Aipotu: a Simulated Microworld Based on a Realistic Model of Gene Expression and Protein Folding.

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Extended Abstract

Aipotu ("utopia" reversed; pronounced "ay poh too") is an in silico microworld based on a highly realistic model of gene expression and protein folding.

Aipotian organisms are sexually-reproducing diploid organisms with DNA genomes. Their genes are expressed by transcribing from a promoter sequence until a transcription terminator is reached. The resulting pre-mRNA is then spliced based on intron start and end sequences. The mature mRNA is then translated using the standard genetic code. Proteins produced are folded on a 2-dimensional hexagonal lattice using realistic non-covalent interactions (hydrogen bonds, ionic bonds, and the hydrophobic interaction). The shapes and compositions of these proteins then determine their effect on the phenotype of the organism. In the current prototype version, the phenotype color is determined in a manner analogous to Green Fluorescent Protein: most proteins are colorless (white); a protein with a particular shape can be colored; the particular color depends on the amino acids present.

When the genomes of a population of these organisms are subjected to random mutation and selection based on color, the organisms show a variety of interesting evolutionary behaviors. These include: heterogeneity between runs with the same starting conditions; evolution of one color from another; loss of color in the absence of selection; convergent evolution of proteins with the same color; and evolution of colored from colorless starting proteins.

I have used Aipotu to teach evolution to undergraduate Biology students; I am currently evaluating its impact on students' understanding of evolution. Because it is based on a familiar and biologically reasonable underlying mapping of genotype to phenotype, it is likely to be more effective than other alife simulations used for teaching.

Because the underlying model involves realistic gene and protein sequences, Aipotu also has potential as a research tool. For example, it would be possible to explore and test the assumptions of molecular phylogeny by comparing the actual ancestry of Aipotian organisms with molecular phylogenetic reconstructions under different mutation regimes. Furthermore, because all of the key features of the underlying model of gene expression and mutation are variable, it will be possible to explore the evolutionary effects of changing these parameters. For example, currently, the mutations are only point mutations; the mutational spectrum could be expanded to include insertions, deletions, and gene duplications. It would be possible to add other structure to phenotype mappings besides color. For example, proteins with certain shapes could act as regulators of other genes, encode other phenotypes, or contribute to multi-protein pathways; entire organisms with hundreds of genes are possible. Finally, it would be possible to observe the effects of changing the genetic code or even the rules of protein folding. The underlying molecular genetic engine is fully functional; extensions are only limited by the imagination of the investigator.

Aipotu is open source and freely-available from http://intro.bio.umb.edu/aipotu/