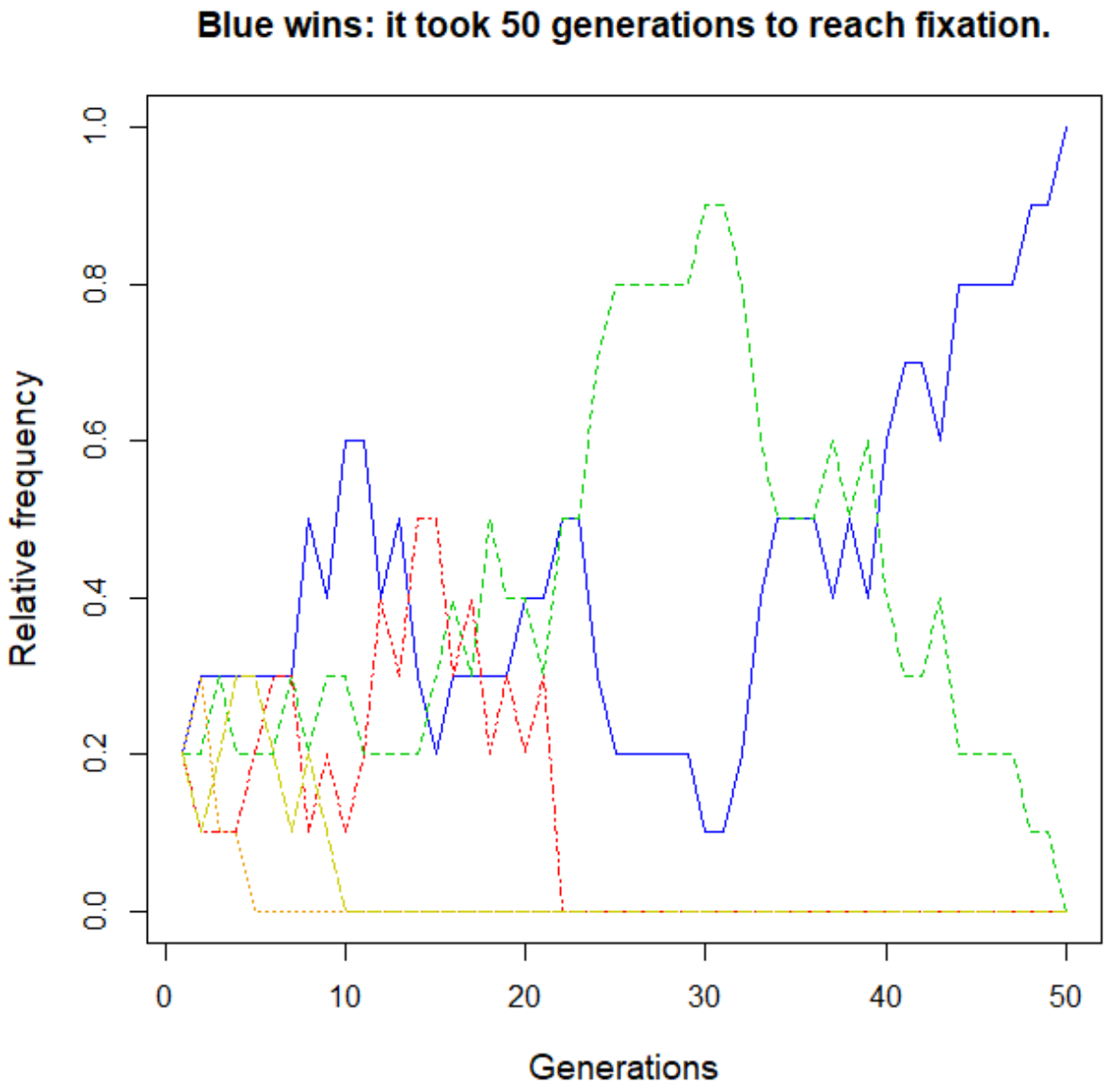
Demonstration of Genetic Drift with M&Ms

Author: Corey D. Anderson, Associate Professor of Biology, Valdosta State University

The following is an exercise from a lab I developed to teach students about genetic drift and, in particular, how genetic drift erodes genetic variation in a gene pool over time, eventually leading to the fixation of a single allele. The students really love this lab, partly because they get to play with and eat M&Ms, but also because it is super effective in demonstrating the power of genetic drift in small gene pools.



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The hardest part of this lab is in teaching the students how to populate and re-populate the gene pools after each generation of drift; it's really not all that complicated, but can be confusing, at first. I would recommend that you walk around and make sure everybody understands it correctly. A simple one-on-one demonstration usually resolves any lingering confusion.

There are three parts to this lab exercise and companion R code.

1) Basic demonstration of drift based on 20 generations of sampling.*
2) Drift with a bottleneck in generation five.
3) The balance of gene flow and drift.

*The R code (as written at the present time) goes with part 1. Since not all students' gene pools will hit fixation by generation 20, it will help to show them that, eventually, drift will lead to fixation (and it will give them a sense of the variation in time it can take). I have considered making a Shiny app so that the students can do this with a nice GUI, on their own (this would be great, IMO). As is, I usually run it on the screen a few times so that they can see what happens. I suppose you could use this as an opportunity to show students how to run R code, but that is not my intention. Feel free to modify the code and use. I just ask that if you modify/add code, you share it with others (as I have done here).

