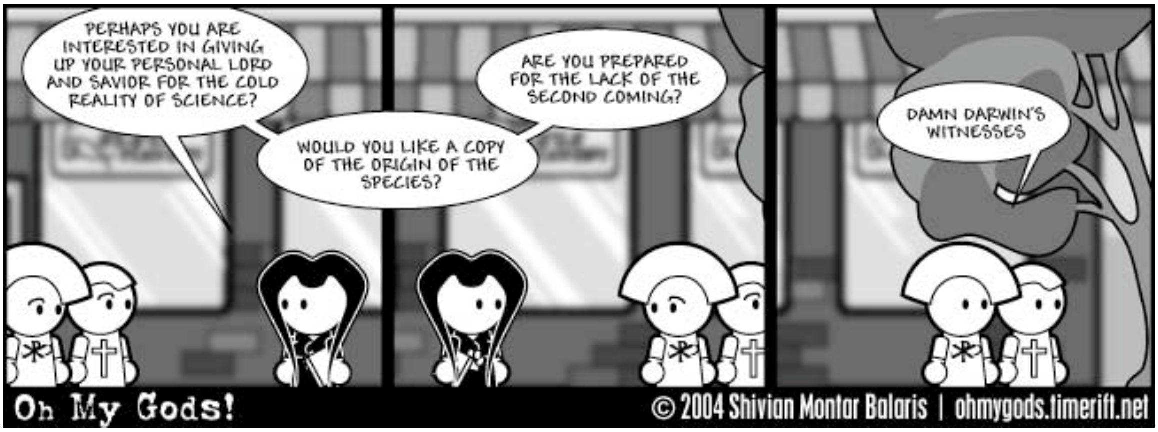
Biology 4415/5415
Evolution

LABORATORY EXERCISE 4:
SELECTION IN POPULATIONS

Charles Darwin opens *The Origin of Species* with a discussion of how humans have produced countless varieties of animals and plants by selective breeding. Humans can consciously produce new varieties of animals and plants with desirable traits, simply by picking out individuals that are close to the desired phenotype, allowing them to breed repeatedly, and culling out individuals that are not close to the standard. Darwin himself experimented a great deal with breeding fancy pigeons, and drew heavily on the writings of stockbreeders and horticulturalists in writing *The Origin of Species*.

This lab involves using computer simulation to look at natural selection. This has the advantage that you can watch evolution of gene frequencies over thousands of generations in just a few seconds.



MATERIALS:

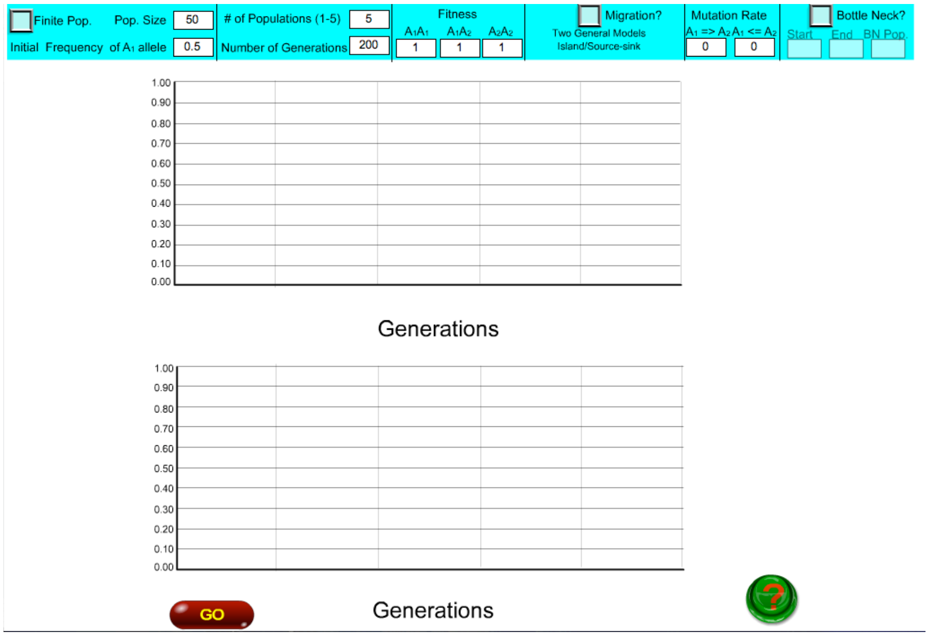
computer with Internet connection

PROCEDURE:

1. Go to

http://www.radford.edu/~rsheehy/Gen_flash/popgen/

and you should get something like the following:



☐ Finite Pop. Pop. Size 50

Initial Frequency of A_1 allele 0.5

# of Populations (1-5) 5

Number of Generations 200

Fitness A_1A_1 1 A_1A_2 1 A_2A_2 1

☐ Migration? Two General Models Island/Source-sink

Mutation Rate $A_1 \Rightarrow A_2$ 0 $A_1 \Leftarrow A_2$ 0

☐ Bottle Neck? Start End BN Pop.

