

2014

Using BioInteractive  
Resources to Teach

# Mathematics and Statistics in Biology

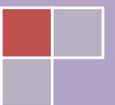
**Paul Strode, PhD**

Fairview High School  
Boulder, Colorado

**Ann Brokaw**

Rocky River High School  
Rocky River, Ohio

Draft: August 2014



# Using BioInteractive Resources to Teach Mathematics and Statistics in Biology

<b>About This Guide</b>	<b>3</b>
Statistical Symbols and Basic Equations	4
<b>Part 1: Descriptive Statistics Used in Biology</b>	<b>5</b>
Measures of Average: Mean, Median, and Mode	6
Mean	6
Median	7
Mode	
When to Use Which One	8
Measures of Variability: Range, Standard Deviation, and Variance	8
Range	9
Standard Deviation and Variance	
Understanding Degrees of Freedom	9
Measures of Confidence: Standard Error of the Mean and 95% Confidence Interval	13
<b>Part 2: Inferential Statistics Used in Biology</b>	<b>19</b>
Significance Testing: The $\alpha$ (Alpha) Level	19
Comparing Averages: The Student's $t$ -Test for Independent Samples	19
Analyzing Frequencies: The Chi-Square Statistical Analysis Test	23
Measuring Correlations and Analyzing Linear Regression	26
<b>Part 3: Commonly Used Calculations in Biology</b>	<b>34</b>
Relative Frequency	34
Probability	34
Rate Calculations	36
Hardy-Weinberg Frequency Calculations	38
Standard Curves	39
<b>Part 4: BioInteractive's Mathematics and Statistics Classroom Resources</b>	<b>43</b>
Links to Classroom-Ready Resources	43

## About This Guide

Many state science standards encourage the use of mathematics and statistics in biology education, including the newly designed AP Biology course, IB Biology, Next Generation Science Standards, and the Common Core.

Two high school biology teachers, Paul Strode and Ann Brokaw, conceived this guide to help other biology teachers implement math and statistics in the classroom. It is not meant to be a textbook of statistics; it covers topics most relevant to high school biology, focusing on methods and examples rather than theory.

The guide is organized in four parts:

- Part 1 covers **descriptive statistics**, methods used to organize, summarize, and describe quantifiable data. They include methods to describe the typical or average value of the data and the spread of the data.
- Part 2 covers statistical methods used to draw inferences about populations on the basis of observations made on smaller samples or groups of the population—a branch of statistics known as **inferential statistics**.
- Part 3 describes other mathematical methods commonly taught in high school biology, including frequency and rate calculations, Hardy-Weinberg calculations, probability, and standard curves.
- Part 4 provides a chart of activities on the BioInteractive website that use several of the math and statistics methods covered in this guide.

A first draft of the guide was published in July 2014. The guide will continue to be updated with additional materials and examples. Subsequent versions of the guide will include the ANOVA test and guidelines for using spreadsheet programs to calculate statistics and graph data.

## Statistical Symbols and Basic Equations

Listed below are the universal statistical symbols and equations used in this guide. The calculations can all be done using scientific calculators or the formula function in spreadsheet programs.

$N$ : Total number of individuals in a population (i.e., the total number of butterflies of a particular species)

$n$ : Total number of individuals in a sample of a population (i.e., the number of butterflies in a net)

$df$ : The number of measurements in a sample that are free to vary once the sample mean has been calculated; in a single sample,  $df = n - 1$

$x_i$ : A single measurement

$i$ : The  $i^{\text{th}}$  observation in a sample

$\Sigma$ : Summation

$\bar{x}$ : Sample mean  $\bar{x} = \frac{\Sigma x_i}{n}$

$s^2$ : Sample variance  $s^2 = \frac{\Sigma(x_i - \bar{x})^2}{n - 1}$

$s$ : Sample standard deviation  $s = \sqrt{s^2}$

SE: Sample standard error, or standard error of the mean (SEM)  $SE = \frac{s}{\sqrt{n}}$

95% CI: 95% confidence interval  $95\% \text{ CI} = \frac{1.96s}{\sqrt{n}}$

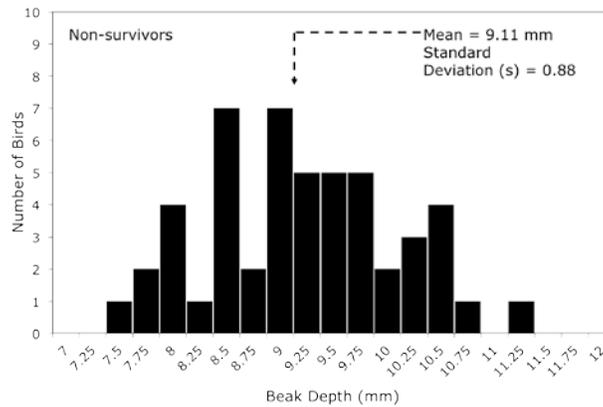
## Part 1: Descriptive Statistics Used in Biology

It is rarely practical for scientists to measure every event or individual in a population. Instead, they typically collect data on a sample of a population and use these data to draw conclusions (or make inferences) about the entire population. Statistics is a mathematical discipline that relates to this type of analysis.

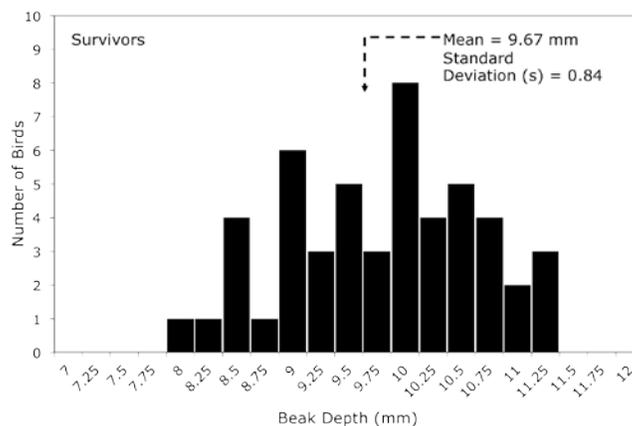
One of your first steps in analyzing a small data set is to graph the data and examine the distribution.

**Figure 1** shows two graphs of beak measurements taken from two samples of medium ground finches that lived on the island of Daphne Major, one of the Galápagos Islands, during a major drought in 1977. The graph on the top shows beak measurements of finches that died during the drought. The graph on the bottom shows beak measurements of finches that survived the drought.

### Beak Depths of 50 Medium Ground Finches That Did Not Survive the Drought



### Beak Depths of 50 Medium Ground Finches That Survived the Drought



**Figure 1:** The distributions of beak depth measurements in two groups of medium ground finches.

Notice that the measurements tend to be more or less symmetrically distributed across a range, with most measurements around the center of the distribution. This is a characteristic of a **normal**

**distribution.** The statistical methods covered in this guide, except for the measures of average and the range, apply to data that are normally distributed, like the beak measurements above; other types of distributions require either different kinds of statistics or transforming data to make them normally distributed.

Also, in the two graphs, the center and spread of each distribution is different. **Descriptive statistics** allows you to describe and quantify these differences.

### Measures of Average: Mean, Median, and Mode

A description of a group of observations can include a value for the mean, median, or mode. These are all measures of **central tendency**—in other words, they represent a number close to the center of the distribution.

#### Mean

You calculate the mean (also referred to as the **average** or **arithmetic mean**) by summing all the data points in a data set ( $\sum X$ ) and then dividing this number by the total number of data points ( $N$ ):

$$\bar{X} = \frac{\sum X}{N}$$

What scientists want to understand is the mean of the entire population, which is represented by  $\mu$ . They use the **sample mean**, represented by  $\bar{x}$ , as an estimate of  $\mu$ .

#### Application in Biology

Students in a biology class planted eight bean seeds in separate plastic cups and placed them under a bank of fluorescent lights. Fourteen days later, the students measured the height of the bean plants that grew from those seeds and recorded their results in Table 1.

**Table 1. Bean Plant Heights**

Plant No.	1	2	3	4	5	6	7	8
Height (cm)	7.5	10.1	8.3	9.8	5.7	10.3	9.2	8.7

To determine the mean of the bean plants, follow these steps:

- I. Find the sum of the heights:  
 $7.5 + 10.1 + 8.3 + 9.8 + 5.7 + 10.3 + 9.2 + 8.7 = \mathbf{69.6 \text{ centimeters}}$
- II. Count the number of height measurements:  
  
There are eight height measurements.
- III. Divide the sum of the heights by the number of measurements to compute the mean:  
**mean =  $69.6 \text{ cm} / 8 = 8.7 \text{ centimeters}$**

The mean for this sample of eight plants is 8.7 centimeters and serves as an estimate for the true mean of the population of bean plants growing under these conditions. In other words, if the students collected data from hundreds of plants and graphed the data, the center of the distribution might be around 8.7 centimeters.

### Median

When the data are ordered from the largest to the smallest, the median is the midpoint of the data. It is not distorted by extreme values, or even when the distribution is not normal. For this reason, it may be more useful for you to use the median as the main descriptive statistic for a sample of data in which some of the measurements are extremely large or extremely small.

To determine the median of a set of values, you first arrange them in numerical order from lowest to highest. The middle value in the list is the median. If there is an even number of values in the list, then the median is the mean of the middle two values.

### Application in Biology

A researcher studying mouse behavior recorded in **Table 2** the time (in seconds) it took 13 different mice to locate food in a maze.

**Table 2. Length of Time for Mice to Locate Food in a Maze**

Mouse No.	1	2	3	4	5	6	7	8	9	10	11	12	13
Time (sec.)	31	33	81	33	28	29	33	27	27	34	35	28	32

To determine the median time that the mice spent searching for food, follow these steps:

- I. Arrange the time values in numerical order from lowest to highest:

27, 27, 28, 28, 29, 31, **32**, 33, 33, 33, 34, 35, 81

- II. Find the middle value. This value is the median:

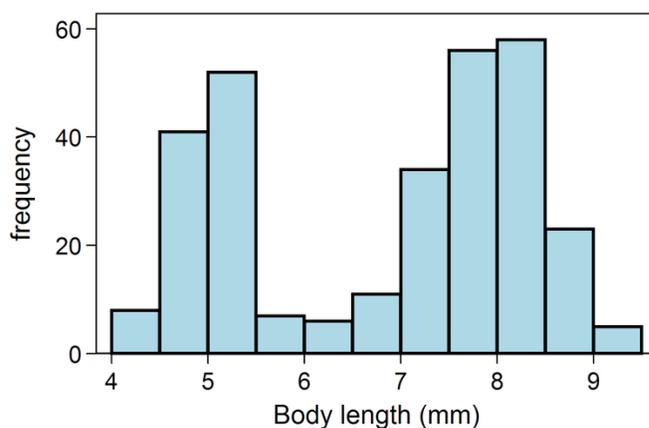
**median = 32 seconds**

In this case, the median is 32 seconds, but the mean is 35 seconds. The mean is larger than the median because a very slow mouse distorts the mean in the direction of that large value.

## Mode

The mode is another measure of the average. It is the value that appears most often in a sample of data. In the example shown in **Table 2**, the mode is 33 seconds.

