

Fall 2015

Genetic Drift Simulation

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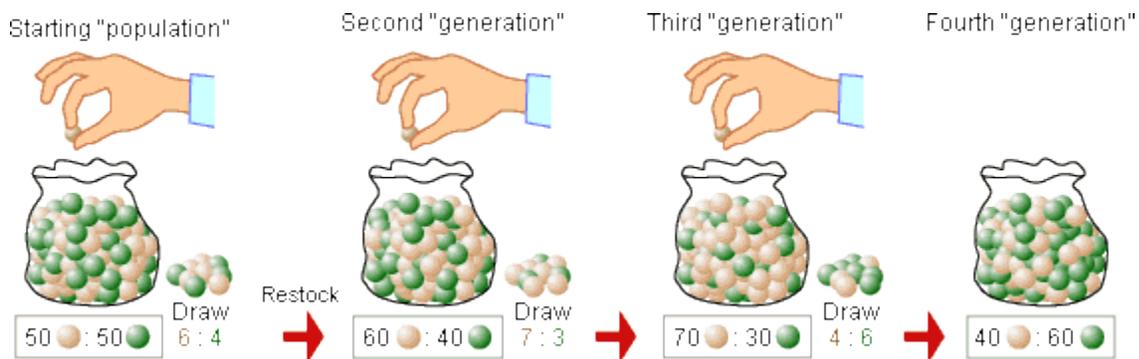
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Genetic Drift Demonstration

Genetic drift can be defined as a random fluctuation in gene frequency. More specifically, it tells us that different alleles may increase or decrease in a population in proportion to one another over time, just by chance, rather than due to any fitness advantage.

The following activity and questions will help you “see” how these fluctuations work and impact a population.



<http://evolution.berkeley.edu/evosite/evo101/IIID1Samplingerror.shtml>

Directions:

1. Collect a mix of 100 beads, 50 of each color. These 100 beads represent the alleles for 50 diploid individuals in a population.
2. Without looking at the color, draw 10 beads out of your pile. Count up how many of each color you have.
3. Use the proportion you determine from the beads you pulled to “restock” your population. For example, if you pulled 6 black and 4 blue, then 60%, or 60 beads, in your next generation would be black.
4. Repeat and collect your ratios for 4 generations.
- 5.

| Generation # | Allele 1 | Allele 2 |
|--------------|----------|----------|
| 0 | 50% | 50% |
| | | |
| | | |
| | | |
| | | |

1. Why did you have to “restock” your bag between generations? How does this relate to genotypes and inheritance?
2. When you look at your chart, what did you notice about the fluctuations? What would you expect to see over time? Were you ever close to losing an allele?
3. How would you expect your answer for number 2 to change in an even smaller population, say, 10 individuals? Why? What about a very large population with 1000+ individuals?
4. What would be different about this simulation if you were trying to model natural selection instead of genetic drift? What would you have to consider? How would you expect the trends over time to change?
5. How would mutation change this simulation? Where would the mutations come from, and how would they get passed on? What impact might it have on allele frequencies?
6. What might you have to change if you incorporated genetic flow? What impact would this have on allele frequencies?