^+$ and $CD4^+$ T cells, suggesting a decrease in the immunosuppressive capacity of the myeloid cells. Currently, I am investigating the mechanism by which JAK/STAT3 pathway disruption impairs tumor growth.

Life Sciences: Cell/Molecular Biology

Regulation of MLK3 during Ovarian Cancer Cell Cycle Progression

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Luis Cedeno-Rosario*; David Honda; William Taylor and Deborah Chadee, *The University of Toledo*

Abstract: Mixed lineage kinase 3 (MLK3) is a serine/threonine MAP3K that promotes the activation of multiple mitogen-activated protein kinase pathways, and is required for invasion and proliferation of ovarian cancer cells. Often, ovarian cancer patients are diagnosed when ovarian cancer is in the late stages and treatment options are limited. Therefore, understanding the molecular mechanisms that cause aberrant division of ovarian cancer cells will give us insights to create novel cancer therapies. Recent studies showed that inhibition of MLK activity causes G2/M arrest in HeLa cells; however, the regulation of MLK3 during ovarian cancer cell cycle progression, and specifically during mitosis, is not known. Based on this, we hypothesize that a Cyclin-dependent kinase (CDK) regulates MLK3 during ovarian cancer cell division. To investigate this regulation, ovarian cancer cells were treated with nocodazole to arrest cells in mitosis, and MLK3 was analyzed by western blot. Interestingly, we found that MLK3 exhibited a mobility shift in the nocodazole-treated cells. To test whether this is a phosphorylation event, we performed a phosphatase treatment assay. We found that phosphatase treatment eliminated MLK3 mobility shift, which suggests that the shift is due to phosphorylation. Furthermore, we tested several kinase inhibitors for their effects on MLK3 phosphorylation and found that inhibition of CDK1 prevented MLK3 phosphorylation. This suggests that CDK1 promotes phosphorylation of MLK3 in mitotic ovarian cancer cells. Based on these findings, we want to further characterize the mechanisms by which CDK1 regulates MLK3, and the significance of this phosphorylation in mitotic progression.

Circadian Clock Protein BMAL1 Regulates Melanogenesis through Mitf

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Soumyadeep Sarkar* and Shobhan Gaddameedhi, *Washington State University*

Abstract: Solar ultraviolet radiation B (UVB) is a leading cause of various types of skin diseases, including sunburn erythema, photoaging, and skin cancer. As a protective response against UVB, the skin has various inbuilt defense mechanisms, including DNA repair, cell cycle, apoptosis, and melanin synthesis. Previously, the efficiency of DNA repair and cell cycle has been shown to vary according to time of the day in a 24-hour circadian fashion, which is due to direct transcriptional regulation of essential genes by an internal timekeeping mechanism called the circadian clock. As melanin is a primary UVB protectant, we wanted to investigate the role of the circadian clock in regulating the ability of the skin to synthesize melanin. We hypothesized that crucial gene/s involved in melanin biosynthesis is transcriptionally regulated by the circadian clock protein BMAL1, a rate-limiting clock protein. In this study, using various in vitro and in vivo models, we established that the microphthalmia-associated transcription factor (MITF), which is a rate-limiting protein in melanin synthesis, is expressed in a 24-hour rhythmic fashion in the presence of core clock protein, BMAL1. Our chromatin immuno-precipitation and qRTPCR assays further demonstrated that BMAL1 binds to the promoter region of *MITF* and transcriptionally up-regulates its expression. Finally, we report that BMAL1 overexpression increases melanin synthesis, which protects human melanocytes and melanoma cells from UVB radiation. In conclusion, our findings provide novel insights into the circadian clock influence of melanin synthesis and its role in protection against UVB mediated DNA damage and genomic instability.

A Mouse Model for a Telomeropathic Mutation in ACD/TPP1

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Jacqueline Graniel* and Jayakrishnan Nandakumar, *University of Michigan*

Abstract: Chromosome ends face two problems: the end-protection (end-to-end fusions) and the end-replication (progressive telomere shortening) problems. To combat these problems: the shelterin complex and telomerase exist. Mutations in genes important for telomerase and/or shelterin function result in diseases termed telomeropathies, the most prominent example being dyskeratosis congenita (DC). Severe shortening of telomeres in patients with DC results in depletion of stem cells and bone marrow failure, the primary cause of death.

ACD/TPP1 is the only shelterin component known that protects chromosome ends AND recruits telomerase to telomeres. We have previously defined regions of ACD/TPP1 that are critical for recruiting telomerase and characterized the consequences of a patient-derived DC mutation in ACD/TPP1 (K170Δ) resulting in decreased telomerase activity, impaired recruitment, and short telomeres in cells. While these studies provide a direct cause-effect relationship, they do not provide insights into stem cell dysfunction *in vivo*.

Using CRISPR/Cas9 technology we generated mice with an equivalent patient mutation in ACD/TPP1 (K82Δ). Using flow cytometry & fluorescence *in situ* hybridization (Flow-FISH), we measured telomere length from bone marrow in Generation 1 (G1)-Generation 5 (G5) mice and found decreasing telomere length with increasing generations. As we continued to breed G4 and G5 mutant mice, we observed a striking decrease in fertility including defects in litter size, testicular size, sperm counts and sperm morphology. Typically, patients with DC do not live long enough for us to know if fertility defects are a hallmark. More work needs to be done to understand the differences seen here.

Life Sciences: Ecology/Evolutionary Biology I

Projected Climate Change Amplifies Non-Native Bee Invasion in Hawaii

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Jesse Tabor[*], *University of Hawai'i at Hilo* and Jonathan Koch, *University of Hawaii Hilo*

Abstract: Island ecosystems may be particularly sensitive to the ecological impacts of invasive bee species. Invasive bees can disrupt the novel environment through disease spread and competition for resources with native fauna. Based on the niche conservatism principal, species distribution models are used to predict the potential invasive range of an adventive species. We analyzed the native and invasive niche spaces for eight adventive bee species in Hawai'i, to test the hypothesis that species conserve their native climatic niche in the invaded range. Furthermore, we predicted climatically suitable niche spaces for invasive bees under future climate scenarios in Hawai'i. Models were calibrated from the species novel niche in Hawai'i.

Cross continental data shows that a shift in the observed climatic niche occurred between native and introduced ranges, providing evidence that invasive bee species can occupy a climatically distinct niche space following its introduction into a new area. Under future climate scenarios, climatically suitable regions for the investigated invasive bees will expand in Hawai'i. Our models suggest climate change will remove current climate barriers thus allowing invasive bees to enter new habitats. Therefore, management of invasive bees in Hawai'i should account for the potential of climate change induced biological invasions into new areas around the Hawaiian archipelago.

Dietary Isotopic (δ13C, δ15N) Values of Muscle Tissue from Cayo Santiago Macaques Sampled before and after Hurricane Maria

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Eva Mann[*1]; Alex DeCasien[2]; Michael Platt[3]; Michael Montague[3]; Susan Antón[2]; Rhonda Quinn[4] and James Higham[2], *(1)New York University, (2)Department of Anthropology, New York University, (3)Department of Neuroscience, Perelman School of Medicine, University of Pennsylvania, (4)Department of Sociology, Anthropology & Social Work, Seton Hall University*

Abstract: Dietary isotopic analysis of primate tissues is a powerful tool in understanding responses to environmental changes and the utilization of fallback foods by primate populations. Biobanking primate tissues provides comparative samples for current and future populations facing ecosystem disruptions related to climate change. This study analyzed muscle tissue δ^{13}C and δ^{15}N values from two cohorts of rhesus macaques from Cayo Santiago, Puerto Rico from before and after Hurricane Maria in 2017, as well as food sources collected on the island in 2018 (species=8). Macaque samples included biobanked, RNA*Later* treated muscle tissues of HH group (n=29) from 2016, and both fresh and RNA-later preserved samples of KK group (n=47) from 2018. We first compared δ^{13}C and δ^{15}N values between the 2018 fresh and RNA-later preserved muscle replicates to understand effects on the biogenic dietary isotopic signal. Our results show a significant (p<0.001) decrease in δ^{15}N values (3.9‰) and a slight but significant (p<0.01) increase in δ^{13}C values for RNA*Later* preserved tissues (0.20‰). Comparisons between the HH and KK group δ^{15}N and δ^{13}C values from muscle tissue preserved in RNA*Later* revealed a slight (0.34‰) but significant (p<0.001) increase in the average δ^{13}C value from 2016 to 2018, and no significant difference in the average δ^{15}N value. We interpret our results to indicate that the vegetative loss from Hurricane Maria influenced a modest increase in C$_4$ resource consumption. Based on behavioral observations and food isotopes, potential food items that were consumed at higher levels included seaweed, C$_4$ grasses and commercial monkey chow.

The Effects of Nutrient Enrichment and Herbivory Pressure on *Ramicrusta Textilis*-Interactions in St. Thomas, USVI

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Alexys Long[*] and Tyler Smith, *University of the Virgin Islands*

Abstract: Coral reefs are undergoing phase shifts from coral to algal dominance as a result of pressure from many anthropogenic activities. These shifts result in a decline in ecosystem services, including shoreline protection from wave energy, aesthetic value for the tourism industry, and nursery habitat for commercially important fish species. In the NE Caribbean, an invasive macroalga, *Ramicrusta textilis*, is rapidly proliferating across reefs and overgrowing live corals as it spreads. As an emerging aggressive benthic competitor, it is imperative that we gain insight into the factors promoting its expansion and herbivore communities required to repress its growth. A presence/absence experiment will be conducted to test the effects of nutrient enrichment and herbivory pressure on *R. textilis* overgrowth rates of living coral colonies (n=40) for 6 months. The second experiment will observe a regression of *Diadema antillarum* densities (0-10 urchins/m^2) in cages with *Acropora cervicornis* fragments being overgrown by *R. textilis.* Colonies and fragments will be recorded and photos from the videos will be used to make 3D models using Agrisoft Photoscan software. *R. textilis* surface area will be measured from these models. Understanding the drivers of *R. textilis*'s spread and ideal *Diadema* densities for decreasing the alga's cover can help us to manage urchin restoration efforts and Caribbean coral reef health in the future.

The Acclimatization of the Fused Staghorn Coral *Acropora Prolifera* to Non-Natal Locations, within the US Virgin Islands.

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

COLIN HOWE*, *Penn State University* and Mónica Medina, *The Pennsylvania State University*

Abstract: Following the population decline of both Caribbean Acropora species, recent evidence has shown a population increase of a third hybrid taxa called *Acropora prolifera* or fused staghorn coral. Earlier studies describe *A. prolifera* as a viable and reproductive hybrid, which can have implications for future restoration efforts of this threatened taxa. This study aimed to test hybrid viability of *A. prolifera* using a common garden transplant experiment between two geographically distinct locations in St. Thomas, USVI. The transplanted group of coral fragments were outplanted with an equal number of natal fragments directly to the substrate (1 x 2 m). Among the donor colonies, three genotypes from each location were verified using genetic analysis. Every month for nine months, health metrics including growth rates, number of apical tips, and signs of stress including mortality, predation, bleaching, and disease were compared between populations and across genotypes. We hypothesized that transplanted fragments would have reduced health metrics or more signs of stress compared to the natal group. Using linear mixed effects models, transplanted fragments showed no significant differences in growth rates compared to natal fragments. Transplanted fragments did however, show higher predation than natal fragments ($z = 2.12$, $p = 0.033$). Overall, across genotypes there was no significant reduction in health of transplanted *A. prolifera* fragments to a non-natal location. Despite concerns of genetic incompatibilities associated with this hybrid, we found that *A. prolifera* can be successfully propagated to distinct reefs and can be carefully incorporated in current and future restoration programs.

Life Sciences: Ecology/Evolutionary Biology II

Effects of Invasive Plants on Native Plant Phenology and Pollination Success

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Jo'lene Saldívar* and Jeff Diez, *University of California, Riverside*

Abstract: Invasive plant species are one of the largest contributors to global pollinator declines as they often outcompete native annual plants. By altering the flowering time of natives, invasive plants can disrupt native plant-pollinator synchrony, leading to decreased seed set and the eventual decimation of native plant communities. Understanding the degree to which invasives shift native phenology and influence insect pollinator visitation rates will have implications on land management and restoration efforts. Thus, I asked whether invasive plants are effective disruptors of native plant-pollinator communities in southern California and tested the hypotheses that (1) the phenology of native plants and their pollinators will be altered when invaders are present, and (2) removal of invasive plants will result in increased pollinator visitation rates and seed set for native plants. I established 2m x 2m paired plots consisting of two treatments (invasive flowers removed and invasive plants removed entirely) and a control for a total of 15 plots. I recorded plant phenology, flower abundance, and pollinator visitation. This presentation will report the findings of my season-long experiment. By examining the entire growing season, I aim to quantify changes in plant-pollinator interactions such as interaction turnover and rewiring to better inform invasive plant management and habitat restoration.

Long-Term Nutrient Cycling in a Materially Closed Ecosystem

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Luis Miguel de Jesús Astacio*; Kaumudi Prabhakara; Zeqian Li and Seppe Kuehn, *University of Illinois at Urbana-Champaign*

Abstract: Closed Microbial Ecosystems (CES) are hermetically sealed microbial communities that support self-sustaining nutrient cycles using only light as an input. CESs have been proposed as controlled model systems to understand the principles governing ecosystem organization and persistence. However, we do not yet understand how the nutrient cycling capabilities of a CES depend on its community structure and composition. To address this question, we present a new method for making precision measurements of carbon cycling in CES using low-cost piezoresistive pressure sensors. With these devices, we quantify carbon cycling rates in a set of CESs over periods of months. Our data show that previously studied synthetic CES comprised of model organisms exhibit declining carbon cycling rates on long-timescales. We go on to self-assemble CESs using the phototrophic alga *Chlamydomonas reinhardtii* combined with complex, soil-derived, bacterial communities. We find that these CESs persistently cycle carbon on timescales of many weeks. Also, we characterize the limiting nutrients in these CESs as well as their community-level metabolic capabilities. Finally, we use next-generation sequencing to characterize the taxonomic and metagenomic composition of these persistent microbial biospheres.