The mode is not typically used as a measure of central tendency in biological research, but it can be useful in describing some distributions. For example, **Figure 2** shows a distribution of body lengths with two peaks, or modes—called a **bimodal distribution**. Describing these data with a measure of central tendency like the mean or median would obscure this fact.



**Figure 2: Graph of body lengths of weaver ant workers** (Reproduced from <http://en.wikipedia.org/wiki/File:BimodalAnts.png>.)

## When to Use Which One

The purpose of these statistics is to characterize “typical” data from a data set. You use the mean most often for this purpose, but it becomes less useful if the data in the data set are not normally distributed. When the data are *not* normally distributed, then other descriptive statistics can give a better idea about the typical value of the data set. The median, for example, is a useful number if the distribution is heavily skewed, like top running speeds of four-legged animals. The mode is not used very frequently in biology, but it may be useful in describing some types of distributions—for example, ones with more than one peak.

## Measures of Variability: Range, Standard Deviation, and Variance

Variability describes the extent to which numbers in a data set diverge from the central tendency. It is a measure of how “spread out” the data are. The most common measures of variability are **range**, **standard deviation**, and **variance**.

### Range

The simplest measure of variability in a sample of normally distributed data is the range, which is the difference between the largest and smallest values in a set of data. You can use the range for data that are not normally distributed.

### Application in Biology

Students in a biology class measured the width of eight leaves from eight different maple trees and recorded their results in **Table 3**.

**Table 3. Width of Maple Tree Leaves**

Plant No.	1	2	3	4	5	6	7	8
Width (cm)	7.5	10.1	8.3	9.8	5.7	10.3	9.2	8.7

To determine the range of leaf widths, follow these steps:

- I. Identify the largest and smallest values in the data set:  
largest = 10.3 centimeters, smallest = 5.7 centimeters
  
- II. To determine the range, subtract the smallest value from the largest value:  
**range = 10.3 centimeters – 5.7 centimeters = 4.6 centimeters**

For any data, a larger range value indicates a greater spread of the data—in other words, the larger the range, the greater the variability. However, an extremely large or small value in the data set will make the variability appear high. The standard deviation provides a more reliable measure of the “true” spread of the data.

### Standard Deviation and Variance

The standard deviation is the most widely used measure of variability. The **sample standard deviation** ( $s$ ) is essentially the average of the deviation between each measurement in the sample and the sample mean ( $\bar{x}$ ). The sample standard deviation is an estimate of the standard deviation in the larger population.

The formula for calculating the sample standard deviation follows:

$$s = \sqrt{\frac{\sum(x_i - \bar{x})^2}{(n - 1)}}$$

### Calculation Steps

1. Calculate the mean ( $\bar{x}$ ) of the sample.
2. Find the difference between each measurement ( $x_i$ ) in the data set and the mean ( $\bar{x}$ ) of the entire set:

$$(x_i - \bar{x})$$

3. Square each difference to remove any negative values:

$$(x_i - \bar{x})^2$$

4. Add up (sum,  $\Sigma$ ) all the squared differences:

$$\Sigma(x_i - \bar{x})^2$$

5. Divide by the **degrees of freedom**, which is 1 less than the sample size ( $n - 1$ ):

$$\frac{\Sigma(x_i - \bar{x})^2}{(n - 1)}$$

Note that the number calculated at this step provides a statistic called **variance** ( $s^2$ ). Variance is an important measure of variability that is used in certain statistical methods. It is the square of the standard variation.

6. Take the square root to calculate the standard deviation ( $s$ ) for the sample.

## Application in Biology

You are interested in knowing how tall bean plants (*Phaseolus vulgaris*) grow in two weeks after planting. You plant a sample of 20 seeds ( $n = 20$ ) in separate pots and give them equal amounts of water and light. After two weeks, 17 of the seeds have germinated and have grown into small seedlings (now  $n = 17$ ). You measure each plant from the tips of the roots to the top of the tallest stem. You record the measurements in Table 4, along with the steps for calculating the standard deviation.

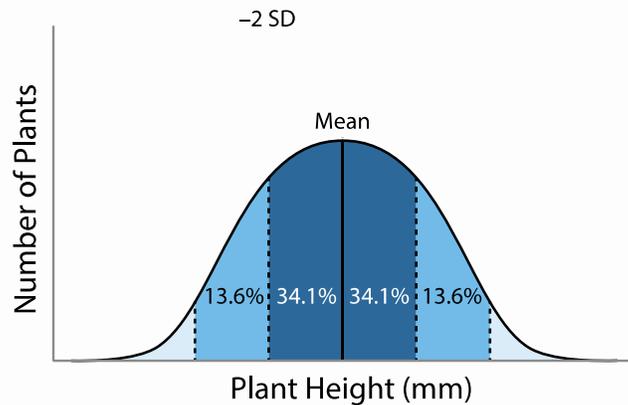
**Table 4. Plant Measurements and Steps for Calculating the Standard Deviation**

Plant No.	Plant Height (mm)	<i>Step 2: <math>(x_i - \bar{x})</math></i>	<i>Step 3: <math>(x_i - \bar{x})^2</math></i>
1	112	$(112 - 103) = 9$	$9^2 = 81$
2	102	$(102 - 103) = (-1)$	$(-1)^2 = 1$
3	106	$(106 - 103) = 3$	$3^2 = 9$
4	120	$(120 - 103) = 17$	$17^2 = 289$
5	98	$(98 - 103) = (-5)$	$(-5)^2 = 25$
6	106	$(106 - 103) = 3$	$3^2 = 9$
7	80	$(80 - 103) = (-23)$	$(-23)^2 = 529$
8	105	$(105 - 103) = 2$	$2^2 = 4$
9	106	$(106 - 103) = 3$	$3^2 = 9$
10	110	$(110 - 103) = 7$	$7^2 = 49$
11	95	$(95 - 103) = (-8)$	$(-8)^2 = 64$
12	98	$(98 - 103) = (-5)$	$(-5)^2 = 25$
13	74	$(74 - 103) = (-29)$	$(-29)^2 = 841$
14	112	$(112 - 103) = 9$	$9^2 = 81$
15	115	$(115 - 103) = 12$	$12^2 = 144$
16	109	$(109 - 103) = 6$	$6^2 = 36$
17	100	$(100 - 103) = (-3)$	$(-3)^2 = 9$
<i>Step 1: Calculate mean.</i>	$\bar{x} = 103$		<i>Step 4: <math>\sum(x_i - \bar{x})^2 = 2,205</math></i>
		Variance ( $s^2$ )	<i>Step 5: <math>\sum(x_i - \bar{x})^2 / (n - 1) = 2,205 / 16 = 138</math></i>
		Standard deviation ( $s$ )	<i>Step 6: <math>\sqrt{s^2} = \sqrt{138} = 11.7</math></i>

The mean height of the bean plants in this sample is 103 millimeters  $\pm$  11.7 millimeters. What does this tell us?

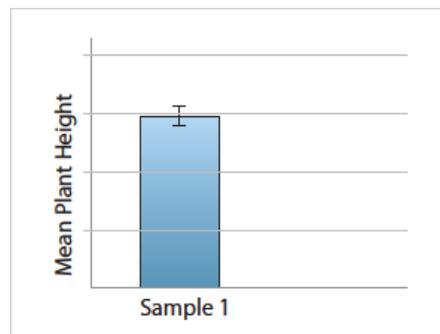
In a data set with a large number of continuous measurements that are normally distributed, 68% of the measurements are expected to fall within 1 standard deviation from the mean and 95% of all data points lie within 2 standard deviations of the mean on either side (**Figure 3**). Thus, in this example, if you

assume that this sample of 17 observations is drawn from a population of measurements that are normally distributed, 68% of measurements in the population should fall between 91.3 and 114.7 millimeters and 95% of the measurements should fall between 80.1 millimeters and 125.9 millimeters.



**Figure 3:** For normally distributed data, 68% of data points lie between  $\pm 1$  standard deviation of the mean and 95% of data points lie between  $\pm 2$  standard deviations of the mean.

You can graph the mean and the standard deviation of this sample of bean plants using a bar graph with error bars (**Figure 4**). Standard deviation bars reflect the *variation* of the data and not the error in the measurements—the latter is a common misconception. On the other hand, error bars based on the standard error of the mean and 95% confidence interval reflect the *uncertainty* in the sample mean when estimating the population mean, and they are dependent on sample size. (These statistics are discussed further in “Measures of Confidence: Standard Error of the Mean and 95% Confidence Intervals.”)



**Figure 4:** This bar graph shows the mean plant height of a sample of bean plants and an error bar that represents  $\pm 1$  standard deviation. Sixty-eight percent of measurements in this population fall in the range indicated by the bar.

**Note:** Another common misconception that standard deviation decreases with increasing sample size. Standard deviation can either increase or decrease as sample size increases; it just depends on the measurements in the sample. If there is a lot of variation in a population, the standard deviation will be large.

## Understanding Degrees of Freedom

Calculations of sample estimates, such as the standard deviation and variance, use degrees of freedom instead of sample size. The way you calculate degrees of freedom depends on the statistical method you are using, but for calculating the standard deviation, it is defined as 1 less than the sample size ( $n - 1$ ).

To illustrate what this number means, consider the following example. Biologists are interested in the variation in leg sizes among grasshoppers. They catch five grasshoppers ( $n = 5$ ) in a net and prepare to measure the left legs. As the scientists pull grasshoppers one at a time from the net, they have no way of knowing the leg lengths until they measure them all. In other words, all five leg lengths are “free” to vary within some general range for this particular species. The scientists measure all five leg lengths and then calculate the mean to be  $x = 10$  millimeters. They then place the grasshoppers back in the net and decide to pull them out one at a time to measure them again. This time, since the biologists already know the mean to be 10, only the first four measurements are free to vary within a given range. If the first four measurements are 8, 9, 10, and 12 millimeters, then there is no freedom for the fifth measurement to vary; it has to be 11. Thus, once they know the sample mean, the number of degrees of freedom is 1 less than the sample size,  $df = 4$ .

## Measures of Confidence: Standard Error of the Mean and 95% Confidence Interval

The standard deviation provides a measure of the spread of the data from the mean. A different type of statistic reveals the *uncertainty* in the calculation of the mean.

The **sample mean** is not necessarily identical to the mean of the entire population. In fact, every time you take a sample and calculate a sample mean, you would expect a slightly different value. In other words, the sample means themselves have variability. This variability can be expressed by calculating **the standard error of the mean** (abbreviated as  $SE_{\bar{x}}$  or SEM) or **the 95% confidence interval** (95% CI).

To calculate  $SE_{\bar{x}}$ , divide the standard deviation by the square root of the sample size:

$$s = \sqrt{\frac{\sum(x_i - \bar{x})^2}{(n - 1)}}$$

$$SE_{\bar{x}} = \frac{s}{\sqrt{n}}$$

$$95\% \text{ CI} = \frac{1.96s}{\sqrt{n}}$$

The equation for 95% CI is  $\frac{1.96s}{\sqrt{n}}$  but is typically rounded to  $\frac{2s}{\sqrt{n}}$ .