You simulate the evolution of the frequencies of two alleles, called $\mathbf{A_1}$ and $\mathbf{A_2}$. The top graph measures the frequency of $\mathbf{A_1}$, and the bottom measures the frequency of $\mathbf{A_2}$ (which means that they will look like mirror images of each other, reflected through the horizontal plane). Obviously, you click the "GO" button to start a simulation.

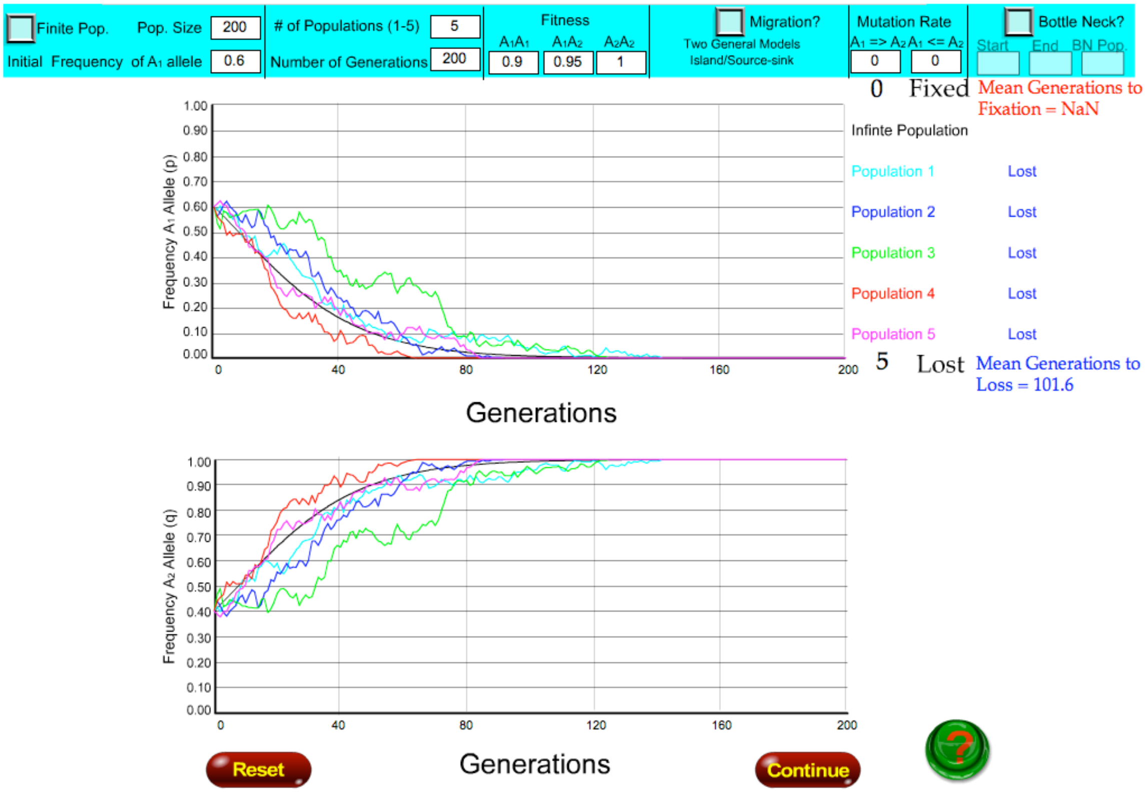
On the upper left of the control window is a box labeled "Initial Frequency of A_1 allele" in which you can enter any number between 0 and 1. (Obviously, you don't have a control to adjust the frequency of allele $\mathbf{A_2}$. Why not?) Next to it are boxes where you can set the starting population size, the number of populations, and the number of generations; these are pretty self-explanatory. Then there are boxes for the relative fitnesses of the three possible genotypes, $\mathbf{A_1A_1}$, $\mathbf{A_1A_2}$, and $\mathbf{A_2A_2}$. These are the same as the **w**-values you've already learned how to set. The highest of these fitness must be set to 1; the other two may be anywhere between 0 and 1.

Under "Mutation Rate", you can enter the $\mathbf{A_1} \Rightarrow \mathbf{A_2}$ mutation rate (the probability that any given $\mathbf{A_1}$ allele will mutate to $\mathbf{A_2}$ in any one generation), and the $\mathbf{A_1} \Leftarrow \mathbf{A_2}$ mutation rate. Both of these are numbers between 0 and 1. You can think of them as the probabilities that, in each generation, a migration or mutation event will occur.

