

For this homework, use the PopG program available at:

<http://evolution.gs.washington.edu/popgen/popg.html>

It will run on Unix/Linux, any version of Windows, or MacOSX. If you have any difficulty downloading or running this program, please get in touch with me right away.

For this homework I do **NOT** want printouts of PopG results, or hand-drawn pictures of PopG results. Only numbers and words, please! Also, please remember that the frequency of a brand new allele (one copy) depends on the population size. All organisms in this HW are diploid.

1. Orange and blue butterflies form an underdominant system: AA is blue, aa is orange, and Aa is a muddy color attractive to predators. The fitnesses are:

Genotype	AA	Aa	aa
Fitness	1.0	0.9	0.95

Suppose that a population starts with 1 copy of the A allele and all the rest are a. (Assume 1 copy in each case, no matter what the population size is. This simulates the fate of a new mutation. Note that this will require a different value for the allele frequency of A in each case.)

- (a) If the population is of size 10, what percentage of the time will it fix A? (Run at least 200 populations to get an estimate.)
 - (b) If the population is of size 50 instead, what percentage of the time will it fix A? (You may need several sets of 200 to get a good estimate. Be sure to change the allele frequency of A!)
 - (c) We cannot run a population of size 1 billion, but what percentage would you expect?
2. Consider a neutral allele (no selection) in a case with no mutation. The starting frequency of A is 0.6. Population size is 100, and we'll run exactly 200 populations at once.
 - (a) What percentage of populations eventually fix A?
 - (b) Add a tiny amount of migration ($m = 0.0001$) among the populations, and describe the results after 1000 generations.
 - (c) Add a much larger amount of migration ($m = 0.1$) and describe the results after 1000 generations.
 - (d) Experiment with different values of the migration rate and give an approximate value at which the behavior of the system changes.
 - (e) How do the results differ if you use populations of size 1000 instead?
 - (f) In words, why does high migration rate give such different results from low migration rate?
 3. In lecture I gave a formula for the fixation chance of an allele with an advantage g in the heterozygote. I didn't give a formula for a purely recessive advantageous allele. For a population size of 100, investigate newborn advantageous recessives with an advantage of 0.5, 0.1 and 0.01. Be sure to run enough cases for a good generalization, and start with a single copy of the new mutation.
 - (a) From your experiments, what is the chance that a new allele with such an advantage will fix?
 - (b) How does this compare to the fixation chance of a new neutral allele?