"Fishing" out the Exomes: An Analysis of Genes Under Selection in Endangered Tidewater Gobies

Discipline: Life Sciences

Subdiscipline: Ecology/Evolutionary Biology

Benjamin Ha*; Marco Morselli; Elizabeth A.C. Heath-Heckman and David Jacobs, *University of California, Los Angeles*

Abstract: The endemic and federally endangered tidewater gobies, *Eucyclogobius newberryi* and *E. kristinae*, inhabit lagoons along the California coast. A recovery plan for *Eucyclogobius* established by U.S. Fish and Wildlife distinguishes six separate management units, each of which contains one or more metapopulations. Intermittent connections and extirpations of lagoonal populations yield local metapopulation dynamics, such as extirpation-recolonization processes. Previous research has analyzed microsatellite and mitochondrial data, which indicated that local populations have high genetic differentiation despite close proximity to one another. Currently, no research has examined the exomes of tidewater goby populations despite the strong likelihood that local isolated populations are subject to different selective pressures, which could potentially be reflected in the gene sequences. I propose to use Expressed Exome Capture Sequencing (EecSeq) to seek SNPs in the DNA coding regions, or exomes, that may be under selection in *Eucyclogobius* populations and management units. EecSeq synthesizes mRNA as “bait” to hybridize and capture relevant exomes *in vitro* from extracted genomic DNA. I will apply EecSeq to historical samples of tidewater gobies collected in the 1990s available in the Jacobs Lab. I plan to identify potential variants in osmoregulatory genes and other unannotated genes. While this study will be the first to examine the exomes of tidewater gobies, it will also provide an understanding of genes under differential selection and illuminate adaptive differences between the populations and management units under investigation. Understanding how interactions between metapopulations function through time is an important factor to the conservation of the tidewater goby.

Improving Trap Design and Placement for Overwintering Spotted Wing Drosophila (*Drosophila suzukii*)

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Ariana Hernandez*; Juan Huang; Larry Gut and Matthew Grieshop, *Michigan State University*

Abstract: Monitoring traps are essential tools for growers and researchers to estimate population levels of pests in agriculture. Spotted wing drosophila (*Drosophila suzukii*) is a detrimental pest of soft fruits that’s caused millions of dollars in damage. Trap design and placement of monitoring traps are of extreme concern to obtain maximum yields of *D. suzukii* and to minimize damage seen on crops. The standard hanging deli cup trap design has been used for both summer and winter morphs of *D. suzukii,* without literature supporting that the trap was optimized for both morphs. With winter morph taking refuge under the leaf litter, a ground trap may be better suited for overwinter trapping. To compare two trap types, the standard cup trap and a dome trap were evaluated in laboratory and field settings. Our laboratory experiment showed that regardless of trap design, placement of the trap was the determining factor for the number of winter morphs captured; furthermore, if a trap was placed on the ground it was six times more likely to capture winter morphs than a hanging trap. In the summer field experiment, the hanging cup trap was the favored trap for wild *D. suzukii* summer morphs and in the winter field experiment the ground cup trap was preferred for wild *D. suzukii* winter morphs, similar to laboratory findings for both morphs. Overall, the morph of *D. suzukii* being targeted should be the determining factor for where traps should be placed to accurately estimate population levels.

Life Sciences: Ecology/Evolutionary Biology III

Coevolutionary History of Coots, Feather Lice, and Bacterial Endosymbionts

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Stephany Virrueta Herrera*[1]; Robert Wilson[2] and Kevin Johnson[1], *(1)University of Illinois at Urbana-Champaign, (2)USGS*

Abstract: Coots (Fulica) are a group of water birds (Gruiformes:Rallidae) comprised of ten species. Like most birds, coots are host to a wide variety of parasites. We obtained samples of one group of ectoparasites, feather lice in the genus Rallicola, from all extant coot species. Achieving this complete species sampling of feather lice presents a unique opportunity to compare the complete evolutionary histories at three scales: birds, parasitic lice, and bacterial endosymbionts of the lice. A phylogeny for the coots was estimated from targeted sequencing of both mitochondrial and nuclear genes. We next estimated the phylogeny coot feather lice (Rallicola) using data from whole genome sequencing. A phylogenomic data set from 1,107 targeted gene assemblies was analyzed using concatenated and coalescent methods and compared that to coot phylogenetic tree. While we found some evidence of cospeciation, host-switching of these parasites has also occurred. Finally, we constructed a phylogeny of the bacterial symbionts in the coot lice using the same genome sequencing reads, which contain genomic reads from these bacteria. Feather lice typically have a single symbiont species which likely provides nutritional supplementation to the feather diet of the lice. We found evidence that different louse species harbored different genera of bacteria, suggesting endosymbiont replacement over the evolutionary history of these parasitic lice.

Unearthed: Exploring the Size of the Rooted World Beneath Our Feet

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Shersingh Joseph Tumber-Dávila* and Robert B. Jackson, *Stanford University*

Abstract: Very little is known about the space occupied belowground by plants in natural systems; however, the size and shape of plant root systems has major implications for our understanding of the earth system and the global cycles of carbon, water, and nutrients. Our aim is to find scaling relationships that can be used to predict the size of plant root systems according to the aboveground size of plants and the environment in which the plants were observed. Generally, much more is known about the size and traits of aboveground plant organs. Furthermore, biomass allocation above- and belowground, commonly referred to as the root:shoot ratio, has been comprehensively studied, whereas the same relationships are not well understood for plant volume or shape. To address these gaps, we created an extensive global dataset including over 2,500 observations of plant volumetric allometry describing the size and shape of plant growth both above- and belowground. The volumetric data was produced using a biometric machine learning algorithm, originally created to trace retinal scans, and a novel plant image analysis software to trace and measure plant profile images gathered from across the globe. Our results show that the volume of plant tissues scales allometrically following universal scaling power laws, similarly to biomass allometry. We also found significant shifts in plant shape above- and belowground across global water availability gradients. This study helps us understand the space taken up by roots in the soil matrix, and how this may change across plant species and climates.

Evolution of a Tandem Gene Family upon Fixation: The Structural and Functional Population Dynamics of a Novel Complex Genomic Region

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Bryan Clifton*; Jamie Jimenez; Ashlyn Kimura; Zeinab Chahine; Carolus Chan; Christine Vu; Shu-Dan Yeh and Jose Ranz, *University of California, Irvine*

Abstract: Species-specific gene expansions are key for adaptation, genetic innovation, and phenotypic diversification; however, high sequence similarity among duplicates has previously impeded their accurate characterization. *D. melanogaster* uniquely harbors such a complex genomic region that is under sexual selection through an impact on sperm competition, *Sdic*. Scrutinizing *Sdic* in 20 geographically diverse populations using reference-quality genome assemblies, read-depth methodologies, and qPCR –which allowed further analysis of 83 individuals– we found 4-8 copies in ~97% of individuals examined. In strains with genome assemblies reliable enough for precise gene annotation, copy number and TE insertion variation result in a unique *Sdic* region per genome. These genomes harbor 31 protein-coding duplicates falling into 13 paratypes with variable 3’ ends and no evidence of pseudogenization. Despite rampant gene conversion, a single paratype has become fixed in all populations examined, functionally diverged at both coding and regulatory levels under positive selection. While doubling copy number within the same genomic background increased male expression over 2-fold, we saw no correlation between CNV and expression across different genomic backgrounds from different natural populations, suggesting that differential genome modifiers play a central role in shaping *Sdic* expression levels. Further, this doubling did not enhance sperm competitiveness, suggesting a fitness cost at high expression levels or a plateau effect. Beyond maintaining a minimally optimal expression level, duplication of *Sdic* copies appears to act as a catalyst of protein and regulatory diversity, detailing a possible evolutionary path that novel gene families can follow toward long-term consolidation within eukaryotic genomes.

Microbial Extracellular Enzyme Activity Across a Climate Gradient

Discipline: Life Sciences
Subdiscipline: Ecology/Evolutionary Biology

Bahareh Sorouri* and Steve Allison, *University of California, Irvine*

Abstract: Understanding the consequences of environmental change for the microbial regulation of carbon and nutrient cycling is a critical need. Specifically understanding microbial community traits, such as extracellular enzyme (EE) activity, can help inform nutrient cycling models and address critical knowledge gaps. We collected data on EE activities and litter decomposition from an 18-month experiment where microbial communities were reciprocally transplanted along a Southern California climate gradient. Communities were from desert, scrubland, grassland, pine-oak, and sub-alpine ecosystems. We aimed to test whether the enzyme activities and decomposition rates of these microbial communities depended on climate variables. Our first hypothesis proposed a “home field advantage” (HFA) of enzyme activity and litter decomposition, whereby microbial communities show highest rates of enzyme activity and decomposition in their home ecosystem. Alternatively, microbial communities might be functionally resilient, whereby transplanted communities produce enzymes and decompose litter at the same rate as native communities. Microbial community EE activities were evaluated with analysis of variance. Enzyme datasets yielding a significant ($p < 0.05$) site by microbial community interaction were further analyzed with Tukey post hoc tests within sites to compare the microbial community EE activities. Results mostly supported functional resilience. Significant interaction effects did not support HFA and instead indicated a home field disadvantage, where transplanted microbial communities displayed higher EE activity than native communities. These enzymatic patterns are consistent with litter decomposition rates, which also supported functional resilience. Our findings are crucial for understanding climate change effects on microbial functioning and improving predictive nutrient cycling models.

Life Sciences: Environmental Science

Insights from Coastal Wetland Restoration: Fungi Help Remove Nitrogen and Microbial Community Analysis Matters in Assessing Restoration Success

Discipline: Life Sciences
Subdiscipline: Environmental Science

Sommer Starr*[1]; Behzad Mortazavi[1]; Saysha Sebren[2]; Taylor Ledford[1]; Erin Smyth[1]; Abigail Griffin Wood[1]; Corianne Tatariw[1]; Lorae Simpson[3]; Julia Cherry[1] and Kevin Kuehn[2], *(1)University of Alabama, (2)University of Southern Mississippi, (3)Florida Oceanographic Society*

Abstract: Coastal wetlands help mitigate the devastating effects of anthropogenic nutrient runoff by removing nitrogen (N), yet these ecosystems are being rapidly degraded or destroyed. While marsh construction has increased, function is not always restored, and little is understood on the role of fungi in marsh N removal through denitrification. We conducted an experimental study on a 33-year-old constructed salt marsh and an adjacent natural marsh from the northern Gulf of Mexico – measuring N removal and fungal biomass at both sites to assess a) the relative contribution of both groups to total N removal and b) whether differences in fungal communities corresponded to functional loss in constructed marshes. N removal was significantly 3x lower in the constructed marsh than the natural marsh ($p < 0.0005$). Both fungal and bacterial denitrification were stimulated when one group of microbes were inhibited in the natural marsh ($p > 0.05$) but neither group experienced competitive release in the constructed marsh ($p < 0.00001$). Additionally, fungal biomass was higher in the natural marsh than the constructed marsh across seasons ($p < 0.05$). Our data suggest that in natural marsh ecosystems, fungi and bacteria compete for N in and each group experiences a release from competition when the other is suppressed and that fungi may contribute as much as 73% of total N removal. Additionally, while denitrification is limited by nitrate availability in natural systems, our data suggest that microbial biomass rather than nitrate availability may limit N removal in constructed marshes.

Assessing the Effects of Using Sheep to Manage Vineyard Cover Crops in Soil Health and Greenhouse Gas Emissions

Discipline: Life Sciences
Subdiscipline: Environmental Science

Noelymar Gonzalez-Maldonado* and Cristina Lazcano, *University of California Davis*

Abstract: California vineyard soils experience a unique set of challenges that make them susceptible to degradation. Cover crops and no-tillage are proposed practices for improving soil health in vineyards; however, their success is dependent on management and termination strategies. Sheep grazing is an alternative for managing cover crops, especially in organic no-till systems; yet, the effects of grazing cover crops in tilled vs not-tilled soil health remain unclear. Also, is it thought that increased cover cropping, no-tillage and sheep grazing could increase soil greenhouse gas emissions (N_2O and CH_4) which are of serious concern in today's drastically changing climate. Therefore, we developed an on-farm full factorial trial testing the following treatments: tillage intensity (tillage, no-tillage) and cover crop termination (grazing, mowing). Soil samples were collected (0-15cm and 15-30cm depth) for quantification of soil biological health (organic matter, active C, NH_4^+, NO_3^-, microbial activity, microbial biomass, and biodiversity). Gas samples were collected for quantification of N_2O and CH_4 emissions. We expect an increase in soil health in grazed no-till soils due to manure inputs and potential organic matter accumulation. These organic material inputs can enhance microbial activity and release of root exudates for nutrient cycling, and potentially promote soil carbon sequestration. However, grazing will likely increment N_2O and CH_4 emissions due to increased biological activity from manure inputs. The results from this project will help us improve soil management recommendations for California wine grape growers to build healthier and resilient soils which are essential for sustaining agricultural, environmental and health quality.

Differentiating Methane Emissions from California Dairy Farms and Their $\delta^{13}C_{CH4}$ Source Signatures from the Farm-Scale to Regional-Scale

Discipline: Life Sciences
Subdiscipline: Environmental Science

Valerie Carranza*[1]; Brenna Biggs[2]; Amy Townsend-Small[3] and Francesca Hopkins[1], *(1)University of California, Riverside, (2)University of California, Irvine, (3)University of Cincinnati*

Abstract: Since 2007, the global mole fraction of atmospheric methane (CH_4) has steadily increased meanwhile the $^{13}C/^{12}C$ isotopic ratio (expressed as $\delta^{13}C_{CH4}$) has shifted to more negative values. This suggests that methane emissions are primarily driven by biogenic sources, however more *in situ* isotopic measurements of CH_4 are needed at the local level to identify which biogenic sources dominate CH_4 emissions. In California, dairies contribute to a substantial amount of CH_4 emissions from enteric fermentation in dairy cows and manure management. In this study, we present seasonal atmospheric measurements of $\delta^{13}C_{CH4}$ from dairy farms in the San Joaquin Valley (SJV) in California using a mobile platform, with cavity ring-down spectrometers, GPS unit for geolocation, and 2D sonic anemometer for wind direction and wind speed. We used $\delta^{13}C_{CH4}$ to characterize emission signatures from enteric fermentation by measuring downwind of cattle housing (e.g., corrals, freestall lanes) and from manure management areas (e.g., anaerobic manure lagoons). Across seasons, enteric fermentation from corrals and freestall lanes were consistently more depleted of $\delta^{13}C_{CH4}$ than manure

lagoons. The mean $\delta^{13}C_{CH4}$ from manure lagoons ranged from -43.16‰ to -47.99‰, whereas the mean $\delta^{13}C_{CH4}$ from cattle housing ranged from -50.71‰ to -60.54‰. Preliminary results at the regional-scale suggests that $\delta^{13}C_{CH4}$ signatures can be used to identify CH_4 emissions from both enteric fermentation and from anaerobic manure lagoons from individual dairy farms. Our findings could improve spatial allocation of CH_4 emissions from dairy farms and constrain the relative contributions from these different sources of emissions in the methane budget.

