

# 1. Evolution lab

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## BACKGROUND

This lab has two parts: a longer section to demonstrate principles of microevolution, and a shorter part to demonstrate the evidence for evolution discussed in lecture.

## CONCEPTS

Hardy Weinberg Equilibrium (HWE) is a “null model” of no evolution within a population, i.e. allele frequencies remain constant through generations. Certain conditions must be met.

Microevolution is any case breaking the rules of HWE. Relevant lecture information: [How populations evolve](#)

There are four general categories of evidence for evolutionary theory. Relevant lecture information: [The theory of evolution](#)

## A. Evolution prequiz

1. List the five conditions required for Hardy-Weinberg equilibrium (Outline 2 How populations evolve, point 3)

2. List the four categories of evidence for evolution and their definitions (outline 1 Theory of evolution, point 3).

## B. Microevolution: Hardy-Weinberg simulation

GOALS: You will use a model of a population's gene pool to test three of the five types of **microevolution** discussed in class. Remember that "no evolution" is represented by the **Hardy-Weinberg equilibrium**. so violating one of the assumptions behind this equilibrium will lead to one type of microevolution. In essence, we are performing the examples found on p268 of your textbook.

### 1. Model introduction procedure

This is a short demonstration to show you the model we will use for simulating genetic changes in populations using beads.

Work in pairs. Obtain a bag of beads from the side bench. There should be 50 of each color. Each bead represents one **allele** of a particular **gene**. The entire bag therefore represents the **gene pool** of the **population**. Therefore your starting frequency of the alleles is 50:50.

Your instructor will tell you which of the colors is dominant. Record that information here: \_\_\_\_\_. We will refer to this color as A, and the other color as a. This is the same capital letter/lower case letter notation you used for studying the genetics of individuals in the first term.

Any given individual would have two alleles for this gene. if they have two of the same allele they are be **homozygous**. If they have two different alleles they are **heterozygous**.

We will first test whether the population's **allele frequency** stays the same after one generation of sexual reproduction. That is, after mixing up all the genes, will the allele frequencies still be 50:50?

1. One partner draws one individual (two beads) out of the bag without looking and states its **genotype** (AA, Aa, or aa). You may find it easier to say "Dominant", "heterozygote," or "recessive."
2. Record this allele in the table provided.
3. Return the beads to the bag and shake the bag to mix up the beads. We call this sampling with replacement, and it gives us an effective population size larger than 50 (100 beads/2).
4. Repeat this 50 times total.
5. Count the number of times you got each genotype, then calculate its frequency.
6. Calculate the new allele frequency. This is normally done using the Hardy-Weinberg equilibrium. However, a quicker way is to calculate  $(2 * \text{homozygous}) + (\text{heterozygous})$  and divide by the total number of alleles. So if you got 31 dominant, 17 heterozygous and 2 recessive your allele frequency for A is  $((2*31)+17)/100$  or 79%.
7. Compare this frequency to the 50:50 frequency from the beginning.

### 2. Does sexual reproduction change the allele frequency in a population?

### 3. Genetic drift procedure

The question here: what if you try the same thing with a small population? Small populations undergo **genetic drift**.

1. Work as a bench (two pairs). One pair's bag will become the gene pool of interest, the other pair's bag becomes spare beads.
  2. Pull out one individual (two beads) as before and record the genotype. This time though, **DO NOT PUT THE BEADS BACK IN THE BAG YET**.
  3. Repeat for a total of 5 times. That was one generation.
  4. Compute the allele frequencies for this generation.
  5. Adjust the allele frequency in the bag to match the allele frequency you calculated for this generation. For example, if your allele frequency was A:a 30:70, then take out 20 beads of the dominant color and store them in your reserve bag. Replace with 20 beads of the recessive color from your reserve bag. (Yes, you put back the beads you pulled out for this)
  6. Repeat this for 5 generations, each time calculating your allele frequency and then adjusting the bag.
  7. Graph your results on the board. All groups should use the same graph, just each group should use a different color marker or different symbols.
- 4. Data tables (see the end of the lab)**
- 5. Does allele frequency change among generations in this case? In which direction? Why?**

- 6. Did all groups get the same pattern? Why or why not?**

**7. Natural selection procedure**

What happens if some alleles make the individual less likely to survive or reproduce?

