

# Computer Program Simulates Protean Creation

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David E. Thomas

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[globalflood.org/origins-debate.html](http://globalflood.org/origins-debate.html)

Editor:

In his letter of June 11 ("The real issue is macroevolution"), John Baumgardner asks, "To go from a bacterium, built from about 1,000 different kinds of widgets, to a mammal, built from 100,000 different kinds of widgets -- some new widgets surely need to be added. How does this happen"? Then, he describes one specific "widget" (say, a new mammal protein) composed of 200 amino acids. Of the 200 amino acid sites on the widget, he assumes that 100 must be exactly as specified. Baumgardner states that trying out billions of random sequences over billions of years would not turn up even one of the specified proteins.

I actually simulated John's problem on my computer, and the solution does not take "billions of years." Using the basic processes of evolution, I can obtain an exact match for the specified protein in less than 10 minutes! Unlike Baumgardner, I used the systems that nature uses: selection, mutations, heredity and time.

I devised a numerical test for the computer program to model "selection." It provides an objective, impartial number for how close a given sequence is to a desired sequence.

I also used mutations to stir the genetic pot by picking a random amino acid site and altering the acid there. Most mutations are "harmful," but every once in a while, a mutation makes the sequence a better match.

For each "generation" of 80 widgets, the results of the tests for the group are sorted, and the top 40 sequences automatically earn a slot in the next generation. The remaining 40 positions are filled by "mutating" the top 40 sequences at one amino acid site each. Thus, each member of a new generation is very closely related to its "parents," just as generations are in

nature. Children in my computerized world inherit very real benefits from their parents.

With this approach, the computer shows the raw power of heredity, mutation, and selection. Within less than 10 minutes, typically between 1,400 and 1,800 generations, a perfect, exact match for the specified sequence emerges from the process. At 80 widgets per generation, that means that instead of testing billions of sequences for billions of years, I need test only about 150,000 sequences before getting an exact match for the 100 specified sites.

I will be happy to provide the source code for this program to anyone who requests it from me, at [det@rt66.com](mailto:det@rt66.com), or by mail at P.O. Box 1017, Peralta, NM 87042. I encourage Dr. Baumgardner to examine it byte-by-byte for himself. My computer system is designed to model nature, just as Baumgardner's "Terra" is.

Reproduction and heredity are real, and life comes with a built-in "test." Nature's "test" does not specify an exact sequence or an exact length to be "matched." Many proteins are nearly equivalent in nature. Rather, the test is simply "Will the organism live." If an organism lives long enough to have children, its genes pass the test. The seeds of evolution are out there in the real world.

David E. Thomas