Assume that there is a population of a species of anole lizards living on an island of the Caribbean. If you were able to measure the length of the hind limbs of every individual in this population and then calculate the mean, you would know the value of the population mean. However, there are thousands of individuals, so you take a sample of 10 anoles and calculate the mean hind limb length for that sample. Another researcher working on that island might catch another sample of 10 anoles and

calculate the mean hind limb length for this sample, and so on. The sample means of many different samples would be normally distributed. **The standard error of the mean represents the standard deviation of such a distribution** and estimates how close the sample mean is to the population mean. The greater the sample size (i.e., 50 rather than 10 anoles), the more closely the sample mean will estimate the population mean, and therefore the standard error of the mean becomes smaller.

The 95% confidence interval (95% CI) is equivalent to 1.96 (typically rounded to 2) standard errors of the mean. Because the sample means are assumed to be normally distributed, 95% of all sample means should fall between 2 standard deviations above and below the population mean, estimated by 95% CI.

What these calculations tell you is that you can be 68% confident that the population mean falls within  $\pm 1$  standard error of the sample mean and 95% confident that the population mean falls within approximately  $\pm 2$  standard errors of the sample mean.

Both  $SE_{\bar{x}}$  and 95% CI can be illustrated as error bars in a bar graph of the means of two or more samples that are being compared. Depicting  $SE_{\bar{x}}$  or the 95% CI as error bars in a bar graph provides a clear visual clue to the uncertainty of the calculations of the sample means.

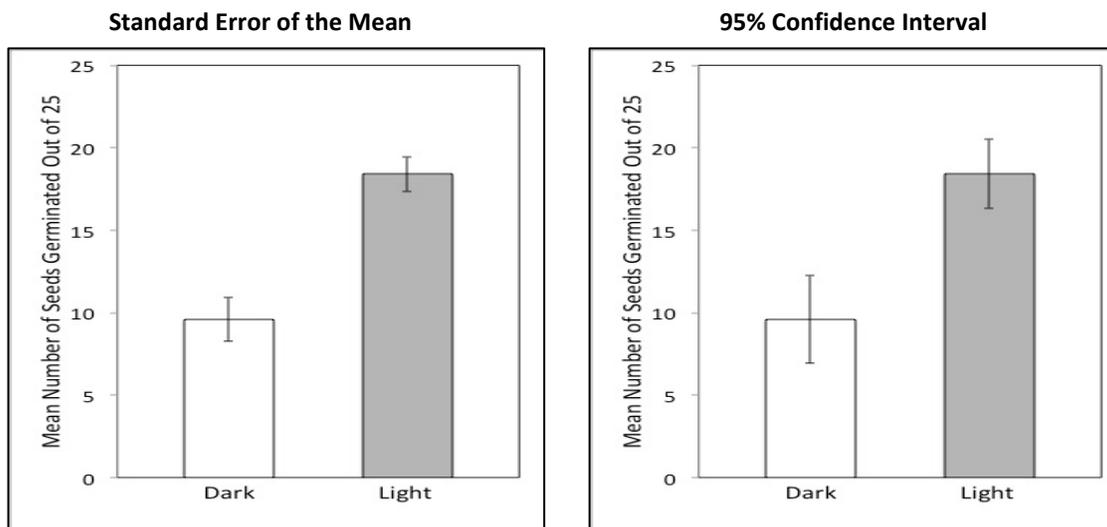
**Note:** Unlike standard deviation, both standard error and 95% CI decrease with increasing sample size. In other words, the greater the sample size the less the uncertainty in the calculations of the sample means.

### Application in Biology—Example 1

Seeds of many weed species germinate best in recently disturbed soil that lacks a light-blocking canopy of vegetation. Students in a biology class hypothesized that weed seeds germinate in response to light. To test this hypothesis, the students placed 25 seeds of crofton weed (*Ageratina adenophora*, an invasive species on several continents) in each of 20 petri dishes and covered them with distilled water. They placed half the petri dishes in the dark and half in the light. After 72 hours, the students counted the number of seeds that had germinated in each dish. The data and calculations of variance, standard deviation, standard error of the mean, and 95% confidence interval are shown in Table 5. The students plotted the data as two bar graphs showing the standard error of the mean and 95% confidence interval (Figure 5).

**Table 5. Number of Crofton Seeds That Germinated after 72 Hours in the Dark and in the Light** (number of replicates [i.e., sample size,  $n$ ] = 10)

Petri Dishes	Dark ( $x_1$ )	Light ( $x_2$ )	Dark ( $x_i - \bar{x}_1$ ) <sup>2</sup>	Light ( $x_i - \bar{x}_2$ ) <sup>2</sup>
1 and 2	12	18	$(12 - 9.6)^2 = 5.8$	$(18 - 18.4)^2 = 0.16$
3 and 4	8	22	$(8 - 9.6)^2 = 2.6$	$(22 - 18.4)^2 = 12.96$
5 and 6	15	17	$(15 - 9.6)^2 = 29.1$	$(17 - 18.4)^2 = 1.96$
7 and 8	13	23	$(13 - 9.6)^2 = 11.5$	$(23 - 18.4)^2 = 21.16$
9 and 10	6	16	$(6 - 9.6)^2 = 13.0$	$(16 - 18.4)^2 = 5.76$
11 and 12	4	18	$(4 - 9.6)^2 = 31.4$	$(18 - 18.4)^2 = 0.16$
13 and 14	13	22	$(13 - 9.6)^2 = 11.6$	$(22 - 18.4)^2 = 12.96$
15 and 16	14	12	$(14 - 9.6)^2 = 19.3$	$(12 - 18.4)^2 = 40.96$
17 and 18	5	19	$(5 - 9.6)^2 = 21.1$	$(19 - 18.4)^2 = 0.36$
19 and 20	6	17	$(6 - 9.6)^2 = 13.0$	$(17 - 18.4)^2 = 1.96$
			$\sum (x_i - \bar{x}_1)^2 = 158.4$	$\sum (x_i - \bar{x}_2)^2 = 98.4$
Mean ( $\bar{x}$ )	$\bar{x}_1 = 9.6$	$\bar{x}_2 = 18.4$	$\frac{\sum(x_i - \bar{x})^2}{(n - 1)} = \frac{158.4}{9}$	$\frac{\sum(x_i - \bar{x})^2}{(n - 1)} = \frac{98.4}{9}$
		Variance ( $s^2$ )	$s_1^2 = 17.6$	$s_2^2 = 10.93$
	Standard deviation $s = \sqrt{\frac{\sum(x_i - \bar{x})^2}{(n - 1)}}$		$s = 4.20$	$s = 3.31$
	Standard error of the mean $SE_{\bar{x}} = \frac{s}{\sqrt{n}}$		$SE_{\bar{x}} = \frac{4.20}{\sqrt{10}} = 1.33$	$SE_{\bar{x}} = \frac{3.31}{\sqrt{10}} = 1.05$
	95% CI = $\frac{2s}{\sqrt{n}}$		95% CI = $\frac{2(4.20)}{\sqrt{10}} = 2.7$	95% CI = $\frac{2(3.31)}{\sqrt{10}} = 2.1$



**Figure 5: Mean number of crofton seeds that germinated after 72 hours in the dark or in the light.** The standard error of the mean graph shows the  $SE_{\bar{x}}$  as error bars, and the 95% confidence interval graph shows the **95% CI** as error bars.

The calculations show that although the students don't know how many seeds of the entire population of crofton seeds would germinate in the dark, it is likely to be a number around the sample mean of 9.6 seeds. But how confident are they of this estimate? They are 68% confident that the dark treatment population mean lies between 8.3 ( $9.6 - 1.3$ ) and 10.9 ( $9.6 + 1.3$ ) and that the light treatment population mean lies between 17.35 and 19.45 seeds. In addition, they are 95% confident that the dark treatment population mean lies between 7 and 12.2 seeds and the light treatment population mean lies between 16.3 and 21.5 seeds.

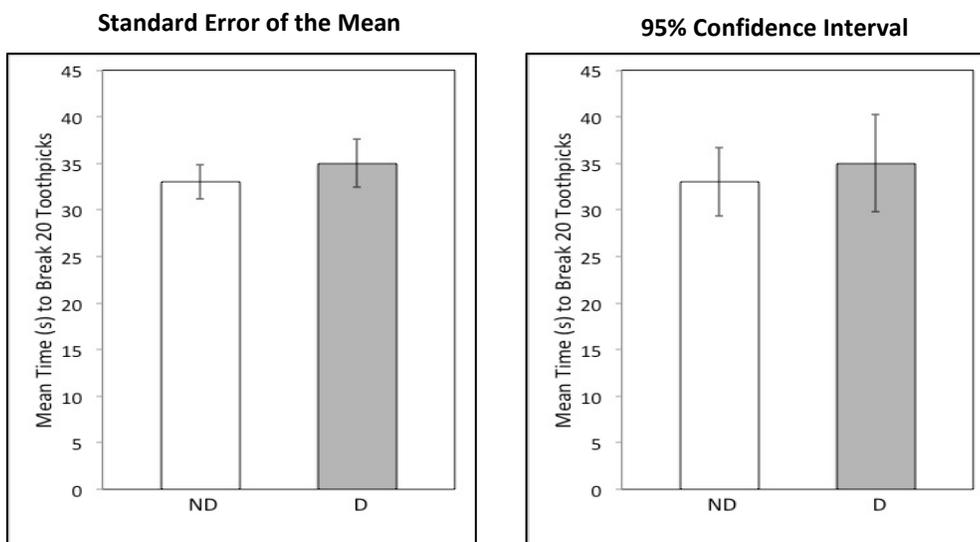
**Note:** By looking at the bar graphs, you can see that the means for the light and dark treatments are different. Can you tell if the differences are statistically significant? If the standard error bars and 95% CI bars overlap, then it is likely that the differences are not statistically significant. In this case, the standard error bars do not overlap; however, this does not necessarily mean that the difference between the means is statistically significant. On the other hand, the fact that the 95% confidence interval error bars do not overlap strongly suggests that the two sample means are *significantly* different. An additional statistical test, the sStudent's *t*-test, is required to be sure.

### **Application in Biology—Example 2**

A teacher had five students write their names on the board, first with their dominant hands and then with their nondominant hands. The rest of the class observed that the students wrote more slowly and with less precision with the nondominant hand than with the dominant hand. The teacher then asked the class to explain their observations by developing testable hypotheses. They hypothesized that the dominant hand was better at performing fine motor movements than the nondominant hand. The class tested this hypothesis by timing (in seconds) how long it took each student to break 20 toothpicks with each hand. The results of the experiment and the calculations of variance, standard deviation, standard error of the mean, and 95% confidence interval are presented in **Table 6**. The students then illustrated the data and uncertainty with two bar graphs, one showing the standard error of the mean and the other showing the 95% confidence interval (**Figure 6**).

