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

**Genetic Drift simulation.**

This simulator simulates genetic drift at a single locus with two alleles, ‘A’ and ‘a’, which have no fitness differences. This simulation simulates panmictic (random mating) populations of constant size. There is no selection, migration or mutation, so all of the allele frequency changes are just due to random chance.

**Input:** The sliders on the left allow you to set up the simulation, including:

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

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

The number of generations to allow the simulation to run

The number of identical populations to simulate

**Output:** There are three 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 top 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.

3-The bottom plot shows genetic diversity (*2pq*)averaged across all of the simulated populations through time. It should be lined up with the plot above it so that you can see how allele frequencies and genetic diversity change together.

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

Press escape to end the simulation when you are done.

1. **Effect of population size.** Population size is an important factor controlling how much random genetic drift affects evolution in a population. To explore its effect, set the number of generations to something close to 100, the number of populations to around 20, the initial allele frequency to anything above 0 and below 1. Change the ‘number of individuals’ (or ‘population size’) from low to high. Answer the following questions:
   1. In the top plot, “Allele frequencies through time”, the dotted line shows the expected allele frequency of the allele through time in a population with no drift. The lines show the allele frequency through time from simulations of populations that are experiencing drift. Do the drifting populations stay closer to the expected frequency when the population is small or when it is large?
   2. The bottom plot, “Genetic diversity through time” shows how genetic diversity changes during the course of the simulation. Does genetic diversity decline faster in small or large populations?
2. **Effect of initial allele frequency.** Set the population size to 500, the number of generations to around 100, and the number of populations to around 20.
   1. Set initial allele frequency to 0— what happens and why?
   2. Set initial allele frequency to 1— what happens and why?
   3. Set initial allele frequency to several intermediate values— how do the simulations track the initial allele frequency?
3. **Ultimate fates of alleles under genetic drift.** Set the population size to around 50, the number of generations to 500, and the number of populations to 100. The plot on the left will probably now be a mess, but that’s okay.

The plot on the far right shows the frequency of the A allele in different populations at the end of the experiment. To see how this plot works, set the initial allele frequency to 0— in this case, all of the populations will have lost the A allele, and the histogram should show one bar on the left over 0 on the x-axis. Set initial allele frequency to 1—now, all populations will have fixed the allele, and there should be a bar on the right over the 1 reflecting this. Use this plot to answer the following questions:

* 1. Set the initial allele frequency to 0.5. How many populations fix the allele?
  2. Set the initial allele frequency to 0.1. Now how many populations fix the allele?
  3. Set the initial allele frequency to 0.9. Now how many populations fix the allele?
  4. Why does the initial allele frequency affect the final outcome in this way?
  5. What happens to genetic diversity in these populations?