

Re: Haldane's Dilemma – clarifications – and Felsenstein [LONG]

Source: <http://sci.tech–archive.net/Archive/sci.bio.evolution/2006–06/msg00293.html>

- *From:* "Perplexed in Peoria" <jimmenegay@xxxxxxxxxxxxxx>
 - *Date:* Thu, 22 Jun 2006 12:18:51 –0400 (EDT)
-

"Joe Felsenstein" <joe@xx> wrote in message [news:e7cbcg\\$234r\\$1@xxxxxxxxxxxxxxxxxxxxxxxxxxxx](mailto:news:e7cbcg$234r$1@xxxxxxxxxxxxxxxxxxxxxxxxxxxx)

I'm not Walter, but do want to comment on the model. It's a straightforward computer simulation of natural selection of mutations, with a few wrinkles. I wonder if you don't want to modify those wrinkles:

1. The alleles are either A or a. In this case the population will, after enough generations, end with with mostly A's but some a's, as there is back mutation at a rate equal to forward mutation. So it will be approaching an asymptotic amount of adaptation. A useful modification would be to have the alleles be integers which are not just characters 'A' and 'a' but can be incremented. Thus we would have alleles 0, 1, 2, ... and this would allow new alleles to be replaced by even better alleles. Mutation would be incrementation of the integer. Or if you wanted to have back mutation as well mutation could sometimes increment and sometimes decrement. The resulting model would gain favorable mutations (with some but not much loss as well) and this would go on indefinitely, or at least until you got near MAXINT.

A great idea. If you decide to implement this, Malcolm, don't forget to introduce a factor of `sizeof(int)` into your memcpy's in the recombination code in the `makechild` function.