

Populations That Evolve to Evolve

w. Menke - 18 Nov 93

1. Goal. Create a population of 'genomes' that are a good starting population for datasets drawn from a known class (e.g. oceanic refraction surveys)

2. Key idea. Mutation rate varies from part of genome to other parts (i.e. from gene to gene). A gene's mutation rate is itself a gene.

3. Discussion.

A. The genome is divided up into segments (i.e. genes).

B. The genes fall into 3 classes:

→ Genes that describe the model: $M_i, i=1, N$

→ Genes that describe the mutation rate of the model genes, $R_i, i=1, N$

→ A single gene, R_0 , that describes the ~~mutation~~ mutation rate of the ~~model~~ R_i genes.

C. The same population of genomes are "trained" on a large number of datasets drawn from the same class. The survivors will tend to be the ones with a low mutation rate for M_i genes that describe features common to the class

Perhaps the mutation rate of R_0 should be zero?

Perhaps the values of R_i should be very roughly quantized - low, medium, high rates.