Pesticides Measured in Roof-Harvested Rainwater from Rural and Urban Communities in Arizona, Using Chromatography-High-Resolution Tandem Mass Spectrometry

Discipline: Life Sciences
Subdiscipline: Environmental Science

Norma Villagomez-Marquez* and Monica Diane Ramirez-Andreotta, *University of Arizona*

Abstract: In arid climates like the Sonoran Desert, rainwater can provide a vital component of water resources. National water quality standards for both potable and non-potable domestic usages of rainwater are thus far undetermined for this new, developing practice. Project Harvest is a co-created citizen science program that educates communities across the state of Arizona on the scientific method. For three years, participants are collecting roof-harvested rainwater samples and sending them to be analyzed for bacteria, organic and inorganic contaminants at the University of Arizona by our team of scientists. Herein the organic chemistry aspect of this project is described, including sample preparation, analytical method development, and preliminary results. We aim to investigate the presence of thirteen target analytes in roof-harvested rainwater by applying liquid chromatography-tandem mass spectrometry (HR-LC-MS/MS). The mass spectrometer was operated in positive and negative modes. Parallel reaction monitoring experiments (PRM) were conducted for pentachlorophenol, glyphosate, nonylphenol, perfluorooctanesulfonic acid, perfluorooctanoic acid, perfluorobutanesulfonic acid, perfluorononanoic acid, and 2,4 dichlorophenoxyacetic acid, in the negative mode. PRM experiments were conducted for chlorpyrifos, prometon, atrazine, simazine, and carbaryl in the positive mode. Other parameters were optimized manually by infusion of standard solutions into the MS. A summary of the detected and non-detected target analyte(s) in roof-harvested rainwater samples in Arizona from 2017 to 2019 will be provided.

Life Sciences: Genetics

Identifying the Genetic Causes of Retinitis Pigmentosa in a Multigenerational Pedigree Using Extremely Low-Coverage Whole Genome Sequencing (XLC-WGS)

Discipline: Life Sciences
Subdiscipline: Genetics

Jose Lazaro Guevara*[1]; Bryan Flores Robles[2]; Javier Hernandez[1] and Marcus Pezzolesi[1], *(1)University of Utah, (2)San Pedro Hospital*

Abstract: Next-generation sequencing (NGS) technologies are powerful for discovering disease-causing variants, although their cost currently limits their utility in a clinical setting. Mitigating the high cost of NGS, extremely low coverage whole-genome sequencing (XLC-WGS) allows investigators to leverage the power of these technologies while significantly reducing overall expense. Here, we investigated the use of XLC-WGS as a cost-effective strategy to identify causal variants within a multi-generational pedigree of individuals with retinitis pigmentosa (RP). RP is a group of genetically heterogeneous eye disorders, with approximately 60 known causal genes, that causes progressive vision loss. We performed XLC-WGS in 17 members of this pedigree, including three individuals with a confirmed diagnosis of RP. Sequencing data were processed using Illumina's DRAGEN pipeline and filtered using genotype quality score (GQX). The resulting variants were analyzed using various variant prioritization tools and disease-causing variants were classified using the ACMG-AMP guidelines. A nonsense mutation (c.1625C>G; p.Ser542Ter) in exon 4 of the *RP1* gene emerged as the most likely causal variant as this variant has previously been identified in a recessive form of RP. We identified two homozygous carriers of this variant among the three sequenced RP cases and three heterozygous individuals with sufficient coverage of the *RP1* locus. In combining pedigree information with XLC-WGS, we validated the utility of this cost-effective approach in identifying disease-causing variants and its potential application in a clinical setting.

Improved β-Cell Function Underlies Resolution of Hyperglycemia in SM/J Mice

Discipline: Life Sciences
Subdiscipline: Genetics

Alex Miranda*; Caryn Carson; Juan Macias; Celine St. Pierre; Heather Schmidt and Heather Lawson, *Washington University in St. Louis*

Abstract: The diabetes-obesity axis centers on glycemic control, where excess adiposity demands elevated insulin production, causing β-cell stress and dysfunction, resulting in chronic hyperglycemia. High fat-fed SM/J mice provide a unique opportunity to study the relationship between obesity and diabetes because they spontaneously transition from hyperglycemic-obese at 20 weeks of age to normoglycemic-obese by 30 weeks. The goal of this study is to understand how insulin homeostasis, β-cell morphology, and β-cell function change during this remarkable transition. To assess how insulin homeostasis changes, we quantified circulating insulin levels, pancreatic insulin content, and insulin sensitivity in high fat-fed SM/J mice at 20 and 30 weeks of age. To assess β-cell morphological changes, we performed immunohistological staining on pancreatic cross-sections to quantify β-cell mass and mitotic index. To understand how β-cell function changes, we assessed glucose stimulated insulin secretion on isolated islets. We find that during the resolution of hyperglycemia, high fat-fed SM/J mice increase circulating and pancreatic insulin levels while simultaneously improving insulin sensitivity. Concurrently, SM/J mice increase β-cell mass, without elevation of β-cell mitotic index. This increase in β-cell mass coincides with improved insulin secretion efficiency and increased islet insulin content. We interpret the increase in insulin levels, β-cell mass, and β-cell insulin secretion efficiency as evidence for dramatic improvement in β-cell health and functionality. Identifying the physiological and genetic mechanisms underlying this remarkable improvement will provide insight into how β-cell functionality can be maintained during glycemic stress and identify novel therapeutic targets for improving β-cell health in diabetic obesity.

A Massively Parallel Reporter Assay to Investigate the Contribution of Noncoding Variation in Autism Spectrum Disorder

Discipline: Life Sciences
Subdiscipline: Genetics

Tomas Lagunas*; Stephen Plassmeyer and Joseph Dougherty, *Washington University in St. Louis*

Abstract: Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder that affects ~1.7% of the population. Current research has made significant investments in sequencing the genomes of ASD families as a diagnostic method and to further understand the genetic architecture of this complex disease. These studies have revealed an enrichment of mutations in the untranslated regions (UTRs) of ASD affected individuals. Assessment of these variations poses a challenge since these regions do not follow the triplet code and, even with prediction algorithms for RNA secondary structure or motif loss, these mutations must be defined experimentally. Furthermore, UTRs are known to have strong cell type dependency for their functionality; therefore, requiring assessment in appropriate cell types. To address these challenges, I have used a Massively Parallel Reporter Assay (MPRA) to functionally assay several hundred mutations in parallel. From a completed assay that looked at 650 3’ UTR mutations from ASD genomes, I report several candidate 3’ UTR variations that appear to have functional effects on mRNA stability. Additionally, these putative ASD risk variants were validated in a fluorescence reporter assay to determine their effects on protein production. These findings indicate that some of these mutations may contribute to disease risk. My research aims to use this technology to identify which elements in UTRs are functional, identify which mutations can alter function, and test which class of elements contributes to ASD risk. This work will report on the burden of noncoding disease mutations and contribute to our understanding of ASD genetic architecture and UTRs.

Assessing Recall in the Informed Consent Process for a Long-Term Tribally-Based Genetics Study

Discipline: Life Sciences
Subdiscipline: Genetics

Krystal Tsosie*[1]; Kylene Martell[2] and Lyle Best[2], *(1)Vanderbilt University, (2)Turtle Mountain Community College*

Abstract: Preeclampsia (PE), a common pregnancy complication, has higher prevalence in US Indigenous women (9.1%) compared to worldwide (~2-8%). Our Genetics and Preeclampsia Study (GPS) constitutes the only PE genetic investigation in Indigenous women with continual enrollment in one US tribal community since 2004. Few genetic studies exist in tribal communities due to distrust, cultural incongruity with research aims, and barriers to equitable partnerships. Because we documented every researcher-participant interaction, the GPS presents a unique opportunity to assess recall of the informed consent process among Indigenous participants.

We employed a non-random sampling strategy to recruit GPS participants with validated PE case-control status (N=29 and 27, respectively). Participants were asked eighteen open-ended questions to recall specifics of their study involvement (to be matched with original consent forms) and educational attainment, income, and general genetics knowledge.

Early results suggest PE cases more accurately recall study details (such as investigator name and biological sample provided) and speak positively of their study involvement, as cases feel affected by the study question (i.e. “It’s important for my daughter to know she’s at risk”). Ascertainment bias exists; women who are supportive or have neutral opinions of the study are more likely to participate, reflected by differential success in recruiting individuals who have consented once compared to repeat participants (37.5% vs 81.8%, respectively, p=0.0001).

As legacy samples are increasingly deposited in open access datasets outside tribal jurisdiction, communities must not rely on institutional memory alone. Studies recruiting a “representative cohort” must also be cognizant of who is excluded.

Life Sciences: Marine Sciences

Impacts of *Egregia Menziesii*, a Foundational Alga, on Intertidal Communities in S. California and N. Washington

Discipline: Life Sciences

Subdiscipline: Marine Sciences

Angelina N. Zuelow* and Jennifer L. Burnaford, *California State University, Fullerton*

Abstract: Canopy-forming seaweeds provide shade for smaller algae and invertebrates in intertidal communities, ameliorating low tide abiotic stressors such as ultraviolet radiation, desiccation, and high temperatures. Conversely, canopies can negatively affect understory organisms by limiting settlement, causing physical disruption, and trapping sand. We are examining the effect of *Egregia menziesii,* a canopy-forming foundation species, on intertidal communities, using manipulative experiments in two portions of its geographic range (southern California and northern Washington). We hypothesized that plots with *Egregia* would have higher abundance and richness of other invertebrates and algae than plots without *Egregia*. At each site, we have set up 25 low intertidal plots, each $0.25m^2$ in size, where we randomly assigned the following five treatments (five replicates of each): Natural *Egregia* (no manipulation), –*Egregia* (*Egregia* removed), No-Natural *Egregia* (no manipulation), +*Egregia* (transplanted *Egregia*), or +mimic *Egregia* (plastic *Egregia* mimic). We have conducted community surveys of sessile and mobile organism cover/abundance for two seasons (Summer 2019 and Winter 2020). We have also measured sand depth and temperature at both sites within all plots. Our data show temperature differences between plots with *Egregia* and without *Egregi*a, confirming that *Egregia* can ameliorate heat stress when present. We predicted *Egregia* plots would trap more sand during the winter at all sites but have seen no strong evidence of sediment trapping in any treatment. We expect differences in understory species composition between southern California and northern Washington but predict plots with *Egregia* in both regions will have higher richness and abundance than plots without *Egregia*.

Staying Local: Small-Scale Environmental History Influences the Metabolic Response of Marine Invertebrates to Increased Temperature

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Racine Rangel* and Cascade Sorte, *University of California, Irvine*

Abstract: As ocean temperatures rise, marine species will be exposed to temperatures that are increasingly exceeding their physiological optima. In order to anticipate species' responses to rising temperatures, we need to know the relationship between metabolic rate and thermal history, which itself may vary at small scales in space and time. We measured metabolic rates of hermit crabs (*Pagurus hirsutiusculus*) and mussels (*Mytilus trossulus*) and evaluated the relationship between thermal sensitivity and thermal history. Organisms were collected from 24 tide pools in Sitka, Alaska in which we also recorded temperature every 5 min for 3 months prior to metabolic rate assays. Using respirometry, we estimated resting mass-specific oxygen consumption (MO_2) at three different temperatures (10°C, 18°C, and 26°C) for one hermit crab and one mussel from each tide pool at four seasonal time points. We tested for linear relationships between thermal sensitivity (individual MO_2 slopes) and the following environmental parameters: average, variance, maximum, minimum, and range of pool temperatures. For both species, there were relationships between thermal sensitivity and thermal history; however, the direction of the relationships and most important thermal parameters differed between species and seasons. These findings show that thermal environmental history at small scales strongly influences metabolic response to temperature increase within populations and in ways that differ notably between species and seasons.

Impacts of Stony Coral Tissue Loss Disease on Reef Communities in St. Thomas, USVI

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Kelsey Vaughn* and Marilyn Brandt, *University of the Virgin Islands*

Abstract: The Caribbean is a hotspot for coral disease with broad and devastating outbreaks (Weil et al. 2006). A new and rapidly emerging disease is stony coral tissue loss disease (SCTLD), which originated in the Florida Reef Tract in 2014 and arrived in the US Virgin Islands in January 2019 (Aeby et al. 2019). SCTLD impacts a vast number of corals and we suggest that it may not follow the diversity-disease hypothesis proposed by Mitchell et al. (2002), which states that coral reefs with high species diversity is negatively correlated with disease prevalence. We suggest that SCTLD may be more prevalent in reefs with high coral species diversity. To test this hypothesis, my Masters of Marine and Environmental Sciences (MMES) 2019 cohort examined the prevalence of SCTLD at reefs with either high or low species diversity (determined by National Coral Reef Monitoring Program, NCRMP, data) within the epidemic zone (categorized as where the disease has recently emerged and intermediate susceptible coral species are recently affected) and the endemic zone (where disease has been present > 9 months and intermediate susceptible species are beyond initial infection). Although analysis is still being conducted for this study, our results suggest that sites with higher pre-disease outbreak diversity demonstrate higher instances of disease. This supports the hypothesis that SCTLD follows the opposite trend that is suggested by the diversity-disease hypothesis. These findings will help resource managers better understand the patterns and dynamics of this disease and may aid in the prevention of its continued spread.

Assessing Coral Reef Diversity and Stony Coral Tissue Loss Disease in St. Thomas, USVI

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Stephanie Hibberts* and Marilyn Brandt, *University of the Virgin Islands*

Abstract: Stony Coral Tissue Loss Disease (SCLTD) is a rapidly spreading and a devastating coral disease. It was first found in the Florida Reef Tract in 2014, and has since spread throughout much of the Caribbean. It was first observed in the US Virgin Islands in January 2019 at Flat Cay, and is now present at reefs surrounding most of the island. Since this disease affects 22 species of stony coral it may not follow the diversity disease hypothesis, meaning the disease could be more prevalent in high diversity reef sites. More than fifty sites previously assessed in 2017 and 2019 under NOAA's National Coral Reef Monitoring Program were surveyed again in 2020. At both times before and after the SCTLD outbreak, benthic and coral demographic surveys were used to calculate coral cover, coral density, coral diversity, and disease prevalence. The sites were split by zone, with the endemic zone as the area where SCTLD was known to be present for longer than 9 months, and epidemic zone as where the disease was more recent, between 2-6 months. Preliminary results show that within the endemic zone, the more diverse sites (from 2017 and 2019 data) had lower change in coral cover, but higher change in diversity. Further work will identify how species composition changed at these sites from before to after the outbreak.

