

NetLogo simulation of genetic drift and mutation

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In this modeling session, we'll build some NetLogo models of populations experiencing genetic drift and mutation. Using the population genetics theory presented earlier, we can also test some of our mathematical expectations using the simulation.

Basic simulation

Open up the basic drift simulation file. The interface should have “setup” and “go” buttons, a slider to set the number of colors or alleles, a plot of the number of alleles, and the population grid. Going to the “code” tab, you'll see the setup function, an initialize-patches function, and the go function. We'll walk through how these work together.

Next, you can perform the following experiments.

1. Running the simulation with any number of initial alleles, what happens to each allele given each time?
2. The plot of the number of alleles over times reveals an important pattern in how genetic drift works as a function of the diversity in the population. What is this pattern? To see this, you will need to have a decent number of alleles initially and not too large a population size.
3. How does changing the population size affect the time for a single type to get fixed?
 - (a) You may start trying to estimate this and notice how labor intensive it could be since there is so much noise in the fixation times. We'll actually automate this to make the pattern easier to see
 - (b) We'll brainstorm what we need to do to make this work together, but it will involve (i) recording the time there is only one type and (ii) averaging these times.
 - (c) Once you have this up and running, what is the pattern? What does this mean for how diversity is lost in large populations?

Adding mutation

Next, we're going to add mutation to the population so that we get a constant amount of diversity evolving over time; in other words, the model will have what is called a "mutation-drift balance".

1. Add mutation so that each patch gets the same rate μ of mutating. You'll need to add a slider too so that you can change the mutation variable.
 - (a) What happens now to the number of types over time? What does the variation in the number of types tell you about how evolution works even without natural selection?
 - (b) Create a running average of the number of types. I'll give you an equation that actually predicts this! Comparing this running average to the plot of the number of types, what does this tell us about making predictions in specific populations?
 - (c) We talked about heterozygosity in the population genetics section. Add a plot to measure the amount of heterozygosity over time. To do this, you'll need an equation for the heterozygosity. Given that you have n alleles each with frequency p_k (for the k^{th} allele), the heterozygosity is

$$H = 1 - \sum_{k=1}^n p_k^2 \quad (1)$$

You'll probably want a running average of this too. Does this match the equation for heterozygosity?