

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.

Just to help you understand population genetics, 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? (Don't turn anything in about these runs).

The exercise that should be turned in concerns the following questions. It is due on Monday, **October 26**. It is worth 25 points, 1/4 of the total number of points you will get from the midterm.

Consider a number of populations (100 of them) that have their population size (N) be 1000 individuals each. You may want to start with a run about 1000 generations long and extend it as needed. In doing the tasks and answering the questions below, if the pattern is not clear from one run, do multiple runs until it becomes clear.

Simulate populations that have no A alleles initially, but have a mutation rate of 0.00001 from a to A . They should have no back mutation, and no migration. Allele A is a dominant allele which is favorable, with fitnesses $AA : Aa : aa$ of 1.02 : 1.02 : 1. Favorable A mutants will occur, and either rise in frequency to fixation or be lost.

Describe the cases run, the outcomes, including how many cases were run for how long, and what happened. Simulate cases to answer these questions:

1. How long does it take before half of the populations reach fixation (use the “Fixed” number at the upper-right of the graph)?
2. How many favorable mutations do you estimate would have occurred in a population by that number of generations?
3. Based on that, what is the approximate probability of a favorable mutant surviving so that it rises to fixation in its population instead of getting lost?
4. What is the effect (in terms of outcome and time for half of the populations to get fixed) of using half as large a mutation rate?
5. What is the effect of using half as large a selection coefficient, so that the fitnesses are 1.01 : 1.01 : 1 ?

6. What is the effect of using twice as large a population size?
7. What is the effect of having the *A* allele be recessive instead, so that the fitnesses are 1.01 : 1.0 : 1.0 ?
8. What is the effect of having a migration rate of 0.001?
9. For each of the last five cases, give an intuitive explanation of why it differs from the initial case.

I am not looking for detailed graphs of all runs (though it is OK to include a graph or two if you want) but a general verbal description, with enough detail to know exactly what was done and what was observed. Do distinguish between what happens with the different parameter values.

To answer the “why” parts of the questions, explain in terms of evolutionary forces such as selection, genetic drift, and migration, why these results are obtained, including your explanation for why results do or do not differ for the different cases.

You should turn in a report in email form (as a PDF or Word format file – PDF is most likely to be readable by me), or as a plain text file if necessary), 2 or 3 pages in length (more if necessary) answering these questions. Don’t forget the “why?” parts of the questions.