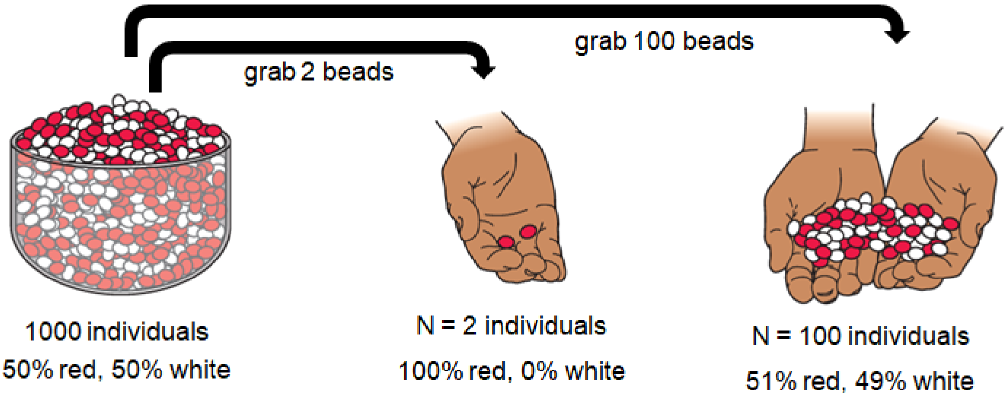
Lab 3 Worksheet: Genetic Drift

In this lab, we will be simulating the effects of genetic drift using coloured pompoms to represent alleles.

Genetic Drift is a random change in the allele frequencies of a population. It is an important mechanism of evolution, because it is *non-adaptive* and can affect *neutral variation*. It generally has a stronger effect in small populations because of random sampling error. For instance, if a small random sample of individuals is separated from a larger population, the allele frequencies (proportion of traits) in that sample may differ significantly from those in the population as a whole, merely because of the luck of the draw (think of the likelihood of flipping a coin twice and getting two heads vs. flipping a coin a hundred times and getting one hundred heads). Because genetic drift is random, the exact change in allele frequency over time is *unpredictable*.



There are two major scenarios where genetic drift is likely to take place: After a **Population Bottleneck** and after a **Founder Event**.

A **Population Bottleneck** is when a large population is drastically reduced in size (by numbers of individuals) due to some natural or anthropogenic disaster which wipes out a significant portion of the population. It is important to remember that this is *random with respect to fitness*. Individuals don't survive the bottleneck because they have useful traits, but rather because they are simply lucky. A **Founder Event** describes the colonization of a new habitat by only a few individuals, causing them to form a new small population. In both scenarios, there is a high likelihood that the new populations contain a different frequency of alleles than the initial population. In fact, these populations may have even lost certain alleles totally from the original gene pool. Even without a Population Bottleneck or Founder Event, alleles are more likely to be lost from small populations rather than large populations due to chance genetic drift. In all these scenarios, the change in allele frequencies is not due to these alleles giving individuals an advantage in survival or reproduction (*i.e.* it is not due to natural selection).

A. Effect of Population Size

In this activity, we will examine the effect of population size on the effect of genetic drift. How do you think genetic drift affects allele frequencies? Come up with a possible explanation (hypothesis) to answer this question.

Hypothesis (3):

How do you think genetic drift will affect the frequency of alleles in a large population? How about in a small population? Come up with a prediction for how allele frequencies might change in each population.

Predictions (4):

Methods:

- You will be given two island populations: a Big Island (with 80 pompoms) and a Small Island (with 16 pompoms).
- **With your eyes closed** (remember that Genetic Drift is random), pick out **40** lucky pompoms from the Big Island (50% of the population) and **8** lucky pompoms from the Small Island (50% of that population) to reproduce.
- Keep the two groups of breeding pompoms in separate piles and empty both of the islands of all of the non-breeding pompoms into the extra bin.
- Let each breeding pompom reproduce one individual of its own kind by adding one pompom of the same colour to the breeding population and place those parents and their progeny (offspring/kids) back into their appropriate islands. The Big Island should again have 80 pompoms and the Small Island should again have 16 pompoms.
- Record the new number of each color of pompom in Table 1 under "Year 2".
- Continue this procedure for three (3) more years (for a total of 5 years).
- Convert the number of pompoms to a frequency in Table 2. Hand in both data tables to the instructor.
- Pool the class data and construct a **line graph** mapping the **frequency of each allele** (pompom colour) in the population **over time**. Consider each group's data as **a separate line**. You should have one graph for each pompom colour and separate graphs for each population size (14).

Using your graphs, answer the following questions (20):

- How did the frequency of each allele (number of each pompom colour) change over time on each of the islands?
- Did the frequency of alleles change more on one island than the other? Explain.
- Were any alleles lost? Is that beneficial or detrimental to the island population? What process(es) could bring those lost alleles back into the population?
- Was your initial hypothesis supported? Why or why not?