**Table 6. Number of Seconds It Took for Students to Break 20 Toothpicks with Their Nondominant (ND) and Dominant Hands (D) (number of replicates [n] = 14)**

Students	ND ( $x_1$ ) Sec.	D ( $x_2$ ) Sec.	ND $(x_i - \bar{x}_1)^2$	D $(x_i - \bar{x}_2)^2$
Josh	33	37	$(33 - 33)^2 = 0$	$(37 - 35)^2 = 4$
Bobby	24	22	$(24 - 33)^2 = 81$	$(22 - 35)^2 = 169$
Qing	35	37	$(35 - 33)^2 = 4$	$(37 - 35)^2 = 4$
Julie	33	28	$(33 - 33)^2 = 0$	$(28 - 35)^2 = 49$
Lisa	42	50	$(42 - 33)^2 = 81$	$(50 - 35)^2 = 225$
Akash	36	36	$(36 - 33)^2 = 9$	$(36 - 35)^2 = 1$
Hector	31	36	$(31 - 33)^2 = 4$	$(36 - 35)^2 = 1$
Viviana	40	46	$(40 - 33)^2 = 49$	$(46 - 35)^2 = 121$
Brenda	28	26	$(28 - 33)^2 = 25$	$(26 - 35)^2 = 81$
Jane	24	28	$(24 - 33)^2 = 81$	$(28 - 35)^2 = 49$
Asa	23	22	$(23 - 33)^2 = 100$	$(22 - 35)^2 = 169$
Eli	44	52	$(44 - 33)^2 = 121$	$(52 - 35)^2 = 289$
Adee	35	29	$(35 - 33)^2 = 4$	$(29 - 35)^2 = 36$
Jenny	36	37	$(36 - 33)^2 = 9$	$(37 - 35)^2 = 4$
			$\sum (x_i - \bar{x}_1)^2 = 568$	$\sum (x_i - \bar{x}_2)^2 = 1,200$
Mean ( $\bar{x}$ )	$\bar{x}_1 = 33$	$\bar{x}_2 = 35$	$\frac{\sum (x_i - \bar{x}_1)^2}{n - 1} = \frac{568}{13}$	$\frac{\sum (x_i - \bar{x}_2)^2}{n - 1} = \frac{1,200}{13}$
		Variance ( $s^2$ )	$s_1^2 = 44$	$s_2^2 = 92$
	Standard deviation $s = \sqrt{\frac{\sum (x_i - \bar{x})^2}{(n - 1)}}$		$s = 6.6$	$s = 9.6$
	Standard error of the mean $SE_{\bar{x}} = \frac{s}{\sqrt{n}}$		$SE_{\bar{x}} = \frac{6.6}{\sqrt{14}} = 1.8$	$SE_{\bar{x}} = \frac{9.6}{\sqrt{14}} = 2.6$
	95% CI = $\frac{2s}{\sqrt{n}}$		95% CI = $\frac{2(6.6)}{\sqrt{14}} = 3.5$	95% CI = $\frac{2(9.6)}{\sqrt{14}} = 5.1$



**Figure 6: Mean number of seconds for students to break 20 toothpicks with their nondominant hands (ND) and dominant hands (D). The standard error of the mean graph shows the  $SE_{\bar{x}}$  as error bars, and the 95% confidence interval graph shows the 95% CI as error bars.**

The calculations show that students can be 68% confident that the population mean for the nondominant hand treatment lies within 31.2 seconds ( $33 - 1.8$ ) and 34.8 seconds ( $33 + 1.8$ ). Likewise, for the dominant hand, students can be 68% confident that the population mean falls within 32.4 and 37.6 seconds.

Students are 95% confident that the population mean for the nondominant hands falls somewhere between 29.5 seconds ( $33 - 3.5$ ) and 36.5 seconds ( $33 + 3.5$ ) and that the population mean for the dominant hands falls somewhere between 29.9 seconds ( $35 - 5.1$ ) and 40.1 seconds ( $35 + 5.1$ ).

**Note:** The fact that the 95% confidence interval error bars for the two sample means overlap, so much so that they include the means, suggests that the two means may not be significantly different. Indeed, if a student reported that she broke 20 toothpicks with one hand, we could not conclude with confidence whether she used her dominant or her nondominant hand because 30 seconds is encompassed by both 95% confidence interval bars.

## Part 2: Inferential Statistics Used in Biology

Inferential statistics tests the statistical hypothesis, which is different from the experimental hypothesis. To understand what this means, assume that you do an experiment to test the experimental hypothesis that “nitrogen promotes plant growth.” To test this hypothesis, you grow 10 bean plants in dirt with added nitrogen and 10 bean plants in dirt without added nitrogen. You find out that the means of these two samples are 13.2 centimeters and 11.9 centimeters, respectively. Does this result indicate that there is a difference between the two populations and that nitrogen might promote plant growth? Or is the difference in the two means merely due to chance because of the 10 measurements collected? A statistical test is required to discriminate between these possibilities.

Statistical tests evaluate the **null statistical hypothesis** (symbolized by  $H_0$  and pronounced H-naught), that  $\bar{x}_1 = \bar{x}_2$ , and therefore by inference,  $\mu_1 = \mu_2$ . In other words, there is no real difference between the populations from which two experimental groups are sampled (i.e., there is no difference between the beans grown with and without nitrogen) and that any apparent difference has occurred by chance. The alternative hypothesis to  $H_0$  is symbolized by  $H_1$  and usually simply states that there is a difference.

### Significance Testing: The $\alpha$ (Alpha) Level

Before you perform a statistical test on the plant growth data, you should determine an acceptable significance level of the null statistical hypothesis. That is, ask, “When do I think my results and thus my test statistic are so unusual that I no longer think the differences observed in my data are due simply to chance?” This significance level is also known as “alpha” and is symbolized by  $\alpha$ .

The significance level is the **probability** of getting a test statistic rare enough that you are comfortable rejecting the null hypothesis ( $H_0$ ). (See the “Probability” section of Part 3 for further discussion of probability.) The widely accepted significance level in biology is 0.05, which translates to a probability of 0.05 or less of calculating a test statistic by chance given the sample data.

### Comparing Averages: The Student’s $t$ -Test for Independent Samples

The section about the 95% confidence interval (see “Measures of Confidence” in Part 1) mentions that if there is no overlap between means and the error bars, then the difference between two data sets is likely to be significant. On the other hand, if there is a large overlap, then the difference between the two sample means likely occurred by chance. But what if the overlap is somewhere in between? You need to use a statistical test to know whether the difference is significant.

The Student’s  $t$ -test compares two sets of quantitative data to help determine if they are significantly different. This  $t$ -test tells you the probability of two data sets being the same. It requires the data to be normally distributed.

Consider an experiment in which students were interested in determining whether the presence of glucose in the growth medium used for growing fruit fly larvae (*Drosophila melanogaster*) affects how quickly the fruit flies complete their larval stage. To investigate this question, the students first grew a group of larvae on glucose-supplemented media and another on media lacking glucose. They then selected 25 larvae from each group and measured the duration of the larval stage. The students then

compared the mean time of the larval stage for larvae grown on media with and without supplemental glucose to see if they are different.

The  $t$ -test assesses the probability that the null statistical hypothesis ( $H_0$ ) can be rejected. The null statistical hypothesis is that the mean of sample 1 is equal to the mean of sample 2, or  $\bar{x}_1 = \bar{x}_2$ . Rejecting  $H_0$  supports the alternative hypothesis,  $H_1$ , that the means are significantly different ( $\bar{x}_1 \neq \bar{x}_2$ ) and that the two populations from which the samples were taken are likely different from each other. In this example, the  $t$ -test determines whether any observed differences between the means of the two groups of larvae are statistically significant or have likely occurred simply by chance.

A  $t$ -test calculates a single statistic,  $t$ , which is compared to a critical  $t$ -statistic ( $t_{\text{crit}}$ ). **Table 7** shows  $t_{\text{crit}}$  for different degrees of freedom for a significance value of 0.05. **The degrees of freedom is calculated by adding the number of data points in the two groups combined, minus 2.** Note that you do not have to have the same number of data points in each group:

$$t_{\text{obs}} = \frac{|\bar{x}_1 - \bar{x}_2|}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

To calculate the standard error for the  $t$ -test, you need to calculate the sample means and the variance ( $s^2$ ) for the two samples being compared, and the sample size ( $n$ ) for each sample must be known:

$$t_{\text{obs}} = \frac{|\bar{x}_1 - \bar{x}_2|}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

### Calculation Steps

1. Calculate the mean of each sample population and subtract one from the other. Take the absolute value of this difference.
2. Calculate the standard error, SE. To compute it, calculate the variance of each sample ( $s^2$ ), and divide it by the number of measured values in that sample ( $n$ , the sample size). Add these two values and then take the square root.
3. Divide the difference between the means by the standard error to get a value for  $t$ .
4. Compare the calculated value to the appropriate critical  $t$ -value in **Table 7**. If the calculated  $t$ -value is greater than the appropriate critical  $t$ -value, this indicates that the means of the two samples are significantly different at the probability value listed (in this case, 0.05). If the calculated  $t$  is smaller, then you cannot reject the null hypothesis that there is no significant difference.

**Table 7. Critical  $t$ -Values for a Significance Level  $\alpha = 0.05$**

Degrees of Freedom (df)	$t_{\text{crit}} (\alpha = 0.05)$
1	12.71
2	4.30
3	3.18
4	2.78
5	2.57
6	2.45
7	2.36
8	2.31
9	2.26
10	2.23
11	2.20
12	2.18
13	2.16
14	2.14
15	2.13
16	2.12
17	2.11
18	2.10
19	2.09
20	2.09
21	2.08
22	2.07
23	2.07
24	2.06
25	2.06
26	2.06
27	2.05
28	2.05
29	2.04
30	2.04
40	2.02
60	2.00
120	1.98
Infinity	1.96

**Note:** There are two basic versions of the  $t$ -test. The version presented here assumes that each sample was taken from a different population and so the samples are therefore independent of one another. In the example of the *Drosophila* larvae, different larvae were used in each of the two treatment conditions, and these samples are therefore considered **independent**. If the same larvae had been used in both treatment conditions, then the samples would be classified as **dependent**. Dependent samples require a different version of the  $t$ -test known as a paired  $t$ -test, a version that many statistical programs default to. The paired  $t$ -test is not discussed in this guide.

## Application in Biology

A small population of crayfish was accidentally released into a shallow pond that was being used in a long-term food-web study. Within a few months, biologists noticed that the underwater plant population was being eaten by the crayfish and had almost disappeared. At the same time, aquatic invertebrates, such as the water flea (*Daphnia* sp.), were also disappearing. From their earlier work, the biologists knew that the main predator of *Daphnia* is the goldfish. They hypothesized that the underwater plants had been providing hiding places for the *Daphnia*, protecting the *Daphnia* from goldfish. As the underwater plants disappeared, the *Daphnia* lost their protection. The biologists designed an experiment to test their hypothesis. They placed goldfish and *Daphnia* together in a tank with underwater plants, and an equal number of goldfish and *Daphnia* in another tank without underwater plants. They then counted the number of *Daphnia* eaten by the goldfish in 30 minutes. They repeated this experiment in 10 tanks per condition (i.e., sample size = 10, or  $n = 10$ , per group). The results of their experiment and their calculations of experimental error (variance,  $s^2$ ) are in **Table 8**.

