For this homework, use the PopG program available at:

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

It will run on Unix, Windows or Macs. 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 newly arising allele depends on the population size.

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.) *(2 pts) Around 5%. I assumed that answers around 10% resulted from thinking that the starting allele frequency is 1/10 rather than 1/20, and marked off a point.*

   (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 choose a new allele frequency of A!) *(2 pts) Around 1%.*

   (c) We cannot run a population of size 1 billion, but what percentage would you expect? *(1 pt) Practically zero. If it were neutral it would fix about 1 time in 2 billion, but as an underdominant allele its chances are even worse.*

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.

   (a) What percentage of populations will fix A? (Again, run at least 200 populations.) *(1 pt) 60% is the theoretical expectation, and most reported results were close to this. I did not give credit for answers which had run only a few generations; if you're trying to assess fixation you need to run long enough for things to fix!*

   (b) Add a tiny amount of migration (m = 0.0001) among the populations, and describe the results after 1000 generations. *(2 pts) Most but not all populations will have fixed, and of those which fixed, about 60% will have fixed A.*

   (c) Add a much larger amount of migration (m = 0.1) and describe the results after 1000 generations. *(2 pts) No fixation. The allele frequencies stay close together and fairly close to 0.6.*

   (d) Can you find the approximate amount of migration at which the behavior of the system changes, by experimenting with different values of migration rate? *(2 pts) Theory predicts a change around 2Nm=1, so with a population size of 100, the behavior should change around m=0.005. Depending on which symptoms you found most important–the failure to fix or the joined-together look of the different populations–students found different empirical answers but mostly in the range 0.01-0.001.*

   (e) How do these results change if you use populations of size 1000 instead? *(2 pts) Much less migration is needed to overcome drift.*

   (f) In words, why does high migration rate give such different results from low migration rate? *(2 pts) With high migration, the system acts as one large population, so drift is relatively slow and all of the populations move together. With low migration, the system acts as several nearly independent populations, so drift is faster and each population drifts on its own. The main difference between low and zero migration is that with low migration,*

populations eventually un-fix due to migrants, so there is no permanent fixation until the entire system fixes. One thing few students commented on is that the entire high-migration system will eventually fix (it takes a very long time, though!) just as any other large population would. Eventually either A or a will be completely lost from the system, and just as before, A is 60% likely to be the winner.

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 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. *I used fitnesses of 0.5, 0.9, and 0.99 for the genotypes other than the homozygous recessive. Some students assumed 50/50 starting allele frequencies here, but this is a NEW allele and the starting frequency should be 1/2N or 0.005.*

   (a) From your experiments, what is the chance that a new allele with such an advantage will fix? *(3 pts) Experimental results reported were 4-8% for an advantage of 0.5, 2-3% for an advantage of 0.1, and less than 1% for an advantage of 0.01. Some people got much higher answers; I believe these come from using a starting frequency of 0.5.*

   (b) How does this compare to the fixation chance of a new neutral allele? *(1 pt) The expected chance for a new neutral allele is 1/(2N) which would be 0.5%. The selected allele does have a higher chance, though for the weak selection (0.01) you would need a large sample to see this. However, it is much less than the 2g chance of a favorable heterozygote. Note that the advantage of 0.5 is too big for our 2g approximation to work, but from the exact table (lecture 9) we see the fixation chance for a gene with 0.5 advantage in the heterozygote is 0.58, whereas these results suggest an equally favorable recessive is 0.06 –a big difference!*

   Those of you who said that a selected recessive would do better than a selected dominant, or that it would do worse than a neutral allele, should give your answers a "smell check" before committing to them. If it smells wrong, it very probably has a mistake somewhere.