Table 1. Number of pompom colours in each year with genetic drift (3)

Island	**Allele (pompom colour)**	**Year 1 (# of each colour pompom)**	**Year 2 (# of each colour pompom)**	**Year 3 (# of each colour pompom)**	**Year 4 (# of each colour pompom)**	**Year 5 (# of each colour pompom)**
Big Island	*White*	10				
	Yellow	10				
	Orange	10				
	Pink	10				
	Red	10				
	Purple	10				
	Blue	10				
	Green	10				
Small Island	*White*	2				
	Yellow	2				
	Orange	2				
	Pink	2				
	Red	2				
	Purple	2				
	Blue	2				
	Green	2				

Table 2. Allele frequency over time with genetic drift (3)

Island	**Allele (pompom colour)**	**Year 1 (allele frequency)**	**Year 2 (allele frequency)**	**Year 3 (allele frequency)**	**Year 4 (allele frequency)**	**Year 5 (allele frequency)**
Big Island	*White*					
	Yellow					
	Orange					
	Pink					
	Red					
	Purple					
	Blue					
	Green					
Small Island	*White*					
	Yellow					
	Orange					
	Pink					
	Red					
	Purple					
	Blue					
	Green					

B. The likelihood of an allele surviving a Population Bottleneck (43)

In this activity, we will explore two factors that affect the likelihood of an allele surviving a population bottleneck: the frequency of the allele in the population and the severity of the bottleneck event.

How do you think these two factors will affect the likelihood of alleles being lost?

Hypothesis (3):

What would you predict about the likelihood of an allele being lost if it at a high frequency vs. a low frequency? How about if the population loses more or fewer individuals?

Prediction (4):

Methods:

- You will pick two colours to represent two alleles in your populations. Write them into Table 3 and 4.
- You will then reset your island to have **45** of one colour pompom and **5** of the other colour pompom according to **Population 1** below.
- **With your eyes closed** (remember that Population Bottlenecks are random), you will simulate a **mild** bottleneck by picking out **25** lucky pompoms that will survive to reproduce.
- Record the number of each color of surviving pompom in Table 3 under "After" for Population 1 in the row for “Mild Bottleneck”.
- Next reset your Population 1 island and simulate a **moderate** bottleneck (**15** lucky pompoms survive) and a **severe** bottleneck (**5** lucky pompoms survive).
- Repeat this procedure for the starting allele frequencies of Population 2 and 3. You should run **9** trials in total (each of the three populations should undergo each type of bottleneck).
- Convert the number of pompoms to a frequency in Table 4. Hand in both data tables to the instructor.
- Construct a **stacked bar graph** mapping the **frequency of each allele** (pompom colour) **before** and **after** the population bottleneck. You should have separate graphs for each population, and each graph should have four bars (*Before, After (mild), After (moderate), and After (severe)*) (10).

Using your graphs, answer the following questions (20):

- How did the frequency of each allele (number of each pompom colour) change after the bottleneck?
- Did the frequency of alleles change more after one type of bottleneck? Explain.
- Did the frequency of alleles change more depending on their initial frequency? Explain.
- How do you think genetic drift would affect your populations after the bottleneck?
- Was your initial hypothesis supported? Why or why not?

Table 3. Number of pompom colours after a bottleneck event (3)

		Population 1		**Population 2**		**Population 3**	
	Allele (pompom colour)	**Before (# of each pompom)**	**After (# of each pompom)**	**Before (# of each pompom)**	**After (# of each pompom)**	**Before (# of each pompom)**	**After (# of each pompom)**
Mild Bottleneck		45		35		25	
		5		15		25	
Moderate Bottleneck		45		35		25	
		5		15		25	
Severe Bottleneck		45		35		25	
		5		15		25	

Table 4. Allele frequency after a bottleneck event (3)

		Population 1		**Population 2**		**Population 3**	
	Allele (pompom colour)	**Before (allele freq.)**	**After (allele freq.)**	**Before (allele freq.)**	**After (allele freq.)**	**Before (allele freq.)**	**After (allele freq.)**
Mild Bottleneck							
Moderate Bottleneck							
Severe Bottleneck							

C. Simulating the Founder Effect (10)

Given the previous two simulations, how would you use the pompoms to simulate the effects of a Founder Event?

How would you assess how the allele frequencies had changed?

For this lab, you will submit a formal lab report of your results. Your write up should include:

- an introduction (10)
    - including your hypotheses and predictions from each section above,
- the methods (5)
    - a summary of what we did for each section
- the class results (15)
    - all the data tables above, your graphs, as well as a written description of the results from each section
- a discussion of the results (15)
    - including answers to the above questions for each section (include the Founder's Effect questions here)
- a conclusion (5)
    - explain what you learned from this lab