At the right is a button labeled "Migration?" Clicking the box will toggle between two different models of migration among separate populations: Island and Source-Sink. Checking the Island model means that each population exchanges migrants with all other populations. Source-Sink means that all populations receive migrants from a source population with a constant allele frequency. In both options, you input the rate of migration—again, this is a number from 0 to 1, equal to the probability that any given individual will migrate in one generation. If you choose Source-Sink, you use the input box labeled "Freq. A_1" to set the frequency of the allele $\mathbf{A_1}$ in the source population from which organisms migrate into the simulated populations. This option might be used to model, say, island populations receiving migrants from a nearby mainland, while Island might model evolution on a cluster of islands far from the mainland (say, Hawaii). **NOTE:** As we'll discuss in lecture later, an "island" doesn't have to be a bit of land surrounded by water! High-altitude mountain forests in the Mojave Desert, glades and meadows surrounded by forest in the Ozarks, patches of metal-rich serpentinite rock and soil in the middle of a field, lakes connected by small narrow streams, isolated thermal vents on the abyssal ocean floor—all of these can be thought of as "islands" for the purposes of evolutionary biology.

The last control, labeled "Bottle Neck?", allows you to simulate a genetic bottleneck, which is a sudden crash in population size. Checking this box lets you enter "Start", the number of generations at which the bottleneck begins; "End", the number of generations at which the bottleneck ends and the population recovers; and "BN Pop", the population size after the crash.

2. For starters, try setting the initial **A_1** frequency to 0.6, and the three fitness values to , 0.8, 0.9, and 1.0. Make sure the Migration and Bottleneck boxes are not checked, and set both the population size and the number of generations to 200. Click the GO button and watch what happens. The colored lines depict the evolution of *p* and *q* in each population. The black line is the "Infinite population", showing how *p* and *q* would change if the population were infinite (i.e. if there were no genetic drift). It should look roughly like this:



☐ Finite Pop.
Pop. Size: 200
Initial Frequency of A_1 allele: 0.6
# of Populations (1-5): 5
Number of Generations: 200
Fitness: A_1A_1 0.9, A_1A_2 0.95, A_2A_2 1
☐ Migration? Two General Models Island/Source-sink
Mutation Rate: $A_1 => A_2$ 0, $A_1 <= A_2$ 0
☐ Bottle Neck? Start, End, BN Pop

0 Fixed Mean Generations to Fixation = NaN

Infinte Population

Population 1 Lost

Population 2 Lost

Population 3 Lost

Population 4 Lost

Population 5 Lost

5 Lost Mean Generations to Loss = 101.6

See what's happening? In a population with no drift (shown by the darker no-drift line), the $\mathbf{A_2}$ allele vanishes within about eighty generations in the face of relatively mild selection against it. However, in this case, one out of the eight populations still retained the allele after 120 generations, due simply to random effects in a small population.

3. Now try fiddling with some of the parameters. What happens if you reduce the size of each population? What happens if you increase or decrease the fitness of one of the genotypes? What if you increase the frequency of migration? What effect do bottlenecks have?

4. Your assignment is as follows: Spend some time fiddling with the simulator. Run several simulations just to "see what happens." Then use it to answer the following questions, citing specific results and settings from simulations whenever necessary.

1. Write down settings that cause the following outcomes to happen, and explain what happens when you try them:
   - **a)** The **a** allele rapidly disappears.
   - **b)** The **a** allele disappears from some populations and the **A** from others.
   - **c, d)** The **aa** genotype is at a disadvantage, but the **a** allele is kept in all populations, even in the absence of migrations. (There are several ways—find two!)
   - **e)** Hardy-Weinberg equilibrium is reached within one generation.

2. What happens when. . .
   - **g)** . . . all populations are small and completely isolated, with no migration?
   - **h)**. . . all populations are small but frequently exchange migrants?

3. Realistic mutation rates are on the order of 10^{-5} to 10^{-8} per gene per generation. How much effect does "realistic" mutation, by itself, have on evolution? How high do mutation rates need to be to have a visible effect?

4. How—if at all—do "stepping-stone" migration, "island" migration, and "source-sink" migration differ in their effects on population-level evolution?

5. In general, what circumstances seem to favor the most rapid divergence of populations from each other? (I.e., how can you get one population's allele frequency to diverge from another's most rapidly and consistently?)

6. What effect do brief bottlenecks have? What effect do long bottlenecks have?

5. Turn in your answers to these questions. Some will require only one sentence; others may need more explication. Be grammatically correct, clear, and concise.