**Table 8. Number of *Daphnia* Eaten by Goldfish in 30 Minutes in Tanks with or without Underwater Plants**

Tanks	Plants (sample <sub>1</sub> )	No Plants (sample <sub>2</sub> )	Plants $(x_i - \bar{x}_1)^2$	No Plants $(x_i - \bar{x}_2)^2$
1 and 2	13	14	$(9.6 - 13)^2 = 11.56$	$(14.4 - 14)^2 = 0.16$
3 and 4	9	12	$(9.6 - 9)^2 = 0.36$	$(14.4 - 12)^2 = 5.876$
5 and 6	10	15	$(9.6 - 10)^2 = 0.16$	$(14.4 - 15)^2 = 0.436$
7 and 8	10	14	$(9.6 - 10)^2 = 0.16$	$(14.4 - 14)^2 = 0.16$
9 and 10	7	17	$(9.6 - 7)^2 = 6.76$	$(14.4 - 16)^2 = 6.76$
11 and 12	5	10	$(9.6 - 5)^2 = 21.16$	$(14.4 - 10)^2 = 19.37$
13 and 14	10	15	$(9.6 - 10)^2 = 0.16$	$(14.4 - 15)^2 = 0.36$
15 and 16	14	15	$(9.6 - 14)^2 = 19.336$	$(14.4 - 15)^2 = 0.36$
17 and 18	9	18	$(9.6 - 9)^2 = 0.36$	$(14.4 - 18)^2 = 12.96$
19 and 20	9	14	$(9.6 - 9)^2 = 0.36$	$(14.4 - 14)^2 = 0.16$
			$\sum (x_i - \bar{x}_1)^2 = 60.4$	$\sum (x_i - \bar{x}_2)^2 = 46.4$
Mean ( $\bar{x}$ )	$\bar{x}_1 = 9.6$	$\bar{x}_2 = 14.4$	$\frac{\sum (x_i - \bar{x}_1)^2}{n-1} = \frac{60.4}{9}$	$\frac{\sum (x_i - \bar{x}_2)^2}{n-1} = \frac{46.4}{9}$
		Variance ( $s^2$ )	$s_1^2 = 6.71$	$s_2^2 = 5.16$

To determine whether the difference between the two groups was significant, students calculated a  $t$ -test statistic, as shown below:

$$SE = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}} = \sqrt{\frac{6.71}{10} + \frac{5.16}{10}} = 1.089$$

mean difference (absolute value) =  $|\bar{x}_1 - \bar{x}_2| = |9.6 - 14.4| = 4.8$

$$t = \frac{|\bar{x}_1 - \bar{x}_2|}{SE} = \frac{4.8}{1.089} = 4.41$$

There are  $(10 + 10 - 2) = 18$  degrees of freedom, so the critical value for  $p = 0.05$  is 2.10 from **Table 7**. The calculated  $t$ -value of 4.41 is greater than 2.10, so the students can reject the null hypothesis that any differences in the number of *Daphnia* eaten in the presence or absence of underwater plants occurred purely by chance. So what can they conclude? It is possible that the goldfish ate significantly more *Daphnia* in the absence of underwater plants than in the presence of the plants.

Note: Count data like the ones used in this example, are not normally distributed. For this reason, a scientist would either log transform the data before analysis or choose a different test (beyond the scope of this Guide) to analyze the data. Another problem with this example is the small sample size. A larger sample size can be achieved by combining data from several classes.

### Analyzing Frequencies: The Chi-Square Statistical Analysis Test

Data can occur in many different forms. Some data, such as plant height, represent a physical measurement that is numerical. Other types of data, such as genotypes, can be classified into categories and counted as frequencies. For frequency data, the chi-square test is the statistical test most often used to determine whether the observed pattern of frequency data could have arisen by chance.

For example, you decide to flip a coin 50 times. You expect a proportion of 50% heads and 50% tails. Based on a 50:50 probability, you predict 25 heads and 25 tails. These are the *expected* values. You would rarely get exactly 25 and 25, but how far off can these numbers be without the results being significantly different from what you expected? After you conduct your experiment, you get 21 heads and 29 tails (the observed values). Is the difference between observed and expected results purely due to chance? Or could it be due to something else, such as something might be wrong with the coin. The chi-square test can help you answer this question.

Note that this test must be used on raw categorical data. Values need to be simple counts and not transformed in any way. Modifying the counts will alter the data and invalidate the test. The size of the sample is an important aspect of the chi-square test—it is generally more difficult to detect a statistically significant difference between experimental and observed results in a small sample than in a large sample. Two common applications of this test in biology are in analyzing the outcomes of a genetic cross and the distribution of organisms in response to an environmental factor of interest.

To calculate the chi-square test statistic, you use the following equation:

$$\chi^2 = \sum \frac{(o - e)^2}{e}$$

$o$  = observed values

$e$  = expected values

$\chi^2$  = chi-square value

$\Sigma$  = summation

## Calculation Steps

1. Calculate the chi-square value. The columns in **Table 9** outline the steps required to calculate the chi-square value and test the null hypothesis, using the coin-flipping example discussed above. The equations for calculating a chi-square value are provided in each column heading.

**Table 9. Coin-Toss Chi-Square Value Calculations**

Side of Coin	Observed ( <i>o</i> )	Expected ( <i>e</i> )	( <i>o</i> - <i>e</i> )	( <i>o</i> - <i>e</i> ) <sup>2</sup>	( <i>o</i> - <i>e</i> ) <sup>2</sup> / <i>e</i>
Heads	21	25	(-4)	16	0.64
Tails	29	25	4	16	0.64
					$\chi^2 = 1.28$ $\chi^2 = \sum(o - e)^2/e$

2. Determine the degrees of freedom value as follows:

$$\text{df} = \text{number of categories minus } 1$$

In the example above, there are two categories (heads and tails).

$$\text{df} = (2 - 1) = 1$$

3. Use the critical values table (**Table 10**) to determine the probability (*p*) value. A *P* value of 0.05 (which is shown in red in **Table 10**) means there is only a 5% chance that there is no real difference between the observed values and expected values and that any differences likely occurred simply by chance.

For example, for *df* = 1, there is a 5% probability (*P* value = 0.05) of obtaining a  $\chi^2$  value of 3.841 or larger. If the  $\chi^2$  value obtained was 4.5, then you can reject the null hypothesis that there is no real difference between observed and expected data. The difference between observed and expected data is considered statistically significant.

If the  $\chi^2$  value was 3.1, then you cannot reject the null hypothesis. The difference between observed and expected data is not statistically significant.

Significance testing in biology typically uses a *P* value of 0.05, which is also referred to as the alpha value (see the "Significance Testing: The  $\alpha$  (Alpha) Level" section in Part 2). A result with the *P* value of 0.05 is called a **statistically significant result**. Some studies use a more stringent 1% as the criterion for rejecting the null hypothesis. A *P* value of 0.01 is called a **highly significant result**.

To use the critical values table (**Table 10**), locate the calculated  $\chi^2$  value in the row corresponding to the appropriate number of degrees of freedom. For the coin-flipping example, locate the calculated  $\chi^2$  value in the *df* = 1 row. The  $\chi^2$  value obtained was 1.28, which falls between 0.455 and 2.706 and is smaller

than 3.841 (the  $\chi^2$  value at the  $p = 0.05$  cutoff); in other words, the result was likely to happen between 10% and 50% of time. Therefore, you cannot reject the null hypothesis, that the results have likely occurred simply by chance, at an acceptable significance level.

**Table 10. Critical Values Table for Different Significance Levels and Degrees of Freedom**

df \ p	0.995	0.975	0.9	0.5	0.1	0.05	0.025	0.01
1	0.000	0.000	0.016	0.455	2.706	3.841	5.024	6.635
2	0.010	0.051	0.211	1.386	4.605	5.991	7.378	9.210
3	0.072	0.216	0.584	2.366	6.251	7.815	9.348	11.345
4	0.207	0.484	1.064	3.357	7.779	9.488	11.143	13.277
5	0.412	0.831	1.610	4.351	9.236	11.070	12.832	15.086
6	0.676	1.237	2.204	5.348	10.645	12.592	14.449	16.812
7	0.989	1.690	2.833	6.346	12.017	14.067	16.013	18.475

### Application in Biology—Example 1

Students just learned in their biology class that pill bugs use gill-like structures to breathe oxygen. The students hypothesized that pill bugs need to live in wet environments. To test the hypothesis, they wanted to determine whether pill bugs show a preference for living in wet or dry environments.

The students placed 15 pill bugs on the dry side of a two-sided choice chamber, and 15 pill bugs on the wet side of the chamber. Fifteen minutes later, 26 pill bugs are on the wet side and 4 on the dry side. The data are shown in Table 11.

**Table 11. Pill Bug Locations on Two-Sided Chamber**

Elapsed Time (min.)	Pill Bugs on Wet Side (no.)	Pill Bugs on Dry Side (no.)
0	15	15
15	26	4

**Experimental hypothesis:** Pill bugs prefer wet environments.

**Experimental prediction:** Significantly more pillbugs will end up in the wet environment than the dry environment after 15 minutes.

**Null hypothesis:** Pillbugs do not prefer either wet or dry environments.

**Expected results if the null hypothesis is true:** An approximately equal number of pill bugs will be found on each side of the chamber after 15 minutes.

**Table 12. Pill Bug Locations Chi-Square Value Calculations**

Side of Chamber	Observed (o)	Expected (e)	(o - e)	(o - e) <sup>2</sup>	(o - e) <sup>2</sup> /e
Wet	26	15	11	121	8.07
Dry	4	15	-11	121	8.07
					$\chi^2 = 16.14$
					$\chi^2 = \sum(o - e)^2/e$

degrees of freedom =  $df = (2 - 1) = 1$

In **Table 12**, the  $\chi^2$  value is 16.14, which is much greater than the critical value of 3.841 (from the critical values table [**Table 10**] for a  $P$  value of 0.05). This means that there is a statistically significant difference between expected and observed data, and it may indicate that the pill bugs prefer one side of the chamber to the other (alternative hypothesis).

Note that an alternative hypothesis is never proven true with any statistical test like the chi-square test. This statistical test only tells you whether the null hypothesis can or cannot be rejected.

## Measuring Correlations and Analyzing Linear Regression

Correlations can suggest relationships between sets of data. The correlation coefficient ( $r$ ) provides a measure of how related two variables are, and it is expressed as a value between +1 and -1. The closer the value is to 0, the weaker the correlation.

