Objectives

Learn basic principles of population genetics and microevolution through the use of a computer model.

Pre-lab assignment

Before lab, read the introductory material below and use your textbook to review the following (chapters 14 and 23).

- Basic terminology and principles of Mendelian genetics (chapter 14).
- Evolution and conditions that influence microevolution including genetic drift, gene flow, mutation, modes of selection in a population, genetic bottlenecks, and random and nonrandom mating (chapter 23).
- Use of the Hardy-Weinberg principle to predict genotype frequencies from allele frequencies (chapter 23).

You may also wish to begin working with the computer model that we will use in lab (see below). It is linked to the Biology 121 Lab page.

Introduction

We’ll start with some definitions. A population is a group of individuals of a species that live together in a particular area and therefore can encounter each other and interbreed. A species is made up of one or more populations. Each population has a gene pool, which consists of the genes of all the members of the population. Population genetics refers to the make-up of the population gene pool- which alleles are present, and how common they are. Allele frequency is defined as the proportion, of all the copies of a particular gene, that is represented by a particular allele. If there is only one allele present, that allele is said to be "fixed" and its frequency is 1.0 (=100%).

The frequency of alleles in a population affects the frequencies of genotypes and phenotypes in predictable ways. This fact was recognized early in the 20th century by Godfrey Hardy, an English mathematician, and Wilhelm Weinberg, a German physician. They (independently) derived simple formulas that can relate frequencies of genotypes to the frequencies of alleles, and vice-versa. For the simple case of a gene locus with two alleles (A and a), the formulas are as follows:

1. \[ p + q = 1.0 \]
2. \[ p^2 + 2pq + q^2 = 1 \]

In this formula, \( p \) is the frequency of allele A, and \( q \) is that of allele a. Remember that allele frequencies are proportions. If these are the only two alleles in the gene pool, then \( p + q \) must equal 1.0. In the second equation, \( p^2 \) represents the probability of an individual having genotype AA, \( 2pq \) the probability of genotype Aa, and \( q^2 \) the probability of genotype aa. This equation is rather like a Punnett square diagram, but it can make predictions for genotypes in populations.

Hardy and Weinberg also recognized that allele frequencies and genotype frequencies could stay the same from one generation to the next, if nothing happened to change them. This condition is called genetic equilibrium. Genetic equilibrium in a population requires some rather unrealistic conditions. These include the following:

1. No mutation.
2. No selection.
3. Population size is infinitely large.
4. All individuals breed and each produces the same number of offspring.
5. Mating is random.
6. There is no net gene flow.
Genetic equilibrium requires that every individual reproduce equally, regardless of genotype, so that allele frequencies stay the same. However, if some genotypes reproduce more than others do, or if certain genotypes are removed from or added to population, the allele frequencies change (evolve). **Evolution** can be defined as a change in the allele frequencies in a population. Several processes can change the allele frequencies to change. Foremost among these processes are selection and genetic drift.

**Selection** is the differential survival or reproduction of a particular genotype because of the selective action of the environment (natural selection) or human intervention (artificial selection). **Genetic drift** is also differential survival or reproduction of a particular genotype, but it is due to chance (not selection). Both processes cause evolution (change the gene pool).

Other processes that can change the gene pool include **gene flow** (net movement of alleles into or out of the population), and **mutation**, although mutation is too rare to significantly alter allele frequencies alone. **Assortative mating** is also a factor, acting as a sort of selection that can reduce or preserve genetic diversity. We will investigate all of these factors using a computer model of population genetics, called PopGenLab.

The PopGen model presents populations of moths and describes the genetics of a locus that determines their color. There are two alleles (A and a) which show incomplete dominance. Therefore, there are 3 phenotypes. Genotype AA is black, aa is white, and Aa is brown.

The moths inhabit stands of trees. In each stand there are three types of trees, which are black, white and brown. Thus, each phenotype of moth has a tree type on which it is best-camouflaged. There are birds present, which exert natural selection on the moths. The birds are more likely to eat those moths that are not matched to their trees. (This model was inspired by real-life research on the moth *Biston betularia*, which has provided well-known examples of natural selection in action).

