**Note: read through the shiny Instructions in the Introduction folder if you haven’t already, or have forgotten how to make shiny run.**

**Selection and genetic drift simulation.**

This simulator combines the previous ones to simulate a more realistic scenario, with both selection and drift simulated together. Again, we follow evolution at a single locus with two alleles, ‘A’ and ‘a’in panmictic (random mating) populations of constant size. There is still no migration or mutation, so all of the allele frequency changes are due to either natural selection or random genetic drift.

**Input:** These should now look familiar, as they are the combined input parameters from the selection and the drift simulators. To help you remember, though, they are listed here:

*p,* the initial frequency of the A allele.

*s,* the selection coefficient acting on the A allele

*h,* the dominance coefficient

*N,* the number of individuals in the population, also known as population size.

The number of generations to allow the simulation to run

The number of identical populations to simulate

**Output:**

**Fitness of Genotypes**: The table on the left shows the fitness scheme.

**Plots** There are two plots, each showing the results of the same simulation in different ways:

1-The top plot on the left shows the frequency of the A allele over generations since the start of the simulation. Results from additional populations are shown as additional lines.

2-The bottom plot on the right shows the outcome of the simulations at the last generation simulated (which depends on what you set in the slider on the left). It shows a histogram of the final allele frequencies for different populations.

Answer the questions below to make sure you understand the simulation.

Press escape to end the simulation when you are done.

1. **How does genetic drift affect natural selection?** Set the initial allele frequency to 0.01, the selection coefficient to 0.1, the dominance to 0.5, and the number of individuals to close to 50, and the number of populations to 100.
   1. For how many populations is the beneficial allele fixed at the end of the simulation?
   2. Now, change s to 0.2— for how many populations is the beneficial allele fixed? Does this change make sense to you?
   3. In a deterministic model, what would be the fate of the beneficial allele? (You can run similar simulations in the ‘Selection.R’ simulator from the selection lecture, or you can set the population size in this simulator to 500 and use that information to guess.)
2. **Fate of beneficial alleles in small vs. large populations.** Set the initial allele frequency to 0.01, the selection coefficient to 0.1, the dominance to 0.5, and the number of populations to 100.
   1. For how many populations is the allele fixed when the population size is 1? Is this substantially different from what would happen if there were no selection at all? (You can set s to 0 and compare the results.)
   2. Change population size to 100 and 500, but keep everything else the same. For how many populations is the beneficial allele fixed in each case? How does this compare to no selection in each case?
   3. Does selection ‘work better’ in small or in large populations? Based on the simulation results, what is meant by ‘work better’?