Partner Preference in the Intertidal: Possible Benefits of Ocean Acidification to Sea Anemone-Algal Symbiosis

Discipline: Life Sciences
Subdiscipline: Marine Sciences

Natalie Coleman*, *Western Washington Unviversity* and Ellie Meyer, *Oregon State Unviersity*

Abstract: Ocean acidification (OA) threatens marine species and is projected to increase severity over 50 years. Areas of Salish Sea that experience seasonal upwelling of low pH water are particularly susceptible to lower pH conditions. While OA literature often describes negative impacts to calcifying organisms, economically important shellfish, and zooplankton, not all marine species may be threatened by OA. Photosynthesizing organisms, in particular, may benefit from OA.

The aggregating anemone, an intertidal organism, hosts photosynthetic symbionts: *Symbiodinium muscatinei* and *Elliptochloris marina.* To determine effects of OA on *A. elegantissima* hosting each symbiont individually, both simultaneously, or no photosymbionts, all types were subjected to one of three pCO_2 levels (600 ppm, 1200 ppm, or 1800 ppm) of OA for 10 weeks. We measured photosynthetic efficiency of symbionts, respiration rate of hosts, reactive oxygen species (ROS), and CZAR score. Over the experiment, photosynthetic efficiency of symbionts did not change in ambient pCO_2 but decreased at high pCO_2 . At intermediate pCO_2, efficiency of green symbionts decreased, but efficiency of the brown symbiont increased. Anemone respiration rate and CZAR score both increased with decreasing pH but were significantly higher in individuals hosting *S. muscantinei* and individuals lacking photosymbionts. ROS concentration increased with decreasing pH and was greatest in *S. muscatinei*. Over the experiment, anemones starting with 50% of each symbiont shifted toward a higher percentage of *S. muscatinei* with decreasing pH. Results suggest *S. muscatinei* will benefit from elevated pCO_2 and *A. elegantissima* hosting them may have a competitive advantage under future OA conditions.

Life Sciences: Microbiology I

Sewer Biofilm Microbiome and Antibiotic Resistance Genes As Function of Pipe Material, Source of Microbes and Disinfection: Field and Laboratory Studies

Discipline: Life Sciences
Subdiscipline: Microbiology

William R. Morales Medina* and Nicole Fahrenfeld, *Rutgers University*

Abstract: Colonization of Sewer biofilms by antibiotic resistance gene (ARG) carrying bacteria may degrade water quality during sewer overflows and threaten the health of utility workers. The objectives of this research were to evaluate the (1) microbiome of sewer biofilms and their potential to accumulate ARGs and (2) susceptibility of sewer biofilms to bleach disinfection. First, field biofilm samples were collected from sewer systems. Next, an annular biofilm reactor was used to simulate the sewer environment while controlling the pipe material (concrete vs. PVC). The reactor was operated either as fed semi-batch with sewer sediment and synthetic wastewater (Sed-SB) or fed with a continuous flow of raw sewage (WW-CF). The abundance of ARGs, human fecal marker, and 16S rRNA gene copies were measured with qPCR. Amplicon sequencing was performed to compare the microbiome between samples. Finally, the susceptibility of reactor biofilm to bleach was evaluated using viability qPCR. Field and WW-CF biofilms contained the most ARG copies. The microbiome composition varied between the different biofilm samples. Sed-SB biofilm had greater diversity but less bacterial concentration than biofilm from WW-CF. Pipe material did not affect the abundance of ARGs. However, log-removal following bleach treatment suggested that biofilms growing on PVC were more susceptible to be dislodged from the surface than on concrete. Following the treatment, viable bacteria carrying ARGs were detected and the microbiome composition shifted. This study showed that sewer biofilms can accumulate bacteria carrying ARGs and that the bleach disinfection protocol tested here do not completely remove the biofilms.

Let’s Talk about Diarrhea Baby, Let’s Talk about Trophs and Cysts

Discipline: Life Sciences
Subdiscipline: Microbiology

Carolina Mendoza Cavazos[*], *University of Wisconsin - Madison* and Laura Knoll, *University of Wisconsin-Madison*

Abstract: *Entamoeba histolytica* is an extracellular parasite that causes amebic dysentery and liver cysts. Globally, 50 million cases are reported per year, impacting mostly the developing world. The infection takes place in the gastrointestinal tract after ingesting infectious cysts in contaminated food or water. The parasite’s life cycle involves interconversion between two morphological stages, essential for disease propagation and pathogenesis. However, no animal model can replicate *E. histolytica’s* life cycle. In this study, we tested the susceptibility of mice with deletions in program cell death, a critical pathway during infection, when orally challenged with *E. histolytica*. Mice received trophozoites via oral gavage. To our surprise, *E. histolytica* cysts were observable in fecal samples via immunofluorescence staining. To determine if the newly generated cysts were infectious, mice received the cysts via oral gavage. Weight loss, a typical symptom of infection, was observed 7 days post-infection (dpi) for the trophozoite challenge and 15 dpi for the cyst challenge. In terms of cysts shedding, the peak of infection was 9 dpi. Lastly, cysts are storable as whole feces at -20° C for up to 6 months. Immediate future work will focus on intestinal inflammation via histological staining. Currently, mouse infections with *E. histolytica* are performed using invasive surgical methods that circumvent the natural infection route and have low rates of success. We provide the first animal model that supports the entire life cycle of *E. histolytica* and results in infectious cysts, a parasitic form previously unable in the laboratory environment.

Pathogenic Allodiploid Hybrids of *Aspergillus* Fungi

Discipline: Life Sciences
Subdiscipline: Microbiology

Jacob Steenwyk[*1]; Abigail Lind[2]; Laure Ries[3]; Thaila dos Reis[3]; Lilian Silva[3]; Fausto Almeida[3]; Rafael Bastos[3]; Thais de Fernanda Campos Fraga da Silva[3]; Bonato Vania[3]; André Pessoni[3]; Fernando Rodrigues[4]; Huzefa Raja[5]; Sonja Knowles[5]; Nicholas Oberlies[5]; Katrien Lagrou[6]; Gustavo Goldman[3] and Antonis Rokas[1], *(1)Vanderbilt University, (2)Vanderbilt University School of Medicine, (3)Universidade de São Paulo, (4)University of Minho, (5)University of North Carolina at Greensboro, (6)Katholieke Universiteit Leuven*

Abstract: Interspecific hybridization substantially alters genotypes and phenotypes and can give rise to new lineages. Hybrid isolates that differ from their parental species in infection-relevant traits have been observed in several human-pathogenic yeasts and plant-pathogenic filamentous fungi, but have yet to be found in human-pathogenic filamentous fungi. We discovered 6 clinical isolates from patients with aspergillosis originally identified as *Aspergillus nidulans* (section *Nidulantes*) that are actually allodiploid hybrids formed by the fusion of *Aspergillus spinulosporus* with an unknown close relative of *Aspergillus quadrilineatus*, both in section *Nidulantes.* Evolutionary genomic analyses revealed that these isolates belong to *Aspergillus latus,* an allodiploid hybrid species. Characterization of diverse infection-relevant traits further showed that *A. latus* hybrid isolates are genomically and phenotypically heterogeneous but also differ from *A. nidulans, A. spinulosporus,* and *A. quadrilineatus*. These results suggest that allodiploid hybridization contributes to the genomic and phenotypic diversity of filamentous fungal pathogens of humans.

In the Search for New Drugs Against Trypanosoma Cruzi Using Cutting-Edge Imaging Technology

Discipline: Life Sciences
Subdiscipline: Microbiology

Karsten Amezcua[*1]; Felipe Rodriguez[1]; Jonathan Dimmock[2] and Rosa Maldonado[1], *(1)The University of Texas at El Paso, (2)University of Saskatchewan*

Abstract: Chagas disease (ChD) is caused by *Trypanosoma cruzi (T. cruzi),* an intracellular protozoan parasite. ChD has a global mortality of 15,000 annual deaths, and approximately, 8-10 million people are infected. There is growing concern in the United States as autochthonous cases of ChD have been reported in the southern region. The two available treatments are only partially effective and highly toxic. N-aroyl derivatives and α, β-unsaturated ketones have been previously tested against *Leishmania,* a closely related parasite, demonstrating selective toxicity towards the microorganism. The objective of this study is to evaluate a drug library consisting of 21 α, β-unsaturated ketones and 15 N-aroyl derivatives as anti-trypanosomal treatments. We hypothesized there will be an effective candidate from the drug collection against *T. cruzi*. High-throughput screening was used to evaluate this. Epimastigote forms of *T. cruzi* CL Brenner Luc were used to assess the anti-parasitic activity of the compounds through a luciferase viability assay. The compounds showed low toxicity to human osteoblast cells (U2-OS). Thirteen of α, β-unsaturated ketones and three N-aroyl compounds showed good anti-trypanosomal activity with an EC50 ranging from 0.016 to 1 µM and a selectivity index (SI) ranging from 16.5 to 3,125. Our future directions include a) to determine the compounds activity against amastigotes (intracellular form of the parasite) by High-Content imaging (HCI), b) tested in the murine model of Chagas disease and c) to explore the possible mode of action of the lead(s) compounds.

Life Sciences: Microbiology II

Genomic Analysis of *Bacillus Cereus* isolates

Discipline: Life Sciences
Subdiscipline: Microbiology

Naomi Niyah[*] and Jasna Niyah, *The Pennsylvania State University*

Abstract: *Bacillus cereus* group isolates have been associated with diseases in animals and humans, as well as possessing insecticidal and probiotic properties. Molecular methods such as 16S rRNA sequencing lacks the ability to differentiate between species of the *B. cereus* group. Hence, the goal of this study was to utilize whole-genome sequencing (WGS) to characterize *B. cereus* group isolates from diverse sources, and evaluate the distribution of virulence genes across phylogenetic clades.

197 isolates from various sources underwent WGS using Illumina and 109 sequences were retrieved from NCBI or obtained from the CDC. Sequences were assembled using SPAdes, and analyzed using BTyper. Phylogenetic clades were identified based on *panC* gene sequence and species were identified using ANIb.

Clade I was represented by 5 isolates, clade II by 43, clade III by 74, clade IV by 82, clade V by 45, clade VI by 45, and clade VII by 12 isolates. 98% of isolates carried one or more of the enterotoxin genes, 74% carried one or more *hbl* genes, 94% one or more *nhe* genes, 16% *cytK-1*, 42% *cytK-2*, and 27% one or more *ces* genes. Based on the Fisher's exact test, isolates from clades III and IV had a significantly higher occurrence of *hbl* operon ($p<0.001$), while clades IV and VII had significantly higher occurrence of *cytK-1* and *cytK-2*, respectively ($p<0.001$). Consistent with previous studies, we found a broad distribution of virulence genes across all clades. However, further work is needed to assess the relationship between virulence gene profiles and cytotoxicity.

Discovery and Characterization of Novel Ecotype of Pandemic *Vibrio Parahaemolyticus* with Increased Cold Sensitivity

Discipline: Life Sciences
Subdiscipline: Microbiology

David Silva[*1]; Jordan Wolfkill[2]; Hailey wallgren[1]; Boris Ermolinksy[2]; Daniele Provenzano[2] and Jeffrey W. Turner[3], *(1)Texas A&M University Corpus Christi, (2)University of Texas Rio Grande Valley, (3)Texas A&M University-Corpus Christi*

Abstract: *Vibrio parahaemolyticus* is the leading cause of gastroenteritis worldwide, partly as a result of clonal expansion of the highly pathogenic O3:K6 serotype. Genomic analysis of environmental *V. parahaemolyticus* 03:K6 strains isolated from the Pacific Northwest (PNW) led to the discovery of a novel ecotype harboring a deletion of seven genes (VP1884 through VP1890), all of which have been found previously to be upregulated upon bacterial culture at cold temperatures. This is noteworthy because, in the PNW, the virulent O3:K6 has been displaced by the O4:K12 serotype as the principal cause of *V. parahaemolyticus* gastroenteritis, perhaps as a result of its inability to survive on ice upon seafood harvest. Allelic exchange with the *lacZ* reporter gene from *V. cholerae* and the *tetR* selection marker from pBR332 was employed to generate VP1884-VP1890 null clones in clinical *V. parahaemolyticus* RIMD 2210633 and BAA-238 strains to test the hypothesis that this set of genes affects bacterial viability at cold temperatures. The VP1884-VP1890 mutants grown at 10°C displayed impaired growth kinetics compared to their WT counterparts. Similarly, survival of the mutant strains at 4°C was severely affected compared to WT counterparts. The rationale for undertaking these experiments is to uncover the molecular underpinnings that reveal the comparative lack of gastroenteritis caused by O3:K6 serotype in the PNW compared to other locations worldwide. The significance of the project is global because favorable selection for temperature sensitivity in *Vibrios* is likely caused by environmental conditions, public health measures and seafood handling practices characteristic of the PNW.

Bifidobacterium Breve'S Unique Role in Vaginal Health and Disease

Discipline: Life Sciences
Subdiscipline: Microbiology

Nicole Jimenez[*1]; Abigail Glascock[2] and Jennifer Fettweis[1], *(1)Virginia Commonwealth University, (2)University of Pennsylvania*

Abstract: *Bifidobacterium* species are key players in early infant gut development via transmission from maternal body sites and the environment. Most of what is currently known about *Bifidobacterium* species comes from studies of gut isolates. Thus, we sought to elucidate the role of *Bifidobacterium* species in the vaginal microbiome. Through a 16S rRNA study of 3094 samples from the Vaginal Human Microbiome Project (VaHMP) and 9205 samples from the Multi-Omic Microbiome Study-Pregnancy Initiative (MOMS-PI) pregnancy cohort, we identified a rare vagitype dominated by *Bifidobacterium breve*. We isolated ten strains of *B. breve* and performed bacterial whole genome sequencing. Comparative genomic analyses with publicly available *B.breve* sequences showed that while genomic architecture and most genes were conserved across all *B. breve* strains, phylogenetic and cluster analysis showed potentially two distinct subclades of *B. breve*. Additionally, vaginal isolates exhibited differences in GC content, additional metabolic genes, and types of mobile elements present. These analyses may reflect preliminary mechanisms of adaptation to the vaginal environment. Intriguingly, clinical and demographic associations differed between women who had high and low abundance levels of *B. breve*. *B. breve* was also found to co-occur with both pathogenic bacterial species and beneficial commensals alike. Thus, *B. breve* may provide a differential function at the interface of vaginal health and disease. This work furthers the understanding of non-lactobacilli microbial dominance in the vaginal microbiome and *B. breve*'s relation to reproductive health and maternal-infant transmission.