The first screen shows a table of input parameters. The table lists the parameters that you can manipulate when setting up your experiments. You must be familiar with the input parameters, because you will manipulate and study their effects in each assignment. A brief description of each parameter is provided below. Refer back to this section as needed when you are working on the different procedures.

Click on the Change Inputs button to see all the parameters you can manipulate. A new page will open with buttons for each of the input parameters located at the left side of
each page (genotype frequency will be open as the first input parameter). Click on each input parameter and read the descriptions below. Change each parameter so that you can become familiar with how each input parameter operates.

1. **Genotype Frequency** - A pie chart shows the initial phenotype frequencies of the population. These frequencies can be changed by left-clicking and dragging the red triangles on the perimeter. Try it. The allele frequencies are shown in the upper right. You can't change these directly, but notice that they change in accordance to the genotype frequencies that you set: AA (black moths), Aa (brown moths), and aa (white moths). The default frequency is 50% for each allele, which gives a 1:2:1 phenotype ratio.

2. **Tree Types** - These trees provide habitat for the moths. Three different types are available. Each has a different color of bark, which corresponds to the color of each of the three moth genotypes. Moth survival depends on camouflage. If they don't happen to land on the right tree, the birds get em! The default value is equal proportions of each tree type.

3. **Number of Stands** - the number of groups (stands) of trees can be varied from 1 to 100. This value determines the number of moth populations. The default value is one tree stand (one moth population).

4. **Stand Size** - the number of trees in an individual stand. The stand size determines "carrying capacity". This gets a little confusing. Basically, the number of trees that you pick determines the maximum number of moths in the population. The default value is 4000, but it can be set anywhere between 1 and 4000.

5. **Migration Rate** - controls the rate of migration and mixing of populations between different tree stands. This parameter is for modeling gene flow. For example, if it is set to "10%", that means that 10% of the moths move between populations in each generation. Note: The Migration Rate button is shaded and inactive unless you select more than one population (tree stand).

6. **Mating Pattern** - the type of mating can be selected as either assortative (similar phenotypes prefer to mate), random, or disassortative (dissimilar phenotypes prefer to mate). The default is random mating. You can alter the degree of assortative or disassortative mating.

7. **Disaster Frequency** - this one controls "disasters". It abruptly reduces population size at random intervals. The moths usually soon bounce back to carrying capacity, but they can go extinct! (Actually, it's called extirpation, if only a population is involved). The default value is for a benign environment with no disasters (Never). This frequency can be changed to produce occasional disasters (Sometimes) or frequent disasters (Often).

After you have finished this introduction to the input parameters, click the Reset button at the left of the screen to return all input parameters to their default values.

2- **Testing genetic equilibrium**

Now that you are familiar with the basic parameters in PopGenLab, set up the following experiment to test the Hardy-Weinberg prediction of genetic equilibrium and the factors that influence a state of genetic equilibrium in a population.

Leave all input parameters at their default values. You will begin with equal allele fre-
quencies (A=50%, a=50%). This gene pool results in phenotype frequencies of 25% black, 50% brown, and 25% white. There are equal proportions of each tree type, in a single stand with a carrying capacity of 4000 moths (a large population). Mating is random, and the disaster frequency is set at "Never", which means that the population will remain near the carrying capacity.

1. **Based on these conditions, does each moth genotype have an equal chance of survival? Explain your answer. Don't forget to think about the birds and the trees.**

Return to the initial page of the simulation (if you are still in the Change Inputs view). Find the popup menu, showing the number of generations, in the lower left corner of the screen. Leave generation number set at its default value of 100. Click the Run Experiment button to run this simulation.

When the experiment has finished running, a separate page will appear that presents the results of your experiment (Note: Any of the data views can be saved or printed by clicking the Export button). The following data can be examined:

- **Genotype Frequency** - The data are represented as a pie chart showing the percentage of each phenotype. Click and drag the slider to show how phenotype frequencies changed during the 100 generations. Remember that the three phenotypes reflect the frequencies of the three genotypes; AA (black), Aa (brown), and aa (white). The end point of the test is the result that shows with the slider all the way to the right (i.e. the last of the 100 generations).

- **Allele Frequency** - click on the check boxes to show a plotted view of allele frequency for each allele (A or a). The data are represented as allele frequencies vs generation.

