

Lab 3: Genetic drift

Basic instructions:

For today's lab, two modules of Populus will be used. For question 1, click on 'Mendelian genetics' then click on 'genetic drift'. Set 'runtime' to 3N generations, '# of loci' to 1, and make sure the tab is set to 'Monte Carlo' and not 'Markov'. For questions 2 and 3, click on 'Mendelian genetics' then click on 'Drift and selection'.

Mathematical background:

The mathematical background for today's lab was covered in the lecture on genetic drift. It would be helpful to review that material before arriving and to bring a copy of that material with you to lab.

Questions:

1. In lecture you saw that the expected time to fixation of a neutral allele was given by $\bar{t} = -4N[p \ln(p) + (q) \ln(q)]$.
 - A. Assuming a population size of 200, use this equation to calculate the expected time to fixation for the following allele frequencies: .01, .1, .5, .9, .99.
 - B. Assuming an initial allele frequency of .1, use this equation to calculate the expected time to fixation for the following population sizes: 10, 50, 500.
 - C. Now, instead of using the equation, answer A and B by running **twenty** simulations for each set of parameters in Populus and averaging the time to fixation observed in each. Also calculate the variance in the time to fixation.
 - D. How close were the two sets of results? What accounts for the difference?

2. As part of an effort to restore viable populations of steelhead trout to a particular stream, a team of researchers was interested in introducing an allele, R, that conferred resistance to whirling disease (the normal allele is denoted S). The current population size of these fish was estimated to be ≈ 200 , the resistance allele was shown to be absent, and the fitnesses of the three genotypes were estimated to be: $W_{RR} = 1$, $W_{RS} = .98$, and $W_{SS} = .96$. Three different regimes were suggested for introducing the R allele:

Regime #1 — Releasing 5 homozygous resistant (RR) fish
Regime #2 — Releasing 15 homozygous resistant (RR) fish
Regime #3 — Releasing 45 homozygous resistant (RR) fish
 - A. What is the initial frequency of the R allele in each of the three regimes?

- B. Run **twenty** simulations for each regime. For each of the three regimes, what % of simulations result in the fixation of the R allele?
- C. Which regime presents the best opportunity for introducing the resistant allele and why?

3. A group of conservation biologists was concerned that an important genetic polymorphism might be lost in an endangered population of ground sloth. This polymorphism is quite similar to the sickle cell polymorphism found in humans. Sloths with the AA genotype are resistant to a protistan parasite that causes a hemorrhagic fever, but they also suffer from moderately severe anemia. Sloths with the Aa genotype receive the benefits of resistance to the protist and suffer only mild anemia. Sloths with the aa genotype are completely susceptible to the protist, but do not suffer any form of anemia. The fitnesses of the various genotypes are $W_{AA} = .98$, $W_{Aa} = 1$, $W_{aa} = .98$. In an infinite population, the frequency of the A allele would reach $\frac{1}{2}$, a condition that would maximize the mean fitness of the sloth population. Unfortunately, the current size of the sloth population is only 50.

- A. If the sloth population does not change size and the current frequency of the A allele is $\frac{1}{2}$, how long can this polymorphism be expected to persist? To answer this question run **twenty** simulations and record how many generations it takes for the allele frequency, p , to reach either 0 or 1. Then calculate the mean and variance of these numbers.
- B. If, through conservation efforts, the sloth population is increased to 300, how long can this polymorphism be expected to persist? To answer this question run **twenty** simulations and record how many generations it takes for the allele frequency, p , to reach either 0 or 1. Then calculate the mean and variance of these numbers.
- C. How would your results change if the fitnesses of the various genotypes were $W_{AA} = .90$, $W_{Aa} = 1$, $W_{aa} = .90$?