

Genomic Complexity in Micro Organisms and Digital Organisms

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For years, my group has used microorganisms as models to address fundamental hypotheses about the mechanisms and dynamics of genetic, ecological, and evolutionary processes [1-4]. In these fields, there are many interacting entities and hence a tremendous number of potential interactions. Identifying general rules, if any, that govern the form of these interactions might be important for developing theories of complex systems.

I recently began a collaboration with Christoph Adami and Charles Ofria (physicist and computer scientist, respectively, at Caltech) to explore these issues in a radically different way. They have developed a system of artificial life, called Avida, using digital organisms — computer programs that self-replicate, compete for CPU time, mutate, and evolve by Darwinian selection [5].

Digital organisms provide an opportunity to seek generalizations beyond the organic forms that biologists have studied to date (all of which share the same basic chemistry of DNA, RNA and proteins). Also, there is considerable interest in using computer programs that can evolve in order to solve complex problems where it is difficult to write programs with the desired behaviors.

I will briefly discuss two sets of experiments — one with *E. coli* [6] and one with Avida [7] — in which we measured the extent and form of nonlinear interactions among random mutations with respect to performance. The experiments with bacteria involved several hundred genotypes; those with digital organisms used billions of genotypes. Both systems exhibited a surprisingly high frequency of interactions. Also, contrary to certain theoretical predictions, neither system showed a preponderance of synergistic interactions (in which multiple mutations are worse than expected from the components); instead, interactions in both systems comprised an admixture of synergistic and antagonistic effects. By using digital organisms, with their greater statistical power, we could also examine subtle questions concerning the relationships between the form of interactions and such variables as genome length and functional complexity.

In the future, we will continue to address fundamental questions using these two systems, trying to identify common features as well as essential differences. For example, what genetic processes and environmental features favor the evolutionary emergence of complex communities, comprised of many distinct species that coexist stably because they perform different functions?

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