- **Heterozygosity** - plots the percentage of heterozygous moths (the brown ones) in each generation over time.

- **Population Size** - plots the number of moths over time. Predation tends to reduce the population, but reproduction pushes it back toward carrying capacity. The fluctuations should be small in this experiment.

- **Allele Distribution** - If we had different populations, this graph would show how the frequency of the A allele varied among the populations. Presently, this graph is pretty boring, because in this test we had only one population.

- **Textual Data** - text columns of raw data for allele frequencies.

- **Input Summary** - a summary table of the input parameters for the experiment that you carried out.

2. **Look at the allele and genotype frequencies vs time (generations). Is there any change in allele or genotype frequencies over time? If so, is the change directional? Explain the results.**

3. **How do the actual genotype frequencies compare to the Hardy-Weinberg predictions? Use equation 2 and the allele frequencies to make the predictions.**

Repeat this experiment at least three times to determine if the results are consistent.

Repeat this experiment with a different set of initial genotype frequencies. Adjust the population so that initially you have 50% black and 50% white moths (no brown ones). Note that the allele frequencies for this population are 50:50, just as they were before. But, we are not anywhere near the Hardy-Weinberg prediction.
4. How many generations does it take for a population to reach Hardy-Weinberg equilibrium?

5. Can different initial genotype frequencies lead to the same Hardy Weinberg equilibrium? What about different allele frequencies?

3- Genetic Drift

Random changes in the gene pool of a population are known as genetic drift. By definition, these changes are not the result of selection or any other causal factor other than chance. Genetic drift is more likely to affect small populations than large ones. The following exercise is designed to help you understand important aspects of genetic drift as a potential cause of evolution. Remember that carrying capacity of the environment (the number of trees in our model) determines the population size, and that small populations are more susceptible to genetic drift.

1. Predict the effect of decreased population size on allele and genotype frequencies.

Run a series of tests in which you alter stand size (and therefore population size). Leave the other parameters at their default values. Repeat each test 5 times. Start with the default value for stand size (4000 moths). For each series of tests, reduce the stand by one-half (for example, run a series at 2000 moths [half of the default value], then 1000 moths, and so on). Make a table and write down the allele and genotype frequencies after each test. We are interested in how variable the results are. After you have completed this experiment, answer the following questions.

2. How did allele and genotype frequencies vary in this experiment?

3. What was the effect of reducing the population size? How do these results compare with what you observed for allele and genotype frequencies under the default conditions? Explain.

In the next series of tests, we will expand the number of tree stands (populations). Set the number of tree stands to the maximum value of 100 and perform a series of tests with different stand sizes as before (4000, 2000, 1000, etc). The most interesting results will occur in the smallest populations. Study genotype and allele frequencies that result from each experiment. Use the text box or arrows in the lower right corner to change your view so that you can see the results for each population in each tree stand as well as the average results. For each experiment, go to the “Allele Distribution” view and use the slider to examine allele frequency among the populations. In addition, examine what happens to population size. For each experiment, answer the following questions.

4. What happened to the genotype frequencies? Consider the average and then page through the individual populations. What happened to the allele frequencies - average and in each population? Explain these results.

5. What happened to the average heterozygosity, and the heterozygosity in each population? Explain these results.

6. How did population size affect the changes in genotype and allele frequencies that you observed in these experiments?
7. What do these experiments tell you about the effect of population size on genetic variation?

8. Did any of the populations that you studied become extinct? If so, which ones? Why did these populations become extinct while others did not? What effect does population size have on the risk of extinction?

9. What is the relationship between carrying capacity and the maintenance of genetic diversity and heterozygosity within populations? What about diversity among populations?

4- Influence of Mating Patterns on Population Genetics

One of the conditions required for maintaining genetic equilibrium in a population is random mating. When individuals select mates with a particular heritable trait—for example, color or size—this is known as assortative mating. In this experiment, you will examine how different forms of mating among moths influence Hardy-Weinberg equilibrium.