Using Metagenomics to Explore Patterns of Genomic Variability in Thermophilic Ammonia-Oxidizing Archaea Populations

Discipline: Life Sciences
Subdiscipline: Microbiology

Rebecca S. R. Salcedo* and José R. de la Torre, *San Francisco State University*

Abstract: Ammonia-oxidizing archaea (AOA) are widespread microorganisms that are key players in the Earth's nitrogen cycle, regulating the formation of essential forms of oxidized nitrogen; nitrite and nitrate. Although the past 15 years have seen a dramatic increase in our understanding of AOA, the majority of this work has been based on select laboratory strains. While metagenome-assembled genomes (MAGs) have increased the known diversity of AOA genomes, our understanding of genetic diversity within natural AOA populations remains poor. Thermophilic AOA (ThAOA) are found in hydrothermal systems around the world and represent the deepest branching lineage of AOA. Four major clades of ThAOA have been identified from laboratory cultivation and genome sequencing. Metagenomes enriched in these organisms are available from multiple sites around the world. In this study, we have focused on hot springs from Northern Spain, the Nevada Great Basin, and the Yunnan Province in China. By aligning individual metagenomic reads to appropriate reference genomes, we have identified sequence polymorphisms within each natural population. We focused on reads with a sequence identity of 98% or greater to ensure that we are analyzing reads from very close relatives (near-species). With this data, we can examine which portions of the genome are the most diverse and/or under different forms of selective pressure. In addition, comparisons between geographically distinct populations will allow us to determine whether these observed patterns are specific to each environment or if they indicate similar adaptive pressures. This is invaluable to help us understand how microbial populations evolve and diversify.

Life Sciences: Cell/Molecular Biology, Microbiology & Other

Identifying a Mutant Respiratory Syncytial Virus G Immunogen As a Vaccine Candidate

Discipline: Life Sciences
Subdiscipline: Cell/Molecular Biology

Ana Nunez Castrejon* and Rebecca DuBois, *University of California, Santa Cruz*

Abstract: Respiratory syncytial virus (RSV) is the leading cause of severe respiratory disease in children and infants. RSV utilizes the G glycoprotein antigen to attach to host cells by interacting with the human chemokine receptor CX3CR1. Antibodies that disrupt this interaction are protective in animal models. However, RSV G as a vaccine immunogen leads to enhanced disease upon RSV infection.

The goal of this project is to create a safe RSV G vaccine immunogen. We will use a structure-guided approach to determine which amino acids to mutate within the RSV G central conserved domain, which has a role in promoting enhanced disease. Mutant RSV G proteins should maintain conformational epitopes required to bind and elicit anti-RSV G antibodies, however the mutations should disrupt the interactions with CX3CR1.

Mutant RSV G proteins were created through site-directed mutagenesis PCR and recombinant protein production in mammalian cells. Binding to anti-RSV G antibodies was measured by Octet RED96e Biolayer Interferometry. Assays to evaluate CX3CR1-binding and CX3CR1-dependent chemotaxis in mammalian cells will be used to determine whether the mutations in the RSV G mutants disrupt the interaction with CX3CR1.

Four mutant RSV G proteins have been created and have been shown to bind anti-RSV G antibodies. They will be tested in the cellular assays.

The ability of the mutant RSV G proteins to bind to anti-RSV G antibodies suggests that these proteins could potentially elicit protective antibodies *in vivo* without promoting enhanced disease. Thus, these mutant RSV G proteins could be safe and protective vaccine immunogens.

Single-Cell Dynamics and Regulation of Hepatitis B Virus Subcellular Trafficking

Discipline: Life Sciences
Subdiscipline: Microbiology

Sofia Romero*; Nuruddin Unchwaniwala; Daniel Loeb and Nathan Sherer, *University of Wisconsin - Madison*

Abstract: Hepatitis B virus (HBV) is a 3.2 kb reverse-transcribing DNA virus that infects the liver and is a leading cause of hepatocellular carcinoma. Although a vaccine offers protection against acute infection, it is not therapeutic. Thus, determining novel HBV-host interactions that support infection may expose targets for new antiviral strategies. During replication, HBV pregenomic (pg)RNA is packaged by Core proteins (Cp) into nucleocapsids where pgRNA is reverse-transcribed to generate, relaxed-circular (rc)DNA. How and when pgRNAs are coordinately trafficked to sites of

nucleocapsid assembly remains poorly understood. Here, we carried out a comprehensive analysis of Cp and pgRNA subcellular trafficking over time using immunofluorescence combined with fluorescence in situ hybridization (IF/FISH) and live-cell imaging for three replication conditions: (I) WT HBV genomes, (II) genomes encoding an assembly incompetent version of Cp(Y132A), and (III) genomes that encode functional Cp but lack the pgRNA packaging signal (Eps-). Interestingly, we observed Cp distribution to start in the nucleus at early time points (24h), followed by a marked shift to the cytoplasm (48h); a transition not observed for either the Y132A Cp mutant or WT Cp from Eps- pgRNA. Live cell imaging revealed Cp nucleus-to-cytoplasm re-localization occurs through two mechanisms; (I) predominantly by nuclear escape during mitosis followed by cytoplasmic retention or (II) punctuated release of nuclear Cp in discrete “burst” events occurring at or near the nuclear membrane. These results indicate that nucleocytoplasmic transitions of Cp/capsids are prevalent, typically occur in conjunction with nuclear membrane breakdown; and that pgRNA and Cp trafficking are interdependent.

Elucidating the Role of IL-9 Secreting CD4+ T Helper Cells in Promoting Mast Cell Expansion in Pulmonary Models of Inflammation

Discipline: Life Sciences
Subdiscipline: Other Life Sciences

Abigail Pajulas[*] and Mark Kaplan, *Indiana University - School of Medicine*

Abstract: Mast cells are tissue resident cells with granules that contain histamine and other proinflammatory mediators. Mast cells are important effectors in immediate type I hypersensitivity reactions. In severe allergic reactions, immunoglobulin E (IgE)-mediated mast cell degranulation triggers localized and systemic anaphylaxis. In allergic asthma, mast cells and T cells interact in the generation of long-lasting inflammation. The molecular mechanisms responsible for mast cell expansion has not been fully elucidated. Because T cells are an important source of the mast cell growth factor IL-9, we are interested in understanding the role of IL-9, and IL-9-producing T cells in mast cell expansion and recruitment. We have identified a role of T helper 9 (Th9) cells in influencing mast cell number and function in pulmonary models of inflammation. Using adoptive transfer models, we have defined a contribution of Th9 cells in immediate hypersensitivity. We have demonstrated that IL-9 expands mast cell progenitor numbers in bone marrow and lung, suggesting that there are systemic effects of local IL-9 production. We hypothesize that increased mature mast cells in the pulmonary system are from recruitment and expansion of progenitor cells rather than expansion of mature cells in situ. Ongoing studies will directly examine the relative contribution and function of the two populations during models of allergic airway inflammation.

Life Sciences: Neurosciences & Other

Validity, Reliability, and Transcultural Adaptations of the Bayley Scales of Infant and Toddler Development (BSID-III-NL) for Children in Suriname

Discipline: Life Sciences
Subdiscipline: Neurosciences

Lauren McLester-Davis[*1]; Arti Shankar[1]; Leila Kataria[1]; Alta-Gracia Hidalgo[2]; Edward van Eer[3]; Aloysius Koendjbiharie[2]; Radha Ramjatan[4]; Virginia Hatch[1]; Melissa Middleton[1]; Wilco Zijlmans[2]; Maureen Lichtveld[1] and Stacy Drury[1], *(1)Tulane University, (2)Anton de Kom University of Suriname, (3)Medical Mission Primary Health Care Suriname, (4)Scientific Research Center Suriname, Academic Hospital Paramaribo*

Abstract: A valid and reliable observational measure of child neurodevelopment is needed in Middle-Income Caribbean Countries, like Suriname. The Bayley Scales of Infant and Toddler Development, 3rd edition (BSID-III), was created for evaluation of United States children. This scale was subsequently validated for use in Dutch speaking children of the Netherlands (BSID-III-NL). Given differences of these First World populations to children in Suriname, the aims of this study were to culturally adapt the BSID-III-NL for Suriname and evaluate its reliability and validity. 299 children between the ages of ten and a half months to twenty-six and a half months were assessed in three regions of Suriname between May 2018 and July 2019. Medical personnel and research assistants were trained in administration of the BSID-III-NL, and images were adapted to be relevant in Suriname. Raw scores were collected for the cognitive, communicative (receptive and expressive), and motor (fine and gross) subscales of the BSID-III-NL. Factor structure was evaluated with exploratory factor analysis and cluster analysis, and reliability of internal consistency was assessed using Cronbach’s alpha coefficient for each subscale. Content validity was approved by examiner and psychologist opinions. Construct validity was approved through agreement of items from cluster analysis where at least 81.56% of all variability was explained by clustering with correct or incorrect responses, and mean scores in subscales increased with age group. Cronbach’s alpha coefficient was above 0.77 for all subscales. This internationally validated developmental measure was found to be reliable and valid in assessing neurodevelopment for children in Suriname.

GPER1 Deletion Protects Against 6-OHDA-Induced Dopaminergic Neuron Degeneration *Via* Upregulation of NURR1

Discipline: Life Sciences

Subdiscipline: Neurosciences

Abdulhafiz Imam Aliagan*; Nathalie Tombo; Yansheng Feng and Jean C Bopassa, *University of Texas Health Science Center San Antonio*

Abstract: Parkinson's disease (PD) is a neurodegenerative disease characterized by the gradual and preferential loss of dopaminergic neurons in the substantia nigra of the brain. The G protein-coupled estrogen receptor 1 (GPER1) has been reported to modulate neuroprotective effects in 6-OHDA and MPTP mouse models of PD. However, the exact mechanism by which GPER1 activation confers neuroprotective effects remains elusive. Here, we evaluated the implication of GPER1 deletion in the development of PD. Using unilateral stereotactic injection of 6-OHDA into the medial forebrain bundle of wild type (WT) and GPER1 knockout (KO) mice, we found that GPER1 KO animals exhibited protection against 6-OHDA induced dopaminergic neuron loss. Compared to WT, GPER1 KO mice had increased striatal dopamine levels and locomotor activity as well as exhibited no amphetamine-induced rotational bias. Specifically, the mRNA and protein levels of the rate-limiting enzyme, tyrosine hydroxylase (TH), were increased in the substantia nigra of GPER1 KO mice compared to WT. In addition, shortly after 6-OHDA injection, the lesioned-GPER1 KO mice had reduced pro-inflammatory gene expression and an upregulation of the nuclear receptor-related 1 protein (NURR1) levels. Our results indicate that Loss of GPER1 signaling protects against 6-OHDA-induced dopaminergic neuron degeneration. Repression of the neurotoxic pro-inflammatory gene expression and induction of dopaminergic neurogenesis stimulated by increased NURR1 levels and activity play an important role in GPER1 KO-induced protection. These results might provide novel potential targets for neuroprotective therapeutic development against PD.

Clustered γ-Protocadherins Regulate Cortical Interneuron Programmed Cell Death.

Discipline: Life Sciences

Subdiscipline: Neurosciences

Walter Mancia Leon* and Arturo Alvarez-buylla, *University of California, San Francisco*

Abstract: Cortical function critically depends on inhibitory/excitatory balance. Cortical inhibitory interneurons (cINs) are born outside the cortex, in the medial and caudal ganglionic eminence (MGE & CGE) of the embryonic ventral forebrain. After long tangential migration into cortex, cIN numbers are adjusted postnatally ,during a period of programmed cell death. Population autonomous and activity dependent mechanisms have been proposed to regulate the death of cINs, but the molecules that regulate programmed cell death remain unknown. Here we show that loss of clustered gamma protocadherins (*Pcdhg*), but not of genes in the alpha or beta clusters, increased dramatically cIN BAX-dependent cell death in mice. Surprisingly, electrophysiological and morphological properties of *Pcdhg*-deficient and wild-type cINs during the period of cIN cell death were indistinguishable. Co-transplantation of wild-type with *Pcdhg*-deficient interneuron precursors further reduced mutant cIN survival, but the proportion of mutant and wild-type cells undergoing cell death was not affected by their density. Transplantation also allowed us to test for the contribution of *Pcdhg* isoforms to the regulation of cIN cell death. We conclude that *Pcdhg*, specifically *Pcdhgc3*, *Pcdhgc4*, and *Pcdhgc5*, play a critical role in regulating cIN survival during the endogenous period of programmed cIN death.

Physiochemical Characterization and Rheological Modelling of Novel Rice Bran Wax-Gelatin Bigels

Discipline: Life Sciences

Subdiscipline: Other Life Sciences

Ariana Saffold* and Nuria Acevedo, *Iowa State University*

Abstract: A bigel is a semi-solid biphasic system composed of an oleogel and a hydrogel phase. The combination of gels results in long-term kinetic stability without the use of surfactants, better skin compatibility, and the ability to carry lipophilic and hydrophilic substances. The objectives of this study were to explore the bigel's physico-chemical properties as the oleogel-to-hydrogel (OG:HG) proportion and hydrogelator concentration changes; to determine compatibility between gel components, and to formulate a rheological model to predict the bigel's mechanical properties. A combination of a gelatin hydrogel and rice bran wax (RBW)-based oleogel with soybean oil as the continuous phase was used for bigel preparation. Bigels were formulated with different hydrogelator (gelatin) concentrations (5, 7 and 10% (w/w)), with a constant RBW (oleogelator) concentration of 10% (w/w), and varying OG:HG ratios (50:50, 40:60, 30:70, 20:80). Confocal microscopy images confirmed the formation of an oleogel-in-hydrogel system for all bigel formulations. Fourier transform infrared spectroscopy showed no unique chemical interactions between bigel components, which suggested that the system is a "true" bigel where two distinct phases are present and stabilized kinetically. Rheology and differential scanning calorimetry suggested an increase in physical interactions within phases that led to improved and enhanced physical and mechanical properties in OG:HG ratios 40:60 and 50:50. A modified Boltzmann Sigmoidal equation successfully modelled the bigel rheological behavior and captured the non-linear enhancement in gel strength. The successful characterization of this system can be used to tailor its properties for specific applications in the food, pharmaceutical and cosmetic industries.