Required supplies:

a) A large party bag of regular M&Ms. Our sections at VSU have 14 students/lab. I can usually cover three sections (with some M&Ms to spare) with two party bags. Sending some students home, at the end, with some fresh M&Ms is also a good way to make friends.
b) Brown paper lunch bags.
c) Some clean plastic cups (I use the red keg cups; they work well for the task and the students are familiar with these ;).

Group structure:

I usually have them work in pairs. They can also do this on their own, but I have found that students usually work better if they have a peer to help explain things (in the case that one student is confused). Pairs also cuts down on the number of M&Ms required.

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Part 1: Loss and fixation of M&M alleles.

All parts of this lab (1, 2 & 3) start the same way. You will need some M&Ms, a paper sack, and a (clean) surface to put the M&Ms on (e.g. a glass bowl or paper towel). I usually poor the M&Ms into the red cup, about one-third full, and then give them to each group (= deme). I also usually poor some M&Ms on a paper towel and have them available in the front of the lab, so that if a student runs out of a particular color, they can come get more.

M&Ms come in six different colors (red, orange, yellow, green, blue, and brown). We are going to ignore the brown M&Ms (let them eat these, if they wish); pretend that the remaining five colors represent different alleles: *r*, *o*, *y*, *g*, & *b*. If you are partial to brown, just switch out one of the colors.

- Take four of each of the five colored M&Ms from the red cup (for a total of 20 M&Ms) and put them into the paper bag; this is your gene pool. Your initial relative frequency for each allele in the gene pool should bel 4/20 = 0.2.

- Now shake the bag (gently) and draw 10 M&M alleles from the gene pool (one at a time). Put them on the paper towel (or in a bowl). Taking them out in small numbers ensures that there is no genic bias in replacing the colors if you happen to go beyond 10.

- Poor the remaining 10 M&Ms (in the bag) back into the red cup.

- Assess the frequency of each color that was sampled and use these frequencies to define the new gene pool of the next generation. The total count of M&Ms in the new gene pool from which you will sample should, again, total 20; the easiest way to do this is just to double the count of each color that you drew previously.

    - For example, let's say that of the 10 M&Ms that were drawn, the counts were: 1 red, 2 orange, 2 yellow, 2 green, and 3 blue….you would put back in the (empty) bag: 2 red, 4 orange, 4 yellow, 4 green, and 6 blue.
        - This ensures that the relative frequency of each allele is preserved in the new gene pool (but back at an N of 20) and shows how the effects of drift accumulate through time.
        - Biologically, this is kind of like clonal/vegetative reproduction.

    - For this simple demonstration, there is no need to write down the relative frequencies in each generation (you could do this and have them plot it out for homework, but I do not). The only thing that they must track is the generation number.

Have each group (= deme) repeat this process 20 times. If all of the colors disappear before 20 generations have passed, stop. If more than one color remains after 20 generations, have the students record how many colors you had left.

I have the students answer particular questions for homework that are coupled to the textbook and lecture, but, at the least, you should talk with the students about what happened. Run the R code to demonstrate that, eventually, only one color will remain.

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Part 2: M&M bottleneck

Repeat the simulation above, but this time in generation five only draw two alleles from the gene pool. As before use these frequencies to define the gene pool of the next generation (i.e., generation six), where the total count in the new gene pool should again total 20 (the easiest way to do this is to multiply the count of each color by 10 (if you draw two of the same color the simulation is over). After the bottleneck in generation five, resume the normal procedure (i.e., by drawing 10 alleles).

If time is short, I usually have the students stop after the bottleneck generation. We then talk about how the bottleneck affected genic variation. In this case, there are only two outcomes: one color or two. Make the point that there is always a loss of genetic variation in a bottleneck, but that bottlenecks can also reshuffle relative frequencies. For example, an allele that was rare could become common. Note that, in the case they draw two different colors, drift will eventually, again, lead to one color, but that it might take a long time to reach fixation (since the relative frequency of each allele will begin at 0.5).

Part 3: The balance of gene flow and drift

Have the groups (demes) array themselves in one dimension. Repeat the original M&M experiment (i.e. start the same way), but this time, for each generation, take 6 of the 10 alleles and give three to the deme on your left and three to the deme on your right. Conversely, add in three alleles from the deme on your left and three alleles from the deme on your right. Note that this requires that the entire class samples in unison (I usually play romantic music). I have the groups on the end exchange with each other.

This is similar to a 1D stepping-stone model of gene flow (but circular). A fun twist is to have one of the groups on the end replace a color with brown M&Ms, so that you can track if/how the brown alleles flow through the demes.

The basic idea here is to demonstrate the balance of gene flow and drift, and how gene flow counteracts the effects of drift. Ask them whether they had any colors/alleles that were lost but came back via gene flow. Talk about what would happen if you had more or less gene flow. Perhaps introduce the idea of isolation by distance.

I usually crack a joke at the end about whether or not they would still eat the M&Ms….and then tell them this is the concept of communicable and sexually transmitted diseases and that, next time, they should wear gloves. Send them home with a fresh bag of M&Ms, if they want them.

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