Assortative Mating: Set up a test at default conditions for Hardy-Weinberg equilibrium for all parameters except the number of tree stands. Set tree stand number to 100. Then conduct a series of 4 tests with different degrees of assortative mating (0, 25, 50, 100%). Use the slider to choose values ranging from 0% (random mating) to 100% (only like phenotypes mate). Repeat this series of experiments at 3 different stand sizes (~100, 1000, 4000).


2. How do the effects of assortative mating compare to those created by genetic drift? In particular, are the effects of assortative mating and the effects of genetic drift the same at different population sizes? Why or why not?

3. Explain any differences you encountered between effects of assortative mating, and genetic drift, with respect to population size.

Disassortative Mating: Conduct a series of tests, similar to those above, but with different degrees of disassortative mating (unlike phenotypes tend to mate).

4. What is the effect of disassortative mating?

Genotype Frequencies and Mating Style: For both assortative and disassortative mating, conduct more experiments where you vary the initial genotype frequency. Try experiments where the initial allele frequencies are not equal.

5. Based on the results of these experiments, can you draw any other conclusions about the effects of assortative and disassortative mating on allele frequency?

5- Modes of Natural Selection

Natural selection can have different effects on the gene pool depending on which mode of selection occurs. For example, directional selection favors individuals at one end of the range of phenotypes. For example, black moths are at one end of the phenotype range, while brown moths represent an intermediate phenotype. In balancing selection, extreme phenotypes are selected against and intermediate phenotypes have
higher rates of reproduction or survival. Conversely, diversifying (disruptive) selection favors individuals at both ends of the phenotype range over individuals with an intermediate phenotype.

Begin an experiment with default conditions for Hardy-Weinberg equilibrium for all parameters except the number of tree stands and genotype frequencies. Set the number of stands to 100. (Recall that the survival of the three types of moths depends on the distribution of tree types within the stand). Change tree frequency to set up several different experiments under conditions of directional selection for dark color, directional selection for light color, balancing selection, and diversifying selection. For each experiment, look at genotype and allele frequencies.

Try experiments with the different conditions of selection and initial allele frequencies near zero and one.

1. What happens to allele frequency in the case of directional selection? Does directional selection for dark color produce the same result as directional selection for light color?

2. What happens to allele frequency in the case of balancing selection?

3. What happens to allele frequency in the case of diversifying selection?

4. Are small differences in fitness effective in changing allele frequencies? (Conduct additional experiments with varying proportions of tree types to help answer this question.)

5. Under what mode of selection might genetic variation be maintained? Explain your answer.

6. Under what mode of selection might there be a "founder effect," where the final allele frequency depends on the initial allele frequency? Explain your answer.

6– Effects of gene flow

Genetic drift in isolated populations can be damped by migration. Both emigration and immigration can influence the gene pool. Immigration can result in new alleles being introduced into a population. Conversely, when organisms emigrate out of a population the frequency of certain alleles in the population can decline.

Run an experiment with a large amount of genetic drift occurring in 100 isolated populations. Set the individual stand size to 400 and the number of stands to 100. To create migration among these populations, click on the Migration button and use the slider to change migration rate. Design and carry out experiments where there are different levels of migration occurring among the populations. For each of these experiments, carefully study what has happened to the populations by analyzing each category of results (genotype frequency, allele frequency, etc.).

1. Does migration modify the effects of genetic drift? If so, how? Explain.

Procedure 7- Population Bottlenecks

Occasionally populations undergo "crashes," when the population size is reduced by natural disasters such as flood, fire, tornadoes, drought, and other extreme weather conditions. These natural disasters are frequently unselective in nature—they kill individuals throughout the population and are not selective for a particular phenotype. Even if population numbers recover, the effect of genetic drift during such a
“bottleneck” can impact the gene pool for many generations.

Conduct a test with a high population size, so that there is (initially) very little genetic drift. Use multiple populations. Then repeat the test with moderate and high frequencies of "disasters" that reduce the populations to small sizes.

1. What is the effect of these population bottlenecks?

2. How do these disasters affect the probability of population extinction?

3. Can these effects be mitigated by allowing migration to occur among the populations? Design and carry out experiments to examine this idea. If you were a conservation biologist, what would these data suggest to you about the design of natural reserves?

Assignment

Based on your discussion in lab, the instructor will choose a subset of the questions to be answered in writing.