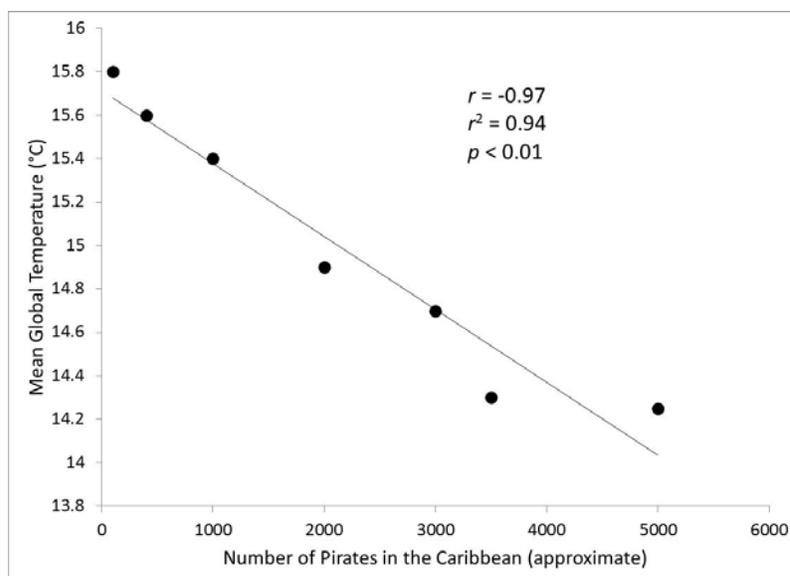
For example, if you plot the area of an oak (*Quercus* sp.) leaf ( $Y$ ) on an  $xy$  scatter plot as a function of the leaf's length ( $X$ ), the correlation coefficient ( $r$ ) indicates how much area depends on length. An  $r$ -value equal to +1 would indicate a perfect positive correlation between area and length. In other words, the longer an oak leaf, the larger its area. An  $r$ -value of -1 would indicate a perfect negative correlation—the longer an oak leaf, the smaller its area. If there is no correlation between two variables, the  $r$ -value equals 0, which would mean that there is no relationship between oak leaf length and area. The null hypothesis ( $H_0$ ) for a correlation is that there is no correlation and  $r = 0$ .

Calculating  $r$  involves determining the sample mean of the predictor variable ( $\bar{x}$ ) and its standard deviation ( $s_x$ ), the sample mean of the response variable ( $\bar{y}$ ) and its standard deviation ( $s_y$ ), and the number of pairs ( $X, Y$ ) of individuals in the sample ( $n$ ):

$$r = \frac{\sum_{i=1}^n \left( \frac{x_i - \bar{x}}{s_x} \right) \left( \frac{y_i - \bar{y}}{s_y} \right)}{n - 1}$$

Another statistic, called the coefficient of determination, uses the square of  $r$ . The  $r^2$  value tells us the strength of the relationship between  $X$  and  $Y$ .

When calculating correlations, it is important for you to remember that correlation does not imply causation. For example, **Figure 7** shows that there is a strong negative correlation between the mean temperature of Earth over the last 190 years and the number of pirates in the Caribbean. Clearly, a decrease in the number of pirates is not the *cause* of global warming.



**Figure 7: Mean global temperature (°C) as a function of the approximate number of pirates in the Caribbean from 1820 to 2000.** The line is the linear regression. Statistics are correlation coefficient ( $r$ ) and the coefficient of determination ( $r^2$ ).

### Calculation Steps

Students wanted to see if there is an association between the mass of the tomatoes on a tomato plant and the number of seeds in the tomatoes. They picked 10 tomatoes from the plant, cut each one open, and counted the seeds. The data and calculations for determining the  $r$ -value are shown in **Table 13**.

**Table 13. Number of Seeds and Mass (g) of Tomatoes**

Tomato No.	Mass ( $x$ )	No. of Seeds ( $y$ )	$\frac{x_i - \bar{x}}{s_x}$	$\frac{y_i - \bar{y}}{s_y}$	$\left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right)$
1	77.5	20	-0.241	-0.530	0.128
2	81.2	26	1.439	1.061	1.527
3	75.9	22	-0.967	0	0
4	78.1	22	0.032	0	0
5	77.1	18	-0.422	-1.061	0.448
6	76.3	20	-0.785	-0.530	0.416
7	75.7	18	-1.058	-1.061	1.123
8	82.3	30	1.938	2.121	4.110
9	78.9	24	0.395	0.530	0.209
10	77.3	20	-0.331	-0.530	0.175
Mean	$\bar{x} = 78.03$ g	$\bar{y} = 22$ seeds			$\sum \left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right) = 8.136$
Standard deviation	$s_x = 2.203$	$s_y = 3.771$			
$r = \frac{\sum \left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right)}{n - 1} = \frac{8.136}{10 - 1} = \frac{8.136}{9} = 0.904$					

1. Calculate  $\bar{x}$ ,  $s_x$ ,  $\bar{y}$ , and  $s_y$  as shown in **Table 13**.
2. Determine  $\frac{x_i - \bar{x}}{s_x}$  and  $\frac{y_i - \bar{y}}{s_y}$ , multiply the two for each tomato sample, and then sum the results as shown in **Table 13**:  $\sum \left( \frac{x_i - \bar{x}}{s_x} \right) \left( \frac{y_i - \bar{y}}{s_y} \right) = 8.136$
3. Calculate  $r = 8.136/9 = 0.904$ .
4. Compare the calculated  $r$ -value with the critical value of  $r$  at  $\alpha$  (the  $H_0$  rejection level) = 0.05. See **Table 14** for critical  $r$ -values. The degrees of freedom is calculated by adding the number of data points in the two groups combined, minus 2.

**Table 14. Critical  $r$ -Values at  $\alpha = 0.05$**

Degrees of Freedom ( $n$ pairs – 2)	$\pm r_{crit}$ (0.05)
1	0.997
2	0.950
3	0.878
4	0.811
5	0.754
6	0.707
7	0.666
8	0.632
9	0.602
10	0.576
11	0.553
12	0.532
13	0.514
14	0.497
15	0.482

Note that  $r$ -values can indicate either positive or negative correlations and can therefore vary between +1 and -1. Therefore, critical  $r$ -values are listed as  $\pm r$  in the table.

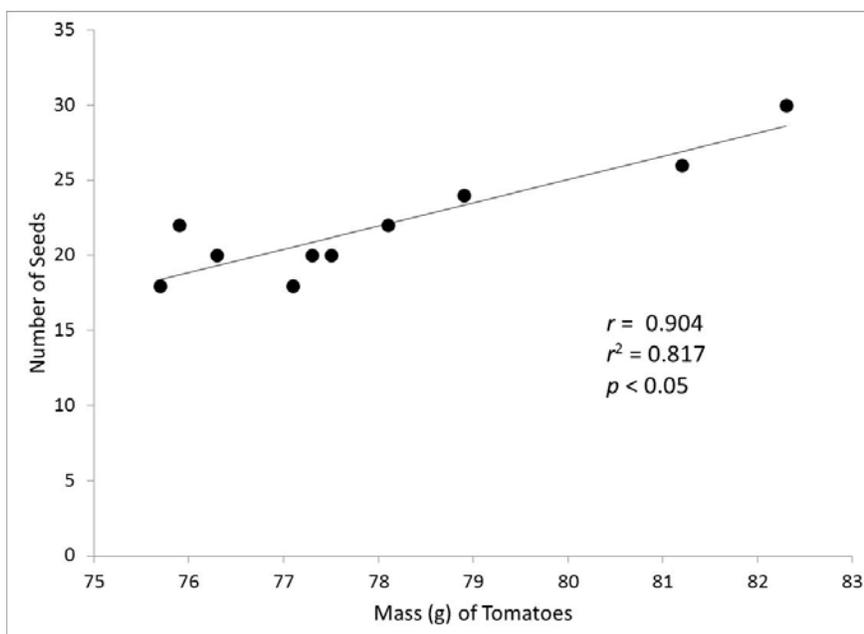
In **Table 14**, the value for  $r_{crit}$  is  $\pm 0.632$  for 8 degrees of freedom (10 pairs of observations – 2). The calculated  $r$ -value is 0.904, which is much closer to +1 (perfect positive correlation) than 0.632. This means that the probability of getting a value as extreme as 0.904 purely by chance if  $H_0$  is true ( $r = 0$ ) is less than 0.05. Therefore, students can reject  $H_0$  and conclude that there is a statistically significant association between the mass of the students' tomatoes and the number of seeds each tomato has.

To go one step further, it is possible to calculate the coefficient of determination,  $r^2$ :

$$r^2 = (0.904)^2 = 0.817$$

The  $r^2$  value of 0.817 denotes the *strength* of the linear association between the mass of the tomatoes ( $x$ ) and the number of seeds ( $y$ ). For example, if students weigh a tomato, they can predict the number of seeds it will have with 81.7% accuracy.

Finally, a scatter plot graph can be used to illustrate the relationship (**Figure 8**). It is possible to draw a straight line that goes through the points—called a line of best fit. The line of best fit may pass through some of the points, none of the points, or all of the points.



**Figure 8: Number of seeds counted in tomatoes as a function of tomato mass.** Statistics are correlation coefficient ( $r$ ) and the coefficient of determination ( $r^2$ ).

The coefficient of determination is a measure of how well the regression line represents the data. If the regression line passes exactly through every point on the scatter plot, it would be able to explain all of the variation. The further the line is away from the points, the less it is able to explain. In **Figure 8**, 81.7% of the variation in  $y$  can be explained by the relationship between  $x$  and  $y$ .

**Note:** Many biological traits (i.e, animal behavior or physical characteristics) vary considerably among individuals in a population. Thus, a coefficient of determination of 0.817 between two biological variables would be considered very high. On the other hand, for a standard curve, as described later, it would be considered low.

### Application in Biology—Example 1

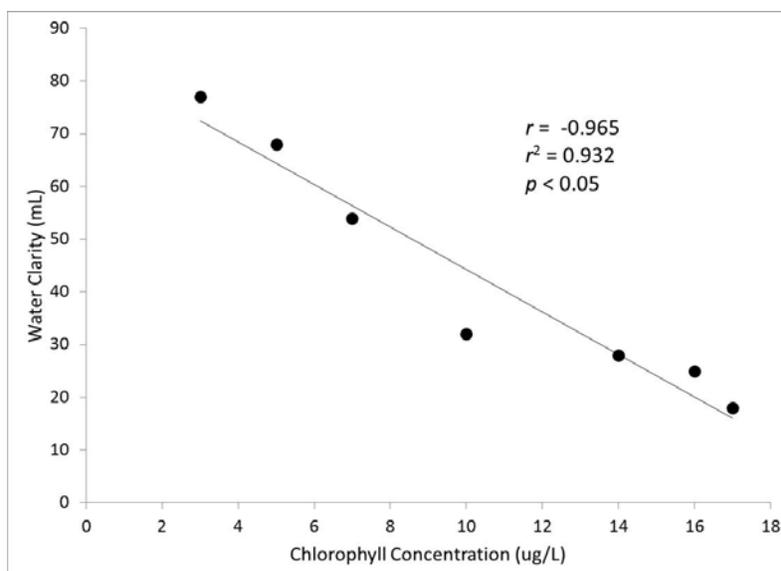
Students were curious to learn whether there is an association between amounts of algae in pond water and the water's clarity. They collected water samples from seven local ponds that seemed to differ in terms of water clarity. To quantify the clarity of the water, they cut out a small disk from white poster board, divided the disk into four equal parts, and colored two of the opposite parts black; they then

placed the disk in the bottom of a 100-milliliter graduated cylinder. Working with one sample at a time, they gradually poured water from each water sample into the cylinder until the disk was no longer visible from above. For each sample, they recorded in **Table 15** the volume of water necessary to obscure the disk—the more water necessary to obscure the disk, the clearer the water. As a proxy for algae concentration, they extracted chlorophyll from the water samples and used a spectrophotometer to determine chlorophyll concentration (**Table 15**).