Life Sciences: Neurosciences, Developmental Biology & Biochemistry

From Human Genetics to Structure and Function: Recurrent SMARCB1 Mutations Reveal a Conserved Baf Complex–Nucleosome Interaction Conserved for Millennia

Discipline: Life Sciences
Subdiscipline: Biochemistry

Alfredo Valencia*, *Harvard University* and Cigall Kadoch, *Dana-Farber Cancer Institute*

Abstract: BAF chromatin remodeling complexes are multi-protein molecular machines that remodel chromatin architecture to regulate gene expression, however the subunit-specific mechanisms by which this activity is achieved remain incompletely defined. SMARCB1 (BAF47) is a core subunit of BAF complexes, and recent genetic sequencing studies have revealed an accumulation of single amino acid mutations in the highly conserved, yet functionally uncharacterized C-terminal domain (CTD) of SMARCB1, which cause the neurodevelopmental disorder, Coffin-Siris syndrome (CSS). Given its conservation through yeast, I hypothesize that these syndrome-associated mutations disrupt the fundamental, nucleosome remodeling activity of BAF complexes. In order to assess my hypothesis, I used a variety of biochemical (peptide pull-down and chromatin remodeling assays), structural (3D-protein NMR), and chromatin mapping (ChIP-seq and ATAC-seq) experiments to define the molecular and genome-wide regulatory consequences of recurrent SMARCB1-CTD single-residue mutations, implicated in CSS. Intriguingly, through peptide pull-down assays we find that the SMARCB1-CTD directly binds nucleosomes and that all CSS-associated mutations disrupt this interaction. Furthermore, single amino acid SMARCB1-CTD mutations significantly abrogate mSWI/SNF complex-mediated chromatin remodeling activity in vitro and DNA accessibility in human cells (by ATAC-seq), without changes in genome-wide complex localization (by ChIP-seq). Lastly, 3D-structural determination of this region through protein NMR revealed an alpha helix structure with a positively charged cluster of amino acids that are highly mutated in human disease. Taken together, these studies provide the first molecular mechanism of the intellectual disability disorder CSS, and unmask a major, evolutionarily conserved function of SMARCB1 that dates back over 900 million years.

Elucidating Novel Roles for the Transcription Factor Sox9b in Cardiovascular Development

Discipline: Life Sciences
Subdiscipline: Developmental Biology

Layra Cintrón-Rivera* and Jessica Plavicki, *Brown University*

Abstract: Congenital heart defects (CHD) are the most common type of birth defect and the leading cause of infant death in the US. CHD result from disruptions to cardiac and great vessel development. The pharyngeal arch arteries (PAA) are the vascular precursors that give rise to the great vessels, the vascular structures that connect the heart to the periphery. Clinical data suggest that human mutations that disrupt SOX9 function are associated with great vessel and cardiac defects. Thus, to study Sox9b functions in cardiovascular development, we have generated transgenic tools to manipulate Sox9b function in a cell-type specific manner. Zebrafish are a great model for studying cardiovascular development as embryos obtain oxygen through passive diffusion from the water in which they develop. As a result, embryos can survive with severe vascular malformations that would otherwise be embryonically lethal in mammalian models. Zebrafish have two *SOX9* orthologues, *sox9a* and *sox9b*. Our findings indicate that global loss of Sox9b function severely disrupts PAA development. Specifically, we observed stenosis of the PAAs, blockage of the outflow tract, and coarctation of the ventral aorta. Currently, we are characterizing the cell types surrounding the PAAs that may also contribute to the observed phenotypes. Thus far, we have found that global loss of Sox9b function disrupts neural innervation of the pharyngeal arches. Additional experiments will address how loss of Sox9b function affects the developing musculature and pericytes. Together, these findings reveal novel functions for Sox9b and contribute to our understanding of the molecular mechanisms underlying CHD.

Hippocampal Modulators of Delayed Recall: Human Connectome Project in Aging at UCLA

Discipline: Life Sciences
Subdiscipline: Neurosciences

Tyler James Wishard*[1]; Timothy Ly[2]; Marcela Caldera[2]; Taylor Kuhn[2] and Susan Bookheimer[2], *(1)University of California, Los Angeles, (2)UCLA*

Abstract: The hippocampus, a vital brain region for memory processing, is composed of distinct subfields. Here, we investigate hippocampal subfield volume alterations at different ages and assessed the correlations with memory capabilities. 278-participants aged 36-96 years were collected as part of the Mapping the Human Connectome During Typical Aging Study at UCLA (mean age = 58.4 years, 57.9% female). We used a 3-Tesla MRI scanner to acquire a MPRage T1-weighted image for visual reference during anatomical segmentation obtained using Freesurfer version 6.0 software (Iglesias et. al, 2015). Memory was measured using the Rey Auditory Verbal Learning Test (Rey, 1941), which verbally presents a list of 15 unrelated words to the participant who is instructed to repeat each word recalled, with five learning trials. Following a second interference list of the same length, a delayed recall of this word list was assessed. A stepwise linear regression was performed to examine the relationship between the delayed recall score and age. We found that age strongly predicted delayed recall performance ($r = -0.355$, $p < 0.0001$), where older adults scored lower. This association is strengthened by NIH Toolbox-Fluid Composite score and left hippocampal subfield CA1 volume ($R^2 = 0.252$). Overall, the

hippocampal fissure volume increased with age, while volumes for other subfields decreased. These findings suggest that a reduction in CA1 subfield volume in conjunction with increased age and declining fluid cognition is associated with a decline in memory abilities. CA1 subfield volume could indicate risk of memory impairment across the adult lifespan.

Characterizing Social and Neuroanatomical Abnormalities in the VPA Rat Model of Autism

Discipline: Life Sciences
Subdiscipline: Neurosciences

Pablo Juarez*; Kayla Horton-Sparks; Vanessa Hull and Veronica Martinez-Cerdeño, *University of California, Davis*

Abstract: Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder characterized by deficiencies in social communication and repetitive patterns of behaviors. Although the pathological basis of ASD is not well known, it has been suggested that deficits in the cortical GABAergic interneuron population may contribute to the ASD phenotype. Exposure to the anticonvulsant drug, Valproic Acid (VPA), during early gestation has been associated with an increased risk of developing ASD. Given its strong association with promoting ASD development, we sought to create a VPA rodent model of ASD to better understand the etiology that governs this disorder. We administered one dose of VPA (400,500 or 600mg/kg) at embryonic day 12.5 (E12.5), representing a crucial time of neurodevelopment. The offspring of VPA exposed dams were then analyzed for behavioral abnormalities and deficits in cortical GABAergic interneurons. Specifically, Parvalbumin (PV+) interneuron subtypes, Chandelier (Ch) and Basket (Bsk) cells, both of which decrease in number in human ASD. Relative to saline treated animals, we found that in utero exposure of 400-600mg/kg VPA doses decreased social interaction in VPA rats. Furthermore, male and female pups exposed to the 400mg/kg VPA dose showed a significant decrease in PV+ Ch cell number (50% and 44%, respectively), while the number of Bsk cell number only decreased in males (18%). The higher VPA doses (500 and 600mg/kg) produced a series of phenotypical abnormalities not consistent with the human ASD phenotype. We conclude that the 400-E12.5 VPA autism rat most closely models a human ASD brain both behaviorally and anatomically.

Life Sciences: Plant Sciences/Botany

Geographic Distribution, Phylogeny and Pathogenicity of Botryosphaeriaceae and Diaporthaceae from *Juglans Regia* in Chile

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Israel Jimenez Luna* and Philippe Rolshausen, *University of California Riverside*

Abstract: Walnut (*Juglans regia*) is a major world nut crop for its production and trade. In the last decade Chile has increased their walnut production reaching 100 thousand tons in 2018. The high incidence of fungal vascular diseases in crop production systems threatens long- term growth and revenue. For example, the family *Botryosphaeriacea*e has been previously reported as a major factor limiting tree/vine productivity in Chile and given its host range we hypothesized that it could also affect walnut production. The goals of our project were to: 1) identify fungal species associated with English walnut limb dieback and canker through morphological characteristics and DNA sequencing comparisons, 2) determine the geographic distribution of fungal species in different walnut orchards across Chile, (3) complete Koch's postulate to determine the degree of virulence of the multiple identified fungal species. We identified three main *Botryosphaeria* species (*N*. *parvum*, *D*. *mutila*, *D*. *seriata*) and two *Diaporthaceae* species (*D*. *cynaroidis*, *D*. *australafricana*) across Southern region in Chile. Furthermore, pathogenicity tests were conducted using the stems of two-years-old Chandler walnut trees and identified *N*. *parvum* and *D*. *australafricana* as the most aggressive species and *D*. *seriata* and *D*. *cynaroidis* as the least aggressive species. This study provides identity and pathogenicity of fungal species in walnut supporting reports from other perennial cropping systems. This research is an essential step towards the development of successful disease management strategies.

Targeted and Controllable Chloroplast Bioengineering By Nanomaterials *in Planta*

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Israel Santana* and Juan-Pablo Giraldo, *University of California, Riverside*

Abstract: Plant nanobiotechnology is an emerging field that utilizes nanomaterials to study and engineer plant biological mechanisms. There is a large potential for applying the unique physical and chemical properties of nanomaterials to chloroplast biotechnology. Chloroplasts are prokaryotic like photosynthetic organelles making them excellent targets for bioengineering technologies due to their high expression of polycistronic genes, lack of silencing mechanisms, and their ability to isolate genes in parental lines. Current chloroplast biotechnologies are limited to a handful of plant species (<10) due in part to the absence of efficient gene delivery mechanisms. Herein, we used two nanomaterial platforms for targeted delivery of transgenes and biochemicals to chloroplasts in *Arabidopsis* thaliana*.* Both nanomaterials contained a rationally designed chloroplast targeting peptide containing biorecognition motifs allowing targeted delivery into organelles. Single-walled carbon nanotubes (SWCNT) were complexed with a polycistronic GFP plasmid. The infiltrated SWCNT complex

demonstrates GFP expression in chloroplasts, confirmed by confocal microscopy and RT-qPCR. Furthermore, functionalized quantum dots (QDs) were used for targeted biochemical delivery into chloroplasts of leaves to bioengineer redox states. The QDs formed inclusion complexes with methyl viologen (MV) a non-specific herbicide and ascorbic acid (Asc) an antioxidant chemical. Treatment with QDs allowed specific tunable changes in chloroplast redox status detected with redox-sensitive fluorescent dyes. Together, these results highlight strategies for detection and targeted delivery of nanomaterials into specific organelles that can allow controllable bioengineering of plant chloroplasts for a broad range of applications from improving the understanding of plant biology, enhancing crop yields, to transform plants into technology.

Rapid Phenotyping of Sweet Corn Ears with Computer Vision for Modern Breeding

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Juan Gonzalez* and Marcio Resende, *University of Florida*

Abstract: Originally grown by several Native American tribes since Pre-Columbian times, fresh market sweet corn is a staple of American culture found in traditional recipes. Fresh market sweet corn is the only corn that is commercialized as a vegetable, picked at milk stage, and sold with little to no processing—resulting in strict ear expectations such as size, color, and shape. Thus, breeders must adhere to these strict demands whilst improving other traits such as disease resistance. Currently, these ear traits are measured by hand and suffer from subjectivity and lack of reproducibility. While genotyping technologies have advanced rapidly in modern plant breeding, phenotyping technologies lag behind. This disparity creates a bottleneck because accurate phenotype information is necessary to leverage useful genomic information. Computer vision tools are useful to develop high-throughput phenotyping in agriculture. We set out to develop a computer vision algorithm using open-source python-based packages to measure yield component traits relevant to fresh market sweet corn from photographs. Overall our algorithm is highly adaptable and automatically and accurately (< 95% for all traits) measures length, width, tip fill, taper, and color for any number for ears against a black background; it can also categorize hybrid ears according to the USDA quality grades. We are working on adapting it as a publically available package. In conclusion, we show that a computer vision approach can be used to rapidly phenotype ears for important fresh market traits. We show that this can be incorporated into breeding programs to reduce cost and resources.

The Population Dynamics and Evolutionary History of the Highly Polymorphic California Endemic *Calochortus Venustus* (Liliaceae)

Discipline: Life Sciences
Subdiscipline: Plant Sciences/Botany

Adriana I Hernandez*; Jacob Landis and Chelsea Specht, *Cornell University*

Abstract: The California endemic *Calochortus venustus* displays striking variation in floral pigmentation, leading us to question the boundaries of species delimitation. Individuals within a population can range in petal color from a continuous spectrum of red to white, and purple or yellow, with variation in petal spots too. This hypervariability is only observed at the southern range, while northern populations are almost exclusively white. The phenotypic spatial distribution is suggestive of a ring species; yet the genetic population dynamics had not been questioned prior to this study. DNA from 190 wild individuals spanning the geographic range was sequenced for RAD-Seq, each with quantified data on floral phenotype and geographic coordinates. A hybrid genome from MinION long reads and Illumina short reads was used to map RAD-Seq reads, and call SNPs and genotypes in Stacks. Various genetic clustering techniques were used to compare floral phenotypes with genotypes to evaluate if various color forms were genetically distinct, to infer population structure, and to assess gene flow between identified populations. Results suggest phenotypic variation is not due to genetic differentiation, rather there is geographic cohesion regardless of phenotype within six populations, which have differentiated from each other due to IBD. While genetic evidence does not suggest *Calochortus venustus* is a ring species, the largest genetic differentiation is between northern populations. Inference of phylogeographic history using SNAPP and RAxML suggest a south to north range expansion around both sides of the Central Valley, indicating parallel evolution toward the white morphotype in the northern range.

Materials Research and Physics

Grain Boundary Engineering $ZnAl_2O_4$ Via Rare Earth (RE) Doping with Varying Ionic Radii

Discipline: Materials Research
Subdiscipline: Materials Research

Luis Sotelo Martin* and Ricardo Castro, *University of California, Davis*

Abstract: Nanocrystalline $ZnAl_2O_4$ powder was synthesized with 0.5 mol% $(RE)_2O_3$ (RE=Nd, Y, Sc, In) using reverse-strike coprecipitation. RE dopants were chosen to span a range of crystal ionic radii (88.5 to 112.3 ppm) in order to study segregation behavior in $ZnAl_2O_4$. Resulting powders were analyzed with x-ray diffraction and electron microscopy where Nd exhibited the highest degree of grain boundary segregation. Microcalorimetry measurements were used to analyze the powders' grain boundary and surface energies. The data showed a correlation between dopant characteristics and

interfacial energies, with consequences to stability against coarsening for doped $ZnAl_2O_4$. Nanoindentation experiments on pellets sintered with high-pressure spark plasma sintering (HP-SPS) revealed Vickers hardness is dependent on doping chemistry which may be explained by the effects of dopants on grain boundaries. These results have implications for the future of grain boundary engineering as we continue to understand mechanical properties of nanocrystalline ceramics.

