

Simulator allows scientists to predict evolution's next best move

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(PhysOrg.com) -- Biologists today are doing what Darwin thought impossible. They are studying the process of evolution not through fossils but directly, as it is happening. Now, by modeling the steps evolution takes to build, from scratch, an adaptive biochemical network, biophysicists Eric D. Siggia and Paul Francois at Rockefeller University have gone one step further. Instead of watching evolution in action, they show that they can predict its next best move.

In Darwinian evolution, even the slightest, infinitesimal beginnings can lead to tools as complex as the human eye. But how do innovations like these get started and propagated by natural selection when their raw material is merely individual random genetic mutations? By looking at the series of mutations in evolutionary space, Siggia, head of the Laboratory of Theoretical Condensed Matter Physics and Paul Francois, a postdoc in his lab, now provide a computational answer to one of Darwin's biggest questions.

In this evolutionary space, Francois and Siggia instructed their algorithm to find a network that worked very much like an eye after adjusting to different levels of light. "The eye is a very good example of adaptation," says Francois. "It admits different amounts of light when light levels change, and after some period of adjustment, your eyes work equally well as before. That's what we selected for; we instructed our algorithm to find a network that after responding to some input, always comes back to its initial value, or level of working. That's perfect adaptation."

To find this network, the algorithm, like Darwinian evolution, showed no mercy. During each generation, the algorithm randomly added, deleted or changed the features of genes in a population of gene networks and selected only those that were the most fit, and thus most likely to reproduce. After duplicating the fittest networks in each generation, it repeated the process of mutation, selection and duplication over and over again until it eventually arrived at the network that adapted perfectly to a random biochemical input.

Francois and Siggia found that certain mutations automatically increased a network's fitness and thus were immediately selected. "When you look at systems like the eye or structures like the human spinal cord, you think how could these have evolved from a simple network," says Francois. In their current study, Siggia and Francois looked at how a complex biochemical network could evolve, and an answer came together: It is built through a specific series of mutations that is repeated over and over again, from scratch, every time they restart their simulations.

"So this is really the idea," says Francois. "From one step to the next, you know, more or less, evolution's next best move. In our simulations, that's what we see."

More information: *Physical Biology*: June 1, 2008

Provided by Rockefeller University

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