

Using Colored Pop-Beads and Four-Sided Dice to Simulate Genetic Drift

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Extended Abstract

The process of genetic drift is one of the more difficult of the classical evolutionary mechanisms for students to grasp. While students generally understand the concept of genetic drift as it occurs in ecological bottlenecks and the founder effect, its occurrence in randomly breeding populations can appear very abstract to some students. Nevertheless, it is one of the most important processes in evolution, as it plays a crucial role in the Neutral Theory and is applied to many evolutionary problems. I have developed a simple method to model genetic drift through random mating in the classroom. The model can be done within the course of a single class period to help students understand the process on a micro-level in a small population. The model can then be expanded to multiple genes or multiple populations. Ultimately it is intended to serve as a bridge to more important computerized models, applications and theory, and a stepping stone to classroom discussions.

In this model, connected pairs of pop-beads represent individuals in a randomly breeding population. The bead colors represent alleles of a gene. Working in groups of two or three, students randomly breed pairs of individuals, produce pre-determined numbers of offspring from each mating, and follow the frequencies of alleles through several generations.

Instructions for the Model

Each group should be provided with multi-colored pop beads of two different colors. The beads are commonly used in chromosome simulation models. Each student group should have sufficient extra pop beads to make more individuals as they continue the exercise and a cup or dish to keep the breeding individuals separate from the other beads. Each group should have one four-sided die. These dice may be purchased at mathematics supply houses and gaming stores. If four-sided dice are not available, six-sided dice may be used, with students ignoring two of the six numbers.

At the outset of the exercise, the students write all the genotypes and all the possible mating combinations of those genotypes. Then they determine the Mendelian ratios for the outcomes of those matings. Some matings will have only one outcome (homozygote X homozygote). Others will have two outcomes (homozygote X heterozygote) and others will have four outcomes (heterozygote X heterozygote). When students perform matings that have more than one possible outcome, they roll a four-sided die to determine each offspring's genotype. They should thus assign numbers one through four to the possible outcomes of the different crosses.

The instructor should determine the size of the population and its genetic make-up. It is best to begin small; a population of eight individuals works well. Allelic frequencies can begin at any number, but it is best to begin with them at 0.500 and a population that is either 100% heterozygous or 50% homozygous for each allele. This is G₀. The instructor should then walk the students in the class through the procedure to produce G₁ and possibly G₂, after which student groups can work independently.

To determine the make-up of a subsequent generation, the students reach into their population and randomly remove two pop-bead pairs, representing two individuals. They then record the genotypes and replace those individuals in the population. Then they mix the cup and remove two more individuals. Each mating will produce two offspring, so the students should repeat this process until they have made four mating pairs.

The students then use the Mendelian ratios and four-sided dice to determine the genotypes of two different offspring from each mating pair. They record the offspring numbers, calculate the allelic frequencies, and make the new generation of individuals using the pop beads. They then use G₁ individuals for another round of random matings. Five to six generations are sufficient for patterns to emerge. The most important data to record are the allelic frequencies. It is useful to graph all the class populations on a common graph (e.g. Futuyma, 2013:262; Herron and Freeman, 2014:247; Zimmer and Emlen, 2013:162).

Students should know that the graph can be interpreted to show either the behavior a specific gene in multiple populations or the behavior of multiple genes within the same population.

By changing the number of individuals in a population, students can explore questions about the relationship between population size and the rate of drift and the end result of drift. By changing the initial allelic frequencies, students can explore questions of the predictability of the end results of genetic drift. Students can also explore multiple alleles by adding further colors.

Outcomes

The ultimate goal for this exercise is to impress on students the process of genetic drift and its relationship to the probabilistic events in breeding. With this background, students should be able to better comprehend the evolutionary and ecological consequences of genetic drift and the research and theory that come from an understanding of the basic process of drift.

Literature Cited

- Futuyma, D. J. 2013. *Evolution*, Third Edition. Sinauer Associates, Sunderland, Massachusetts, 655 pages.
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- Zimmer, C. and D. J. Emlen. 2013. *Evolution: Making Sense Out of Life*. Roberts and Company, Greenwood Village, Colorado, 680 pages.

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