Download the program PopG using the link at the course web site. There are Windows, Mac OS X, and Linux executables available (plus C source code that you are welcome to recompile yourself if you want).

Do runs on the following case, and submit a report of about 5 pages answering the questions I ask below. Please do not print out large numbers of graphs showing all your runs (one or two is fine if you want). This homework is worth 25 points.

Consider a set of 10 populations with 1000 individuals each. Give allele $A$ the initial gene frequency of 0.01 in each population. The populations are connected by migration at rate $m$, and the $A$ allele is favored, with fitnesses $AA : Aa : aa$ of $1 + 2s : 1 + s : 1$. There is no mutation.

Try some runs with different values of $m$ and $s$ and then see if you can choose ones that help you answer the following questions. Runs of at least 1000 generations per graph will be needed. Linux users should note that the X-windows interface of the program sometimes does not accept a new value typed into a box unless you later move the cursor elsewhere (this should not be a problem with Windows or Mac OS X).

1. If there is no selection ($s = 0$) what will happen if $m = 0$? If $m > 0$? For this you don’t need to do any runs but just think about what you already know about genetic drift. Note that in a single population genetic drift causes all alleles to be descended from one of the original copies. What happens to this if there is migration connecting a bunch of such populations? Your existing understanding should tell you the answer, which you can verify by doing runs.

2. Try a number of runs with $s = 0.001$ and $m = 0.01$. What are the possible long-term outcomes?

3. Try lower values of $m$ than 0.01. At what value do we see substantial (say twofold) differences in the time until the $A$ allele fixes in the different populations. How does the value of $m$ compare with the condition $4Nm = 1$ which is usually used as the value beyond which the populations do not have much differentiation of gene frequencies?

4. Running (say) 100 populations of size 1000, with $m = 0$, what does the probability of fixation of $A$ seem to be? How does this compare to the probability you would calculate with equation VII-90?

5. What happens to this fixation probability if you have instead a set of 10 populations of size 1000, connected with migration of rate $m = 0.01$? You can roughly do this by simulation, though this may take many runs of sets of 10. Make sure you run long enough to see whether the populations fix for $A$.

6. For a large enough rate of migration, the set of populations should act like a single population that mates randomly. Use a largish number (say 100) of replicates of populations each of size 10,000 with $m = 0$, to get a sense of what 10 populations of size 1000 would do if migration were high enough. Can you calculate what the fixation probability would be in this limit, using equation VII-90? You will need to run until you are pretty sure how many populations are going to end up fixed.