

### Genetic simulation program exercise

Get the genetic simulation program and get it working on your computer. Detailed instructions are in the documentation file (which is a web page, `popg.html`, that accompanies it). This web page is also reached from a link on the main course web page.

Start by playing around with the parameters. Can you make a run that shows selection with very little genetic drift? Drift with very little or no selection? Mutation with little drift or selection?

The exercise that should be turned in concerns these two questions. It is due on **February 13**. It is worth 25 points.

1. Consider a number of populations (8-10 is fine) that have 1000 individuals and no migration between them. The fitnesses of the three genotypes should all be 1.0, so that there is no selection. Let us look at the mutation rates for  $A \rightarrow a$  and  $a \rightarrow A$ . We want to try different values for them, but always keeping these two rates (the forward and backward mutation rates) equal. The initial gene frequency can be left at its default value of 0.5. What happens when the rates are 0.01? When they are 0.001?, 0.0001? 0.00001? Run at least 1000 generations (though several times more than that may be helpful).
  - Describe the outcomes. I am not looking for detailed graphs of all runs but a general verbal description. However, distinguish between what happens with the different parameter values.
  - Explain, in terms of evolutionary forces, why these results are obtained, including why the different results for different cases are obtained.
  - Consider the number of new mutants arising in a population in one generation. What is it in terms of  $N$  and the mutation rate  $\mu$ ?
  - Is there some value of this number of new mutants, above which the outcome is different than below it? (i.e. some value that is roughly the border between two kinds of behavior of the simulations).
2. Consider 8 populations of size 1000 with the genotypes  $AA$ ,  $Aa$ , and  $aa$  having (respectively) fitnesses 1.2, 1.1, and 1.0. Set the mutation rates both to 0.000001 with no migration. Run 1000 generations, at least (some more may be helpful). Set the initial gene frequency of the favored allele  $A$  to zero.
  - What happens?

- Why?
- Set the migration rate to a small value such as 0.00001. How does this alter the result? What happens with higher migration rates such as 0.0001 and 0.001?
- Consider the number of immigrants into an individual population from all others. What is it in terms of  $N$  and  $m$  ? (remember that  $m$  is the fraction of individuals that are newly arrived in each generation).
- Is there some value of that quantity that is the border between two different kinds of behavior?

You should turn in a report, 5 pages or so in length, answering these questions.

In addition to answering the questions, one of the things you can also do (although not to turn in to us) is to explore the effects of various combinations of natural selection, genetic drift, mutation and migration. You might want to start with no mutation and look at the effects of natural selection including overdominance. Then maybe look at the effect of mutation versus selection. You may also want to examine the effect of genetic drift alone by making all fitnesses equal, and the sizes of the other effects necessary to have a noticeable effect on the outcome in the face of drift. *Be creative*, but with some ability to compare results with other cases that differ in useful ways. The object of this exercise is really to give you some feel for how gene frequencies are expected to change in natural populations.