Let's assume that the dominant alleles lead to a dark phenotype and the recessive alleles lead to a light phenotype. That means the dominant homozygous or the heterozygous genotypes are dark and the recessives are light colored. If the background is dark, and there is a predator that can easily capture individuals that are obvious against this background, what happens to a population of individuals that are largely light colored?

This exercise has more complex calculations from before, so use the datasheet provided.

1. Continue working as a bench.
2. Adjust your gene pool to an allele frequency of 10:90 A:a.

3. Select 50 individuals WITH REPLACEMENT as in the model introduction procedure. Record the genotype frequencies, but do NOT calculate allele frequencies yet.
  4. Now come the predators: 50% of the light individuals get eaten but only 10% of the dark individuals. So reduce the numbers of homozygous recessives by half, but reduce the number of homozygous dominants and heterozygotes each by 10%.
  5. Calculate allele frequencies based on this new total.
  6. Adjust your gene pool allele frequencies to match what you have just calculated. That is one full generation.
  7. Repeat for about 4 generations.
  8. Graph your results on the board as a class, as you did for the genetic drift exercise.
- 8. Natural selection data sheet (see the end of the lab)**
- 9. Does allele frequency change among generations in this case? In which direction? Why?**

**10. Did all groups get the same pattern? Why or why not?**

**11. What would happen if the phenotypes were reversed, i.e. A was light and a was dark?**

**12. What would happen if you started with 100% aa individuals?**

**13. Gene flow procedure**

Now we are going to simulate evolution by gene flow, i.e. individuals moving between populations and bringing alleles with them.

1. Continue working as a bench but each pair uses a bag as their gene pool.
2. Note the initial allele frequencies of each bag, based on the results of the natural selection exercise. If they are close to 50:50, exchange some beads so they are significantly different, at least 70:30.
3. Each round you are going to swap 10 individuals. So draw 20 beads out of the bag WITHOUT REPLACEMENT and put them in a glass dish.
4. Swap dishes with the other pair on your bench. Dump these beads into your bag.
5. Repeat 3-4 times.
6. Count your beads to calculate your new allele frequency.

**14. Does allele frequency change among generations in this case? In which direction? Why?**

**15. Did all groups get the same pattern? Why or why not?**

## C.Evidence for evolution

GOALS: See examples of comparative morphology, comparative embryology and the fossil record to support lectures 1 and 2. Students should be comfortable explaining how these data sets support the theory of evolution, using specific examples from the demos. Note that we do not cover molecular evidence for evolution in this lab.

### 1. Comparative morphology procedure

**Homology** of bones in the vertebrate forelimb. Examine how the ancestral limb form has been modified for various tasks.

1. Examine the skeletons on the side bench (frog, cat, bird, human). Find the forelimbs of each and count how many bones are at each joint.
2. Compare each limb to the ancestral state (frog), region by region, using common terms (fingers, elbows).
3. If you have time, examine the skeletons on display in the ground floor hallway. Can you find the same bones?

### 2. Comparative embryology procedure

Comparative embryology: similarity among embryonic forms. This is different than comparative morphology because embryological form differs from adult form.

1. Examine the slides of pig and chicken embryos.

Identify the three major shared characters visible (pharyngeal slits, somites, post-anal tail)

### 3. Fossil record procedure

The fossil record indicates that evolution has occurred. We can date the appearance and disappearance of similar forms over time by their presence/absence in different **strata**. Through this sequence, we can see a timeline of similar looking species that change in predictable ways.

Examining the fossil record in detail would take more than one lab time, but I wanted you to at least see examples. Note the time frame of each tray (Paleozoic is older than Mesozoic is older than Cenozoic). See p299 of your textbook for descriptions of these time periods.

4. **Which line of evidence for evolution did we NOT examine here? Why is it considered important?**

Table 1. Results from Model Demonstration

Parent populations		New Populations				
Allelic Frequency		Genotype Frequency			Allelic Frequency	
<i>A</i>	<i>a</i>	<i>AA</i>	<i>Aa</i>	<i>aa</i>	<i>A</i>	<i>a</i>

Table 2. Results from Genetic Drift Simulation

	Genotype frequency			Allelic frequency	
	observed			observed	
Generation	<i>AA</i>	<i>Aa</i>	<i>aa</i>	<i>A</i>	<i>a</i>
0				0.5	0.5
1					
2					
3					
4					
5					

**BI102 Lab 1: Evolution**

Data sheet for the Natural Selection exercise