**Table 15. Chlorophyll Concentration ( $\mu\text{g/L}$ ) and Clarity of Pond Water**

Pond	Chlorophyll Concentration ( $x$ ; $\mu\text{g/L}$ )	Water Clarity ( $y$ ; mL)	$\frac{x_i - \bar{x}}{s_x}$	$\frac{y_i - \bar{y}}{s_y}$	$\left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right)$
Sandy's	14	28	0.672	-0.656	-0.441
Herron	5	68	-0.956	1.077	-1.029
Tommy's	10	32	-0.052	-0.482	-0.025
Rocky	7	54	-0.594	0.470	-0.280
Fishing	17	18	1.214	-1.089	-1.323
Lost	16	25	1.033	-0.786	-0.812
Sunset	3	77	-1.318	1.467	-1.933
Mean	$\bar{x} = 10.29 \mu\text{g/L}$	$\bar{y} = 43.14 \text{ mL}$			$\Sigma \left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right) = -5.792$
Standard deviation	$s_x = 5.529$	$s_y = 23.083$			
$r = \frac{\Sigma \left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right)}{n - 1} = \frac{-5.792}{7 - 1} = \frac{-5.792}{6} = -0.965$					

**Note:** Water clarity is given as the volume of water in milliliters (mL) required to obscure a black-and-white disk at the bottom of a 100-milliliter graduated cylinder. A greater volume corresponds to clearer water.



**Figure 9: Clarity of pond water as a function of chlorophyll concentration.** Water clarity was measured as the volume of water necessary to obscure a black-and-white disk in the bottom of a 100-milliliter graduated cylinder. Statistics are Pearson’s correlation coefficient ( $r$ ) and the coefficient of determination ( $r^2$ ).

Just by graphing the data points and looking at the graph in **Figure 9**, it is clear that there is an association between water clarity and chlorophyll concentration. Because the line slopes down, students know it is a negative correlation: as water clarity decreases, chlorophyll concentration increases.

When students calculate  $r$ , they get a value of  $-0.965$ , which is a strong correlation (with  $-1$  being a perfect negative correlation). They can confirm this by checking the critical  $r$ -value on **Table 14**, which is  $\pm 0.754$  for 5 degrees of freedom ( $7 - 2$ ) with a 0.05 confidence level. Since the  $r$  of  $-0.965$  is closer to  $-1$  than  $r_{crit} -0.754$ , they can conclude that the probability of getting a value as extreme as  $-0.965$  purely by chance is less than 0.05. Therefore, they can reject  $H_0$  and conclude that chlorophyll concentration and water clarity are significantly associated.

The coefficient of determination ( $r^2$ ) is 0.932, which indicates that students can predict water clarity based on chlorophyll concentration with 93.2% accuracy.

### Application in Biology—Example 2

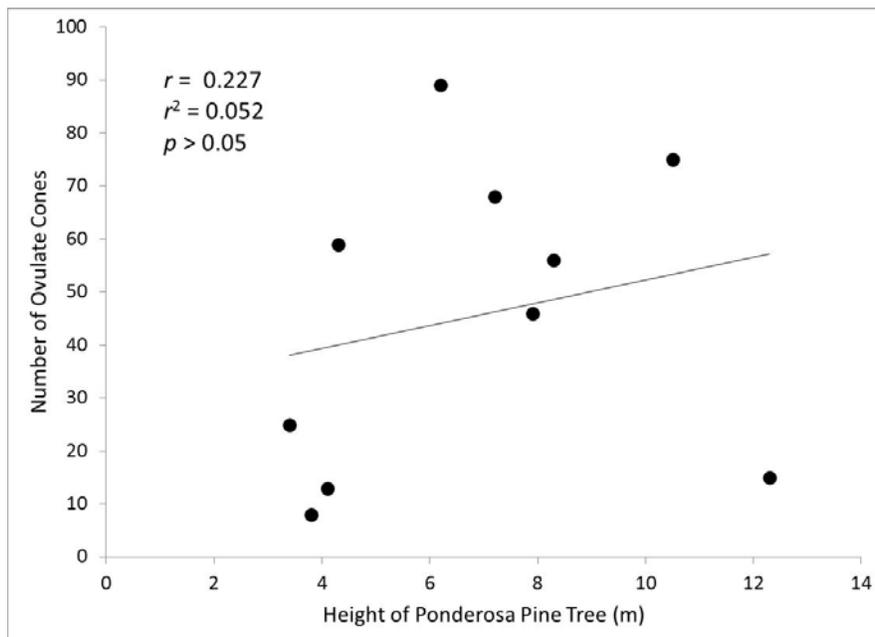
Students noticed that some ponderosa pine trees (*Pinus ponderosa*) on a street have more ovulate cones (female pinecones) than other ponderosa pine trees. They reasoned that older, and therefore taller, trees should have more cones than younger, shorter trees.

To determine the height of a tree, they used the “old logger” method. A student held a stick the same length as the student’s arm at a  $90^\circ$  angle to the arm and backed up until the tip of the stick “touched” the top of the tree. The distance the student was from the tree equaled the height of the tree. Using this

method, the students measured the heights of 10 trees. Then, using binoculars, they counted the number of ovulate cones on each tree and recorded the data in Table 16.

**Table 16. Number of Ovulate Cones on Ponderosa Pine Trees of Different Heights**

Tree No.	Tree Height (m)	No. of Cones	$\frac{x_i - \bar{x}}{s_x}$	$\frac{y_i - \bar{y}}{s_y}$	$\left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right)$
1	10.5	75	1.226	1.034	1.267
2	7.2	68	0.133	0.790	0.105
3	4.3	59	-0.828	0.475	-0.393
4	7.9	46	0.364	0.021	0.008
5	3.8	8	-0.994	-1.307	1.298
6	8.3	56	0.497	0.370	0.184
7	3.4	25	-1.126	-0.713	0.802
8	4.1	13	-0.894	-1.132	1.012
9	12.3	15	1.822	-1.062	-1.934
10	6.2	89	-0.199	1.523	-0.303
Mean	$\bar{x} = 6.8$ m	$\bar{y} = 45.4$ cones			$\Sigma \left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right) = 2.046$
Standard deviation	$s_x = 3.019$	$s_y = 28.625$			
$r = \frac{\Sigma \left(\frac{x_i - \bar{x}}{s_x}\right)\left(\frac{y_i - \bar{y}}{s_y}\right)}{n - 1} = \frac{2.046}{10 - 1} = \frac{2.046}{9} = 0.227$					



**Figure 10: Number of ovulate cones on ponderosa pine trees as a function of tree height (m).** Statistics are Pearson’s correlation coefficient ( $r$ ) and the coefficient of determination ( $r^2$ ).

Just looking at the data points in **Figure 10**, it is hard to know whether there is a correlation or not. If there is a correlation, it is not very strong. Drawing the line of best fit suggests a positive correlation. This is clearly a case in which calculating  $r$  will help determine whether the correlation is statistically significant.

In **Table 14**,  $r_{crit}$  is  $\pm 0.632$  for 8 degrees of freedom ( $10 - 2$ ). The calculated  $r$ -value is 0.227, which is further away from +1 than  $r_{crit}$  0.632, so the probability of getting a value of 0.227 purely by chance is greater than 0.05 ( $p > 0.05$ ). Therefore, students cannot reject  $H_0$  and can conclude that there is not a statistically significant association between the numbers of ovulate cones on ponderosa pine trees and the heights of the trees.

## Part 3: Commonly Used Calculations in Biology

### Relative Frequency

Relative frequency is the ratio of the number of times an event occurs out of a total number of events. This calculated fraction can then be converted into a percentage of the total number of events measured.

$$\text{relative frequency} = (\text{number of times a specific event occurs}) / (\text{total number of events})$$

The result can be multiplied by 100 to give the percentage.

### Application in Biology

Allele and genotype frequencies are commonly calculated by population geneticists. For instance, in a population of 350 pea plants, suppose 112 are homozygous for the dominant yellow pea seed allele ( $YY$ ), 139 are heterozygous ( $Yy$ ), and 99 are homozygous for the recessive green pea seed allele ( $yy$ ).

To determine the relative frequency (and percentage) of plants in this population that are homozygous for the dominant yellow pea seed allele, you should divide the number of plants that are homozygous for the yellow pea seed allele by the total number of plants:

$$\text{relative frequency of the homozygous dominant (} YY \text{) genotype} = 112/350 = 0.32$$

To express frequency as a percentage, multiply the frequency by 100%:

$$\text{percentage} = 0.32 \times 100 = 32\% \text{ of the population has the homozygous dominant genotype}$$

To determine the relative frequency (and percentage) of the recessive green seed allele, divide the total number of green seed alleles in the gene pool by the total number of alleles in the population:

$$\text{relative frequency of the recessive allele (} y \text{)} = [(139 \times 1) + (99 \times 2)] / (350 \times 2) = 337/700 = 0.48$$

$$\text{percentage} = 0.48 \times 100 = 48\% \text{ of the gene pool is the recessive green pea seed allele}$$

### Probability

You learned in the “Significance Testing” section of Part 2 that a probability of 0.05 means that there is a 5% chance for an event to happen—for example, a 5% chance of calculating a particular test statistic by chance. This section provides more information about probability and how to calculate it for different scenarios.

Probability allows scientists to predict the likelihood of the outcome of random events. Probability values ( $p$ ) lie between 1 (the event is certain to happen) and 0 (the event certainly will not happen). The probabilities for all other events have fractional values. For example, the probability of throwing a 2 on a

six-sided die is 1 out of 6 ( $p = 1/6$ ), since the number 2 appears on only one of the six sides. By contrast, the probability of throwing a 7 on a normal six-sided die is 0.

### Rule of Addition

The probability of *either* of two *mutually exclusive* events occurring is equal to the sum of their individual probabilities.

#### Example

Given a normal six-sided die, what is the probability of you rolling *either* a 2 or a 4 on the die? These events are mutually exclusive because they cannot happen at the same time—that is, in a single roll of the die you cannot roll both a 2 and a 4.

There is a  $1/6$  chance of rolling a 2.

There is a  $1/6$  chance of rolling a 4.

The probability of either event occurring is equal to the sum of the probability of each event:

$$p = 1/6 + 1/6 = 2/6 = 1/3$$

There is 1 chance in 3 of you rolling either a 2 or a 4 on the die.

### Rule of Multiplication

The probability of two independent events both occurring is the product of their individual probabilities.

#### Example

Given a normal six-sided die, what is the probability of you rolling a 2 and then a 4 on two consecutive rolls? These events are independent of one another because they have no effect on each other's occurrence—that is, if you roll a six-sided die twice, rolling a 2 on the first roll has no effect on whether you will roll a 4 on the second roll.

On the first roll, there is a  $1/6$  chance of rolling a 2.

On the second roll, there is a  $1/6$  chance of rolling a 4.

The probability of rolling a 2 first and a 4 second follows:

$$p = 1/6 \times 1/6 = 1/36$$

There is 1 chance in 36 of rolling a 2 and then a 4 on two consecutive rolls of the die.

### Application in Biology—Example 1

What is the probability that two parents who are heterozygous for the sickle cell allele would have three children in a row who are homozygous for the sickle cell allele and have sickle cell anemia?

