

Genetic Drift and Gene Flow Illustration

This is a more detailed description of Activity Idea 4, Chapter 3, “If Not Race, How do We Explain Biological Differences?” in: *How Real is Race? A Sourcebook on Race, Culture, and Biology*. Carol C. Mukhopadhyay, Rosemary Henze, and Yolanda T. Moses. 2nd Edition. 2014. AltaMira Press.

<https://rowman.com/ISBN/978-0-7591-2273-4>

These activities were originally developed by or adapted for use here in 2006 by **Scott Smith**, then a graduate student, Department of Anthropology, University of California, Riverside. ©Scott Smith

Genetic Drift Illustration

Objective: To illustrate the effects of genetic drift on allele frequencies in a population.

Conceptual Overview

Genetic drift is one of the four forces of evolution and is defined as the fluctuation of allele frequencies due to random factors. Genetic drift is strongly tied to population size and becomes influential in situations where a small segment of an original population splits off or becomes isolated from the parent population. Sometimes this occurs when a small group founds a new population in geographic isolation from the parent population. This is referred to as ‘founder effect’. Other times this process occurs when a parent population undergoes a devastating population reduction referred to as a population bottleneck.

These processes both produce a situation where a non-representative sample of alleles is carried over to the new population. For example, assume a parent population of

1000 individuals and at one particular locus each individual has one of two forms of a gene, *B* or *b*. In the original parent population 700 individuals have the *B* allele and 300 have the *b* allele. The frequency then of the *B* allele is .7 and the frequency of the *b* allele is .3.

Say 200 individuals become angry with the parent population and decide to leave and start a new settlement far away from the original parent population. Just by chance 180 of these individuals have the *B* allele and only 20 have the *b* allele. The new frequency of the *B* allele in this population is then .9 and the new frequency of the *b* allele is .1. In this case because a random sample of alleles was carried over to a new founder population that is much smaller than the original parent population, allele frequencies were altered. Since evolution is defined as a change in allele frequencies over time we see how genetic drift can be an important evolutionary force.

Materials (per group of students)

- Dry beans of two different colors (they should be as close to the same size as possible) (other materials such two different color marbles may be used alternatively)
- A set of measuring cups
- A large bowl
- A cafeteria tray or a pan of some sort on which to sort beans (something with edges is useful so the beans don't go shooting around the room)

Instructions

- 1) Divide students into groups
- 2) Explain that the beans represent two different alleles (eg. *B* and *b*) at one particular locus on a chromosome. You might say that these beans represent the

- gene for tongue-rolling ability (which is a discrete trait). One type of bean represents the tongue-rollers and the other the non-tongue-rollers. You can use any discrete trait here though.
- 3) Have students take a cup of each type of bean and mix them in the large bowl. Explain to the students that since the alleles are about the same size and the same volume was taken of each there should be the same number of each allele in the bowl (if you want to take the time you can have each group count out even numbers of beans but each group should use about a cup of each type of bean). The beans now in each group's bowl are the original parent population of alleles and the frequency of each type of bean (allele) is .5.
 - 4) In order to simulate the effects of genetic drift students will begin taking samples of beans (alleles) and recording the counts and frequencies of each type of bean on a data table (see example table below). Explain to students that each sample they take represents a group of individuals who have become angry with the original parent population and have decided to leave and settle somewhere else.
 - 5) Groups will begin by taking a $\frac{1}{2}$ cup sample (25%) of the original parent population and counting the number of each type of bean (allele). Students should record this number in their data table and then calculate the frequency of each type of bean by dividing the number of each type by the total number of beans in the $\frac{1}{2}$ cup sample. Explain that the two frequencies should add up to 1.0 (100% of the $\frac{1}{2}$ cup sample). The frequencies of each type of bean (allele) in this sample will probably be close to that of the original parent population of beans (1 cup of each).

- 6) Students should continue by taking a $\frac{1}{4}$ cup sample and recording bean counts and frequencies. Following this a 50 bean sample and then three 20 bean samples should be taken. All samples should be taken without looking at the beans so as to assure that the sample is as random as possible.
- 7) After all groups have finished counting and recording their samples ask students to discuss their results among themselves and report back to the class. Students should find the bean (allele) frequencies vary in general more dramatically from the original parent population frequencies when a smaller sample is taken. Since evolution at the population level is defined as a change in allele frequency over time we can see how genetic drift can be a strong evolutionary force in certain situations. Explain to students that in the new 'founder' populations (the 20 bean samples) allele frequencies can fluctuate more dramatically and it is more likely that a locus will become 'fixed'. That is, it is more likely that one particular allele will vanish from the population. In other words, if there are 1000 beans and we switch 1 bean from one type to another (simulating for example the effects of recombination), it represents a .1% change in the composition of the population. However, if the population is only 10 beans as opposed to 1000, switching 1 bean from one type to another represents a 10% change in the composition of the population. Here we see that a smaller population size can account for a much more dramatic shift in the composition of the population.

Activity Extension – Gene Flow

This can be extended to illustrate another evolutionary force, gene flow. Recall that gene flow is the exchange of genes between populations. Unless the two populations have exactly the same frequencies of a particular gene the overall composition of the resulting population will be altered. Remembering that the evolution is defined as a change in gene frequencies over time we see how gene flow can be an evolutionary force.

We can extend the genetic drift activity to demonstrate the effects of gene flow on gene frequencies.

- 1) Ask each group of students to save their last 20 bean (allele) sample.
- 2) Each group of students from the genetic drift activity should combine with another group to form a larger group. Each larger group should now have two distinct 20 bean samples and a record of the bean (allele) frequencies for their sample.
- 3) Explain that these samples are genetically distinct populations. It is important to emphasize that these genetically distinct populations do not represent different species and that the two distinct theoretical populations can interbreed.
- 4) Explain that our angry populations from the genetic drift activity which split away from the original parent population in that activity have all encountered another split off population and decided to live together. In each large group of students the two 20 bean samples represent the angry populations who split off from the original parent populations. Since now, for each group of students, the two populations become effectively one breeding population, tell students to combine

both 20 bean samples into one bowl which makes one population of 40 beans.

Students should count the number of each type of bean (allele) for this new population and determine the frequencies of each. Students should then compare these new bean (allele) frequencies with those of the two original 20 bean populations and note how they have changed.

- 5) Ask students to discuss these new results among themselves and then report back to the class.

Example of Data Table

		Original Parent Population	½ Cup Sample	¼ Cup Sample	50 Bean Sample	20 Bean Sample	20 Bean Sample	20 Bean Sample
Bean Type 1 (allele <i>B</i>)	Count							
	Frequency							
Bean Type 2 (allele <i>b</i>)	Count							
	Frequency							