Magnetic Resonance Structural Characterization and Transport Studies of Composite Electrolytes for Solid-State Lithium Batteries

Discipline: Materials Research
Subdiscipline: Materials Research

Daniel Morales*, *Graduate Center of City University of New York*; Lauren O'Donnell, *Hunter College of City University of New York* and Steve Greenbaum, *Hunter College of City University of New York, Dept of Physics*

Abstract: The widespread use of lithium-ion batteries in commercial electronics have fueled many years of research into finding a solid-state substitute for the typical liquid electrolytes. Of the many different alternatives, glassy (Li_2S-P_2S_5) and glass-ceramic (Li_3PS_4) electrolytes have shown great promise, with room-temperature ionic conductivities comparable to commercial electrolytes. However, the brittle nature of glasses leads to mechanical stability issues during charge and discharge. To mitigate this issue, it is possible to synthesize the glass-ceramic with Polyethylene Oxide (PEO), forming a glass-ceramic/polymer composite. Polymer electrolytes containing lithium salts show good mechanical stability during battery cycling, at the cost of significantly decreased ionic conductivity, so it is thought that the composite may balance the two constituent parts.

To that end, we utilized Nuclear Magnetic Resonance to understand the effects that the addition of PEO had on the glass-ceramic, using ^{7}Li, ^{31}P, and ^{1}H as probe nuclei. Magic angle spinning (MAS) NMR was used to describe the local environment surrounding both lithium and phosphorus nuclei as a function of PEO content. Subsequent Diffusometry experiments will reveal how the Li ion dynamics, and therefore electrolyte performance, are affected by the inclusion of the polymer.

Computational Study of the 2D Material MoS2 for Application in Space Lubrication

Discipline: Materials Research
Subdiscipline: Materials Research

Enrique Guerrero*; Rijan Karkee and David A. Strubbe, *University of California, Merced*

Abstract: MoS_2 is a layered material with interesting mechanical, electronic, and optical applications. Doping the material with Ni is known to enhance the tribological properties by reducing friction and wear, increasing the lubricant's lifetime and effectiveness. The high lubricity and its ability to withstand low temperatures and pressures mean Ni-doped MoS_2 is a candidate for lubrication in space applications. An understanding of the mechanisms by which Ni enhances these properties in bulk is lacking and rests upon understanding of how Ni dopes 2H-MoS_2. We use quantum-mechanical density functional theory (DFT) computations to determine structural, mechanical, vibrational, and stability properties of bulk Ni-doped MoS2. We find four suitable, meta-stable dopant sites (Mo substitution, S substitution, and two interlayer intercalated sites) of Ni-doped MoS_2. These results will help guide classical simulations of larger-scale sliding, may help experimentalists identify or create variable dopant samples, and may shed insight as to the relationship between atomic-scale structure and high lubricity.

Use of Lyapunov Exponents to Determine the Presence of Chaotic Behavior in Heart Dynamics

Discipline: Physics & Astronomy
Subdiscipline: Physics

Giraldo Pino* and Flavio Fenton, *Georgia Institute of Technology*

Abstract: The heart is a nonlinear biological system whose electrical activity is responsible for its contraction. The electrical activity can be studied through the application of nonlinear dynamics and chaos theory. Arrhythmias are an irregular complex beating of the heart caused by turbulent electrical pulsing and may cause symptoms ranging from shortness of breath, fatigue, and dizziness, to cardiac arrest. We are interested in investigating the heart's electrical signals during induced Wenckebach rhythms, a type of arrhythmia that can lead to irregular contractions in the ventricles. Our intentions are to identify if the exhibited behavior is irregular or chaotic.

If a system is chaotic, it is possible to find periodic orbits in phase space that can be used to control the system with small perturbations applied at the right times. In contrast, this property is not possible for an irregular turbulent system. In the case of heart dynamics, if chaotic, that would mean there are possibilities for control and termination of arrythmias. Lyapunov exponent (LE) is a value that can be calculated to identify and quantify chaos. Thus, we calculate the LE for this Wenckebach example and find regions for which we can identify chaotic rhythms. Furthermore, we show examples of calculated periodic orbits within the chaotic dynamics.

Mathematics: Applied Mathematics & Mathematical Biology

Solving 3D Anisotropic Elastic Wave Equations Using High Order Mimetic Differences.

Discipline: Mathematics

Subdiscipline: Applied Mathematics

Angel Boada Velazco* and Jose E. Castillo, *San Diego State University*

Abstract: In computational geophysics, modeling seismic data sets in complex 3D anisotropic media represents a significant challenge to numerically solve the 3D elastic wave equation in an efficient way. Fluxes involved in this equation are represented on the model as a non-diagonal symmetric and positive definite tensor which can potentially have jump discontinuities over a material boundary that are not aligned with the coordinate axis. High order mimetic difference operators are discrete analogs of the continuous differential operators and have been extensively used in the fields of fluid and solid mechanics. In our scheme, we model anisotropic fluxes using a novel 3D mimetic flux operator. In this talk, we examine the viability of employing an explicit approach to construct a high order mimetic scheme along with second and fourth order temporal discretization for solving a three-dimensional fully anisotropic elastic wave problem on a staggered mesh.

Projection Methods for Monotone Inclusions in Hilbert Spaces

Discipline: Mathematics

Subdiscipline: Applied Mathematics

Oday Hazaimah* and Yunier Bello-Cruz, *Northern Illinois University*

Abstract: In this study, a conceptual algorithm is proposed to modifying the popular Tseng's forward-backward-forward (FBF) splitting method for solving monotone inclusions. The FBF improves the convergence properties of the classical forward-backward (FB) splitting iteration by adding an extra forward step. The proposed conceptual algorithm generalizes the forward-backward-half-forward (FBHF) iteration by choosing two different projection (forward) steps: (I) in the spirit of the cutting plane method, a backtracking search is performed over the FB step to construct a separating hyperplane which could allow larger step sizes; and (II) two special projection (forward) steps onto half-spaces. Convergence analysis of both proposed methods is presented without assuming the Lipschitz continuity on the smooth operator and with relaxing cocoercivity of the nonsmooth operator. Furthermore, the first variant can be seen as a general iteration which recovers the FBHF iteration. The second variant allows the generated iterates: to be contained entirely in a ball with diameter equal to the distance between the initial and the solution set; and to converge strongly to the optimal solution. Only weak convergence is known for the FBHF splitting method.

Modeling the Impact of a Zika Virus Epidemic Including Vaccination

Discipline: Mathematics

Subdiscipline: Mathematical Biology

Wencel Valega Mackenzie*[1]; Suzanne Lenhart[1] and Karen Rios Soto[2], *(1)University of Tennessee Knoxville, (2)University of Puerto Rico Mayaguez Campus*

Abstract: Zika Virus (ZIKV) is a vector-borne disease that during 2016 had rapidly spread in more than 50 countries around the world. The virus is primarily transmitted through mosquito bites, but also through direct contact from human to human. Severe birth defects and brain damages in babies have been some of the terrible side effects caused by ZIKV if women are infected during pregnancy. In this talk we will present a ZIKV vaccination model as an approach to control the spread of a possible ZIKV epidemic, such as in 2016. Although there is no formal vaccine against ZIKV disease, the National Institute of Allergy and Infectious Diseases has been launching vaccination trials since 2016 to 2019 to determine if a vaccine is effective. Our goal is to investigate ZIKV dynamics under vaccination that includes sexual and mosquito transmission. We compute the basic reproductive number of the model to further analyze the impact caused by perfect and imperfect vaccination rates. We will illustrate some realistic numerical scenarios to measure the effect of vaccination efforts by public health officials. Results of this work show that a high level of sexual transmission can produce larger cases of infections within a very short period of time. Nonetheless, in presence of high level transmission from mosquitoes to humans, the number of infections in humans will take longer to be reflected within the population providing opportunities to control the spread of ZIKV by implementing vaccination.

In silico Mouse Model of Infection and Immunity

Discipline: Mathematics

Subdiscipline: Mathematical Biology

Daniel Jonas*; Michael Kirby and Alan Schenkel, *Colorado State University*

Abstract: An organism's immune system tries to protect it by identifying the presence of pathogens and attempting to eliminate them. The defense is twofold: innate immune cells mobilize rapidly, while acquired immune cells slowly develop into pathogen-killing specialists. These responses incur collateral tissue damage, which anti-inflammatory mediators seek to control. This system of checks and balances is responsible for host survival. Experimental research has demonstrated how vastly complex these interactions are, indicating a place for theoretical and computational study. In this work we develop a comprehensive differential equation model of the immune system by considering interactions between immune system components in the presence of pathogen or tissue trauma. Through this step-by-step construction we explore the dependence of the anti-inflammatory mediators on pathogen levels, and also how they temper the immune response at

the end of infection. We then challenge the “virtual mouse” with typical pathogens of varying virulence and observe the outcomes via model simulation. We find that anti-inflammation can downregulate the activation and proliferation of immune cells or promote apoptosis as cessation mechanisms, suggesting the need for *in vivo* experiments. Bifurcation theory describes how the outcomes of infection depend on model parameters, from which we conclude that initial insult and pathogen growth rate allow us to predict whether or not the *in silico* mouse overcomes the disease in a deterministic framework.

Mathematical Biology & Statistics

Deep Learning Methods for Detecting Structural Variants in Related Individuals

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Erica Sawyer* and Mario Banuelos, *California State University, Fresno*

Abstract: Structural variants (SVs) are observed differences between the sequenced genome of an individual as compared to a reference genome for that species. These differences include deletions, inversions, insertions, and duplications. Since some variations are associated with certain diseases, our work focuses on developing methods to detect such genomic changes. Current DNA sequencing methods may be costly and existing methods rely on high quality data. We present machine learning and deep learning methods to identify deletions in DNA based on genomic information of related individuals.

In this talk, we explain the implementation of neural networks to predict SVs. A neural network - a sequence of linear and nonlinear transformations - takes in training data and uses that information to learn how to classify corresponding test data. Our preliminary model incorporates the observed genomic information of two parents and an offspring to predict locations of SVs in the genome of the child. We also investigate the performance of this model under different neural network architectures using various performance metrics. Furthermore, we discuss the generalization of our model to simultaneously predict SVs for both the parents and the child in different classification regimes.

Low Dimensional Structures in Cardiac Alternans

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Hector Velasco-Perez* and Flavio Fenton, *Georgia Institute of Technology*

Abstract: In order to understand how normal electrical waves that produce the heart’s contraction can turn into arrhythmias, it is necessary to investigate the mechanisms responsible for their initiation and maintenance . For example when cardiac tissue is paced at very fast periods, it can develop what is called a period doubling bifurcation where the propagating electrical waves are not constant anymore and instead, its wavelength varies (alternates) from short to long values as it propagates, which can facilitate arrhythmia induction. This well-known arrhythmic mechanism can be investigated mathematically with models in the form of partial differential equations that describe the cardiac cell’s dynamics in space. However, the number of degrees of freedom required to accurately describe this phenomena in space with these mathematical models can be very large and thus complex to understand. Nevertheless, selecting specific observables and using symmetry reduction methods it is possible to greatly reduce the complexity of the system to just a few key degrees of freedom.

Here we illustrate the reduction of two generic models for cardiac tissue exhibiting various levels of alternans. These model reductions are based on data-driven proper orthogonal decomposition and sparse linear regression methods. We show that it is possible to reduce the dimensionality of the system from 2000 degrees of freedom to just 2. The resulted system of two ordinary differential equations have enough information to closely reproduce the dynamics and bifurcations to alternans obtained from the full simulations of the whole PDE system.

Bayesian Parameter Estimation in a Model of the Cardiac Action Potential

Discipline: Mathematics
Subdiscipline: Mathematical Biology

Alejandro Nieto Ramos*, *Rochester Institute of Technology* and Elizabeth Cherry, *Georgia Institute of Technology*

Abstract: Finding appropriate values for parameters in mathematical models of cardiac action potentials is a challenging task. Previous approaches for this problem include ad-hoc techniques as well as a wide variety of optimization methods, including genetic algorithms, which have been shown to be computationally efficient but cannot provide meaningful distributions of the parameters. Towards this end, Bayesian approaches, including Gaussian process emulators, history matching, and approximate Bayesian computation (ABC), have been used to estimate parameters along with their distributions. Our aim is to develop a model of the zebrafish cardiac action potential using a phenomenological model capable of reproducing many crucial properties of cardiac cells and tissue, including information about the distributions of relevant model parameters. We present preliminary results obtained by parameterizing the Fenton-Karma model with the ABC Sequential Monte Carlo (ABC-SMC) method. Specifically, we evaluate the performance of the model for different algorithmic choices, using synthetic data obtained from simulations, where accuracy and robustness can be assessed in

detail, and data from experiments in zebrafish hearts. Our conclusion is that ABC SMC is a promising algorithm to parameterize the Fenton-Karma model, offering good accuracy as well as fast running times and linear scalability in the number of parameters.

Computational Efficiency of Hamiltonian Monte Carlo for Genomic Prediction

Discipline: Mathematics
Subdiscipline: Statistics

Elizabeth Hale*[1]; Adriana Ortiz-Aquino[1]; Lauren White[1]; Nora Bello[1]; Nathan Albin[1]; Stephen Welch[1] and Phillip Alderman[2], *(1)Kansas State University, (2)Oklahoma State University*

Abstract: Genomic prediction (GP) offers advantages for rapid assessment of genetic merit in breeding programs based on genetic markers. However, the implementation of GP models often comes with substantial computational challenges due to the high dimensionality of the problem. Advanced GP models are often fitted using Markov Chain Monte Carlo (MCMC) methods in a hierarchical Bayesian framework that is primarily based on Gibbs sampling. Recent algorithmic developments in MCMC proposed Hamiltonian Monte Carlo (HMC), which uses differential geometry to efficiently guide the sampling process over the typical set of the multidimensional target posterior density. In this talk, we fit GP models using HMC as implemented by Stan software and compare computational efficiency with that of traditional Gibbs sampling MCMC, as implemented in the R package BGLR. Using the metric of effective sample size per second, we show that traditional MCMC with Gibbs sampling is substantially more computationally efficient than HMC for highly hierarchical GP models under the default settings. Further research is needed to tune HMC settings to realize its computational potential. We illustrate these results using wheat grain yield data provided by the International Maize and Wheat Improvement Center (CIMMYT) in Mexico.

