

Investigations dealing with GENETIC DRIFT

I preliminary observations

1. This time we will violate a different assumption of the Hardy-Weinberg, infinite population size. What an infinite population size does is eliminate all sampling error. Sampling error is chance deviation in the real world from theoretic expectations.

For example, the theoretic probability of head with any coin flip is 0.50, so if we flip a coin 10 times we should theoretically get exactly 5 heads and 5 tails. However, we often get 4, 6, or even 10 heads. Those deviations from 5 heads are sample error.

In the same way, Hardy Weinberg calculations are based on theoretical expectations that may not be met in the real world, for example:

- a. The allele frequency calculation $p = \text{freq}(A1A1) + .5 \text{ freq}(A1A2)$. Assumes that the A1A1 and A1A2 individuals will reproduce at exactly their frequencies in the population. In nature, A1A1 individuals might enter into slightly more mating than expected, just by chance --not because they have any advantageous quality. That's sampling error.
 - b. The union of gametes to produce offspring genotype frequencies of p^2 , $2pq$, and q^2 assumes that the gametes will combine at exactly the p and q frequencies. But in nature, just by chance, the allele frequencies involved in making the next generation not exactly p and q . As a result, for example, there may be slightly more A1A1 combinations and the frequency of A1A1 offspring will be a little larger than p^2 . That's sampling error again.
2. To introduce sampling error, set the population size to 20 ("finite" means an element of chance is involved). Keep all other parameters the same as the Hardy-Weinberg conditions. Set generations to 100. Run 5 populations simultaneously all starting at the same initial frequency.

Notice that population 0 is an infinite population and so represents the control treatment.

Notice that the upper graph tells you the number of populations in which the A1 allele was either fixed or lost. If A1 is fixed, then A2 is lost, as you can see on the lower graph.

If not all alleles are fixed or lost, click "continue" to see how many generations it takes.

3. The patterns of evolution that result from sampling error is called genetic drift -- frequencies seem to drift at random. But if we measure averages or percents from lots of populations, we can see that despite the randomness, there are some trends.

Notice you can measure or count various things, such as:

- the number of populations in which an allele is fixed (or lost).
- the time (generations) to fixation (or loss).
- how often the direction of change changes.
- there is no regular slope, but you can measure the maximum and minimum amount of change in N generations.

4. Draw conclusions (generalizations) about how "drifting" populations tend to evolve

II. We will now conduct an experiment where we, as a class, collect and share data. We will address three questions:

- 1) What is the affect of population size on genetic drift?
- 2) What is the affect of allele frequency on genetic drift?
- 3) What affect does gene flow have on genetic drift?

We will start with each person collecting data on the length of time till loss or fixation of alleles at various starting allele frequencies and different population sizes. Each person will run each simulation 5 times and record the following information:

- Number of times A1 allele was fixed.
- Average time till fixation of A1 allele.
- Average time of loss of A1 allele.

Experiment 1:

Set number of populations to 10. Set A1 allele frequency to 0.1. Record the following data for each population size.

[illegible]

Experiment 2:

Set number of populations to 10. Set A1 allele frequency to 0.25. Record the following data for each population size.

[illegible]

Experiment 3:

Set number of populations to 10. Set A1 allele frequency to 0.5. Record the following data for each population size.

	Population size N = 10			Population size N = 50			Population size N = 100			Population size N = 200		
	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss
1												
2												
3												
4												
5												
Mean												

Experiment 4:

Set number of populations to 10. Set A1 allele frequency to 0.75. Record the following data for each population size.

	Population size N = 10			Population size N = 50			Population size N = 100			Population size N = 200		
	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss
1												
2												
3												
4												
5												
Mean												

Experiment 5:

Set number of populations to 10. Set A1 allele frequency to 0.9. Record the following data for each population size.

	Population size N = 10			Population size N = 50			Population size N = 100			Population size N = 200		
	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss	A1 Fix	Mean fix	Mean Loss
1												
2												
3												
4												
5												
Mean												

After collecting your data calculate the means in each column and record these data on the google docs table at the link I sent you on Thursday. Each experiment appears on a different tab (look at the bottom of the web page). The last row will be the calculated means for each column. Draw conclusions (generalizations) about how "drifting" populations tend to evolve. Write a concise summary of your conclusions based on group data.