Mathematics

The Escalator Boxcar Train Method for Time-Dependent Wheat Models

Discipline: Mathematics
Subdiscipline: Applied Mathematics

Adriana Ortiz Aquino*[1]; Elizabeth Hale[1]; Lauren White[1]; Nathan Albin[1]; Phillip Alderman[2]; Nora Bello[1] and Stephen Welch[1], *(1)Kansas State University, (2)Oklahoma State University*

Abstract: With a constant increased demand of wheat production, it is estimated that wheat yields must increase dramatically for the next 30 years to accommodate food security needs. We have created a system of ordinary differential equations (ODE), modeling the growth of wheat by using real environmental factors including the effects of vernalization on grain yield. Even though this is a step in the right direction, solving such a system can be a difficult task due to the large number of individuals being tracked. The Escalator Boxcar Train (EBT) method was introduced by de Roos in 1988 as a way to approximate summary statistics of a large population of individuals with characteristics modeled by an ODE system. The computational benefits of this method come from the significant reduction in dimensionality; rather than modeling each individual in the population, the EBT method predicts the statistics of cohorts of similar individuals. We apply this method to mathematical models of wheat growth, analyzing the accuracy and efficiency by numerical simulation, and exploring the effects of the choice of numerical integration algorithm, temporal step size and adaptive cohort subdivision.

Simultaneous Outlier Detection and Feature Selection Using Mixed-Integer Programming

Discipline: Mathematics
Subdiscipline: Statistics

Ana Kenney*, *Pennsylvania State University*; Luca Insolia, *Scuola Normale Superiore*; Francesca Chiaromonte, *Pennsylvania State University and Sant'Anna School of Advanced Studies* and Giovanni Felici, *IIASI CNR*

Abstract: Contemporary sciences are increasingly data rich, but redundant features in a model can lead to unstable estimates, inference, and prediction. Feature selection methods attempt to avoid this by favoring sparse, interpretable models. However, for many approaches, performance deteriorates in the presence of contaminated units (i.e. outliers) which often go unnoticed in practice. We investigate high-dimensional regression models contaminated by multiple mean-shift outliers affecting both the response and the design matrix. In contrast to existing approaches, which heavily rely on heuristics, we propose a discrete and optimal method to perform simultaneous feature selection and outlier detection using Mixed-Integer Programming. We prove several theoretical properties under this framework and demonstrate its superior performance against competing methods in an extensive simulation study and real data application.

Decompositions of the h*-Polynomial for Rational Polytopes

Discipline: Mathematics

Subdiscipline: Algebra/Number Theory/Combinatorics

Andrés Vindas Meléndez*[1]; Benjamin Braun[1] and Matthias Beck[2], *(1)University of Kentucky, (2)San Francisco State University*

Abstract: A rational convex polytope P is the convex hull of finitely many rational points in d-space. Fundamental data of P is given by its (relative) volume. Computing volume, even for these seemingly simple objects, is surprisingly hard. One approach is to compute the discrete volume of P, i.e., the number of lattice points in each integral dilate of P. This counting function is called the Ehrhart quasipolynomial of P. The Ehrhart quasipolynomial of P can be encoded in a generating function, namely the Ehrhart series of P. The Ehrhart series is a rational function, whose numerator is a polynomial called the h*-polynomial. While the literature on lattice polytopes is vast, there is much work to be done on rational polytopes. In 1985 Ulrich Betke and Peter McMullen proved that the h*-polynomial of a lattice polytope can be decomposed in such a way that it brings together arithmetic data from the simplices of a triangulation and combinatorial information from the face structure of the triangulation. Sam Payne and Alan Stapledon recently proved a series of inequalities for the coefficients of the h*-polynomial coming from lattice polytopes. Building on the work of Betke, McMullen, Stapledon, and Payne, we provide a decomposition of the h*-polynomial for rational polytopes, which generalizes the Betke–McMullen decomposition. Secondly, we present inequalities for the coefficients of the h*-polynomial arising from rational polytopes.

Astronomy & Astrophysics

A Search for Dark Matter Axions with the Admx Detector

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Raphael Cervantes* and Gray Rybka, *University of Washington, Seattle*

Abstract: Dark matter makes up 85% of the total matter in the universe, yet we don't know what dark matter is. Axions are a compelling candidate for dark matter because it's existence would also explain why the neutron has no overall electrical polarity, despite the expectation that it would.

The Axion Dark Matter Experiment (ADMX) is searching for the axion using an ultra-sensitive AM radio inside of a strong magnetic field. Axions in a magnetic field can convert to photons. The frequencies of these photons are proportional to the mass of the axion, but the axion mass is unknown. Thus the ADMX detector must be able to scan over a range of frequencies. The detector consists of a metallic cavity with a tunable resonant frequency. The expected signal is 10^-24 W, so it can be overwhelmed by miniscule amounts of background radiation. To reduce thermal background, the cavity is cooled to 150 mK. The signal out of the cavity is then amplified with minimal added noise using quantum amplifiers.

ADMX has excluded with a 90% upper confidence limit the existence of axions with an associated photon frequency of 650 MHz to 800 MHz. By employing new cavity designs and better quantum detectors, ADMX continues to search for axions at higher frequencies.

Measuring the Eccentricity of GW170817 and GW190425 Using Ligo/Virgo Gravitational Wave Observations

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Amber Lenon*[1]; Alex Nitz[2] and Duncan Brown[1], *(1)Syracuse University, (2)Albert Einstein Institute*

Abstract: The LIGO/Virgo collaborations announced the detection of the first binary neutron star (BNS) merger, GW170817, that ushered in a new era of multi-messenger astronomy and recently announced the detection of a second neutron star merger, GW190425. These systems are most likely field binaries which are expected to have radiated any eccentricity away and circularized by the time their gravitational waves reach the LIGO-Virgo sensitive band. However, binaries formed through interactions in dense stellar environments, like globular clusters or galactic nuclei, may still retain a significant amount of their eccentricity. Eccentric binaries are binaries in elliptical orbits and at merger may have different electromagnetic emission than circular BNS and allow us to probe various formation channels. Although these binaries were detected by searches with waveform models of binaries in circular orbits, they could still have some small eccentricity. We use gravitational-wave observations and Bayesian parameter estimation to measure and constrain the maximum allowed eccentricity of GW170817 and GW190425. Even though these binaries were detected by waveform models in circular orbits, we find that they have a small eccentricity at merger that is negligible. Although these binaries have no significant eccentricity, the proposed third-generation detectors will have the ability to detect these mergers at higher eccentricities and probe the dynamical formation channel.

Searching for Eccentric Supermassive Black Hole Binaries in the Nanograv 12.5 Year Data Set

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Belinda Cheeseboro* and Sarah Burke-Spolaor, *West Virginia University*

Abstract: Gravitational waves (GWs) are small ripples that stretch and compress the fabric of spacetime and travel at the speed of light. They provide more information about binary compact object (i.e. neutron stars or black holes) systems and possibly supernovae. There are several types of detectors that probe various gravitational wave frequency ranges, but the focus of this presentation is on the pulsar timing array regime (10−9 to 10−6 Hz). Pulsar timing arrays monitor an array of millisecond pulsars looking for deviations in the time it takes their signals to reach Earth using radio telescopes. Supermassive black hole binaries (SMBHB) with total masses of 108-1010 M⊙ are one of several gravitational wave sources that could be detected by pulsar timing arrays like the North American Nanohertz Observatory for Gravitational waves (NANOGrav). In the past, the calculation of gravitational waveforms from eccentric SMBHB was computationally expensive as compared to the circular case, thus only circularized binaries have been considered in past all-sky GW searches. Recent algorithmic development has optimized the eccentric waveform search process allowing us to develop an all-sky search pipeline for eccentric gravitational waves. We conduct the first search for gravitational waves from eccentric SMBHB using the NANOGrav 12.5 year data set. Detecting eccentric GWs from eccentric SMBHBs can help us study the inspiral phase of these binaries which gives dynamical information to further understand the evolution of galaxies and their central supermassive black holes.

The Demographics of Wide Planetary-Mass and Substellar Companions and Their Circum(sub)Stellar Disks through Psf-Fitting of *Spitzer*/IRAC Archival Images

Discipline: Physics & Astronomy
Subdiscipline: Astronomy & Astrophysics

Raquel Martinez* and Adam Kraus, *The University of Texas at Austin*

Abstract: The last decade has seen the discovery of a growing population of planetary-mass and substellar companions (~<20 M_{Jup}) to young stars which are often still in the star-forming regions where they formed. These objects have been found at wide separations (>100 AU) from their host stars, challenging existing models of both star and planet formation. Demographic trends with mass and separation should distinguish between these formation models.

The extensive *Spitzer*/IRAC data set of every major star-forming region and association within 300 pc has great potential to be mined for wide companions to stars. In this presentation, I will describe my development of an automated pipeline to leverage this archive and find wide-orbit companions of stars via point spread function (PSF) subtraction in *Spitzer*/IRAC images. My survey is sensitive to companions with masses approaching that of Jupiter at orbital radii of a few hundred AU, discovering wide companions in their birth environments and revealing their circum(sub)stellar disks. I will present a re-analysis of archival *Spitzer*/IRAC images of 9 stars (G0-M4.3) known to host faint planetary-mass and substellar companions (ρ=1.2″-12.3″) through previous high-contrast imaging observations at optical or near-IR wavelengths. I will report new mid-IR photometric measurements of this sample of wide-orbit companion systems, then discuss an automated companion search of all known young stars with existing *Spitzer*/IRAC data, concluding with my ongoing follow-up observations of candidate wide planetary-mass/substellar companion systems with ground-based telescopes and the outlook for future observations with space-based telescopes.

STEM Education & Learning

Rethinking Initiatives for Increasing STEM Diversity: A New Capital Framework Model

Discipline: STEM Education & Learning
Subdiscipline: Other STEM Education & Learning Research

Patricia Jaimes* and Julie C. Libarkin, *Michigan State University*

Abstract: Science educators have long tried to increase the participation of underrepresented minorities (URM's) in STEM, with capital - non-financial and financial resources that help individuals succeed - playing an important role. Historically, STEM initiatives to increase diversity, such as student research programs, focused on providing two types of capital to URM's: 1) social capital (scientific mentors) and 2) cultural capital (scientific knowledge). Although providing these capitals is useful for recruiting URM's into STEM, lack of diversity is still a problem, suggesting that efforts need to also focus on retention. This research explores multiple forms of capital that may contribute to the development of innovative solutions for retaining URM's in STEM.

This study explores the capitals that URM scientists accessed while pursuing their career. Semi-structured interviews were conducted with scientists (N=16) who identified as Latinx, African-American, Queer, or Disabled. Interviews explored participant's STEM career experiences. Interviews were analyzed using a predetermined codebook. The capitals most important to participants were social and intrinsic (internal motivation). Access to cultural capital and economic capital (financial resources) was also important for scientific career advancement but were dependent on access to social capital. Cultural and economic capitals were categorized as external capitals because they derived from outside influences. An interesting finding was that intrinsic capital emerged when participants encountered social barriers such as poverty, racism, ableism, or sexism, allowing participants to defy those challenges and persist in their scientific endeavors. This research presents a new framework model demonstrating the interconnectedness of external capitals and intrinsic capital.

Building a Computer Science Learning Ecosystem: An Exploratory Study Examining the Connections between Culture and Technology with Indigenous Partners across Northern Utah

Discipline: STEM Education & Learning

Subdiscipline: Other STEM Education & Learning Research

Ms. Megan Hamilton* and Breanne Litts, *Utah State University*

Abstract: While many organizations have committed to providing every student with high-quality computer science education, system inequities still persist. For instance, Indigenous peoples continue to remain disproportionately underrepresented in computer science and engineering fields. One strategy to address this inequity is to align computer science education interventions with Indigenous ways of knowing. With these efforts, scholars are finding new ways to center traditional culture, which has historically been marginalized in this field, in computer science activities and communities with the goal of increasing overall interest and sustaining participation of Indigenous peoples in computer science. Building on this work, as a team of Indigenous and non-Indigenous researchers and educators, we are working to build a computer science ecosystem in northern Utah. Inspired by other learning ecosystem models, a key goal of this effort is to build computer science knowledge through engagement of families and community. In this presentation, I will report our early efforts as we explore how Indigenous youths' perceptions of computer science change as a result of their participation in the building and implementation of a computer science ecosystem. Specifically, I draw on ethnographic fieldnotes, educational artifacts, semi-structured interviews, and talking circles to highlight individual experiences of youth participants and how their participation in the ecosystem affected their perceptions of computer science. Insights from our findings reshape how we think about issues of access and equity in computer science interventions for Indigenous youth. This work makes contributions to the fields of computer science education as well as the learning sciences.

The CAR Strategy: Confronting, Addressing, & Replacing (CARing) Master-Slave Terminology in Engineering Education

Discipline: STEM Education & Learning

Subdiscipline: Other STEM Education & Learning Research

Amman Asfaw*; Storm Randolph; Andrew Danowtiz and Jane Lehr, *California Polytechnic State University - San Luis Obispo*

Abstract: "Master-slave" terminology is still present in engineering education and industry. This legacy nomenclature can be found in engineering topics such as brake/clutch cylinder systems in car engines, serial peripheral interface connections in microcontrollers, online git repositories, computer network database architectures, aeronautical missile systems, architectural designs of residential homes, and more. Usage of "master-slave" in academia can make students—especially those who identify as female and/or African-American—feel uncomfortable, potentially evoking Stereotype Threat and/or Curriculum Trauma.

This presentation will report specifically on student perceptions and the effectiveness of the confront, address, replace (CAR) Strategy piloted as a framework for driving out iniquitous terminologies such as "master-slave" in engineering education. Of students surveyed, initial data confirms: 86% either agree or strongly agree The CAR Strategy appropriately confronted the historical significance and origins of "master-slave"; 68% either agree or strongly agree The CAR Strategy helped them realize the technical inaccuracies of "master-slave"; 70% either agree or strongly agree The CAR Strategy is an effective framework for driving out iniquitous terminologies such as "master-slave" in engineering education; and 67% either agree or strongly agree they would like to see all professors use The CAR Strategy when applicable in their classes.

We are currently analyzing student responses using a more sophisticated statistical software in order to extrapolate a data-supported consensus on The CAR Strategy and to determine where further research on iniquitous terminologies is warranted.

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The largest multidisciplinary and multicultural STEM diversity event in the country, 2020 SACNAS – The National Diversity in STEM Conference serves to equip, empower, and energize participants for their academic and professional paths in STEM. From October 19 to 24, 2020, college-level through professional attendees are immersed in cutting-edge scientific research and professional development sessions, motivational keynote speakers, a Graduate School & Career Expo Hall, multicultural celebrations, and an inclusive and welcoming community of peers, mentors, and role models. The conference is a training ground for the next generation of diverse STEM professionals, aiming to level the playing field for first-generation college students of color through mentorship, professional development, and networking opportunities. For more information, visit *2020sacnas.org*.

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