The probability of two parents who are heterozygous for an allele to have a child who is homozygous for that allele is 1 in 4:

$$p = 1/4 \times 1/4 \times 1/4 = 1/64$$

There is 1 chance in 64 that these parents will have three children in a row with sickle cell disease.

## Application in Biology—Example 2

Two pea plants that are heterozygous for the round (*R*) and yellow (*Y*) alleles (*RrYy*) are crossed and produce only a single seed. What is the probability of a seed from this cross having the genotype *RRYy* or *RRYY*?

The probability of getting a seed with the *RRYy* genotype is  $\frac{1}{4} \times \frac{1}{2} = \frac{1}{8} = \frac{2}{16}$

The probability of getting a seed with the *RRYY* genotype is  $\frac{1}{4} \times \frac{1}{4} = \frac{1}{16}$

To obtain the probability of getting a seed with the *RRYy* genotype **or** the *RRYY* genotype, we use the rule of addition:

$$P = \frac{2}{16} + \frac{1}{16} = \frac{3}{16}$$

There are three chances in 16 of these parents having a child with either the *RRYy* or *RRYY* genotype.

## Rate Calculations

Rate is used to express one measured quantity (*y*) in relation to another measured quantity (*x*).

In biology, rates are often calculated to indicate the change in a property of a system over time. For example, the rate of an enzyme-catalyzed reaction is frequently expressed as the amount of product produced by the enzyme in a given amount of time. When you use data plotted on a graph, you calculate the rate in the same way as you calculate the slope.

$$\text{rate} = \Delta y / \Delta x$$

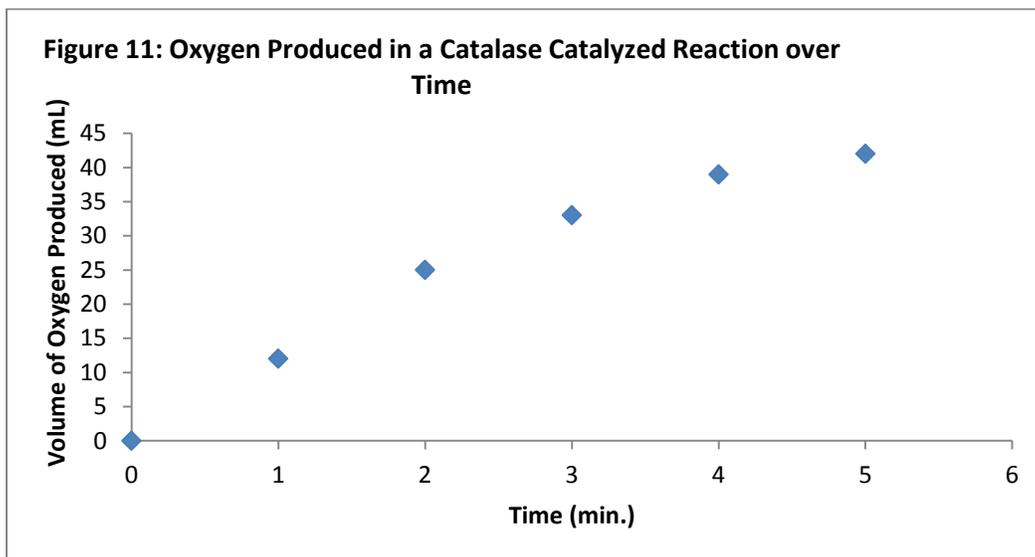
(The delta symbol represents change.)

## Application in Biology

Students in an advanced biology class studied the reaction catalyzed by the catalase enzyme. Catalase degrades hydrogen peroxide ( $\text{H}_2\text{O}_2$ ) to water ( $\text{H}_2\text{O}$ ) and oxygen gas ( $\text{O}_2$ ). The students set up an experiment to measure the amount of  $\text{O}_2$  produced by catalase over 5 minutes when it is added to  $\text{H}_2\text{O}_2$ . Table 17 contains the data collected by a group of students, and Figure 11 shows the corresponding graph. From these data, rates of catalase activity can be calculated over various intervals of time.

Table 17. Volume of Oxygen Produced from the Catalysis of Hydrogen Peroxide by the Enzyme Catalase

Time (min.)	Volume of Oxygen Produced (mL)
0	0
1	12
2	25
3	33
4	39
5	42



To calculate the initial rate of reaction in the first 2 minutes of the experiment, students first subtracted the volume of oxygen produced at 2 minutes from the volume of oxygen produced at 0 minutes:

$$\Delta y = 25 \text{ milliliters} - 0 \text{ milliliters} = 25 \text{ milliliters}$$

Next, they subtracted the number of minutes at 2 minutes from the number of minutes at 0 minutes:

$$\Delta x = 2 \text{ minutes} - 0 \text{ minutes} = 2 \text{ minutes}$$

Finally, they divided the change in oxygen volume ( $\Delta y$ ) by the change in time ( $\Delta x$ ); this is the rate:

$$\text{rate} = 25 \text{ milliliters} / 2 \text{ minutes} = 12.5 \text{ milliliters of O}_2 \text{ produced/minute}$$

Similarly, they can calculate the rate of reaction between the third and fifth minutes of the experiment:

$$\text{rate} = (42 \text{ milliliters} - 33 \text{ milliliters}) / (5 \text{ minutes} - 3 \text{ minutes}) = 9 / 2 = 4.5 \text{ milliliters of O}_2 \text{ produced/minute}$$

## Hardy-Weinberg Frequency Calculations

The Hardy-Weinberg equations are used in population genetics to describe the basic principle that allele frequencies do not change in a large, freely interbreeding population from one generation to the next.

Allele frequencies in a population are in equilibrium (do not change) when all the following conditions are met:

1. The population is very large and well mixed.
2. There is no migration in or out of the population.
3. Mutations are not occurring.
4. Mating is random.
5. There is no natural selection.

To calculate the allele frequencies in a population, you use two equations derived from the Hardy-Weinberg principle:

$$p + q = 1.0$$

$$p^2 + 2pq + q^2 = 1.0$$

where

$p$  = the frequency of the dominant allele ( $A$ )

$q$  = the frequency of the recessive allele ( $a$ )

$p^2$  = the frequency of the homozygous dominant  $AA$  genotype

$2pq$  = the frequency of the heterozygous  $Aa$  genotype

$q^2$  = the frequency of the homozygous recessive  $aa$  genotype

If the observed allele frequencies in a population differ from the frequencies predicted by the Hardy-Weinberg principle, then the population is not at equilibrium and evolution may be occurring.

### Application in Biology

In a hypothetical population of 100 rock pocket mice (*Chaetodipus intermedius*), 81 individuals have light, sandy-colored fur and a  $dd$  genotype. The remaining 19 individuals are dark colored and therefore have either the  $DD$  genotype or the  $Dd$  genotype. Scientists assumed that this population is at equilibrium; they used the Hardy-Weinberg equations to find  $p$  and  $q$  for this population and calculated the frequency of heterozygous genotypes.

Scientists knew that 81 mice have the  $dd$  genotype:

$$q^2 = 81/100 = 0.81, \text{ or } 81\%$$

Next they calculated  $q$ :

$$q = \sqrt{0.81} = 0.9$$

Then they calculated  $p$  using the equation  $p + q = 1$ :

$$p + (0.9) = 1$$

$$p = 0.1$$

To calculate the frequency of the heterozygous genotype, they calculated  $2pq$ .

$$2pq = 2(0.1)(0.9) = 2(0.09)$$

$$2pq = 0.18$$

Based on the calculations, the frequency of the recessive allele is 0.9 and the frequency of the dominant allele is 0.1.

If the scientists had a way to distinguish mice that are heterozygotes from those that are homozygous dominant for the dark colored fur, then they would have a way of determining whether the population is or is not at equilibrium and could apply a statistical test like the chi-square test to see if there is a difference.

### Standard Curves

A standard curve is a method of quantitative data analysis in which measurements of samples with *known* properties are plotted on a graph and then the graph is analyzed to determine the properties of *unknown* samples. Analysis of the graph is performed by drawing a line of best fit through the plotted points of the known samples and then determining the equation of this line (in the form  $y = mx + b$ ) or by interpreting the values of unknown samples directly from the drawn line. The samples with known properties are the standards, and the graph is the standard curve. Two common uses of standard curves in biology are to determine protein concentrations and to analyze DNA fragment length.

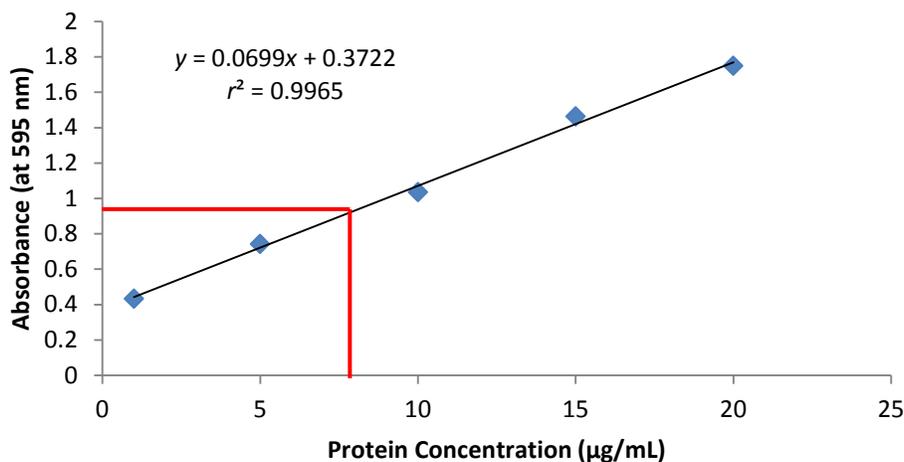
#### Application in Biology—Example 1: The Bradford Protein Assay

The Bradford protein assay is a colorimetric assay that determines the protein concentration of a solution by measuring how much light of a certain wavelength it absorbs. The light absorbance of several samples with known protein concentrations is measured using a spectrophotometer and then plotted on a graph as a function of protein concentration. Using this graph, or linear regression analysis, scientists determined the protein concentration of an unknown sample once its absorbance was measured.

**Table 18. Absorbance Measured at 595 Nanometers of Various Known Protein Concentrations**

Known Protein Concentration (µg/mL)	Measured Absorbance (at 595 nm)
1	0.433
5	0.742
10	1.036
15	1.463
20	1.750

**Figure 12: Protein Concentration as a Function of Absorbance**



In **Figure 12**, absorbance in **Table 18** was plotted as a function of protein concentration for the known samples (standards). The calculated coefficient of determination ( $r^2$ ) and equation of the regression line are included on the graph. The closer the  $r^2$  value is to 1, the better the data fit the curve—or the more likely that the data points  $x$  and  $y$  are actual solutions to the equation  $y = mx + b$ .

In this case, the equation of the line is

$$y = 0.0699x + 0.3722.$$

The absorbance of the unknown protein solution was measured with a spectrophotometer as 0.921 ( $y = 0.921$ ), so the scientists used the equation of the best-fit line to determine the protein concentration ( $x$ ):

$$\text{Protein concentration of unknown: } 0.921 = 0.0699x + 0.3722$$

$$\text{Protein concentration of unknown: } x = 7.85 \text{ micrograms per milliliter}$$

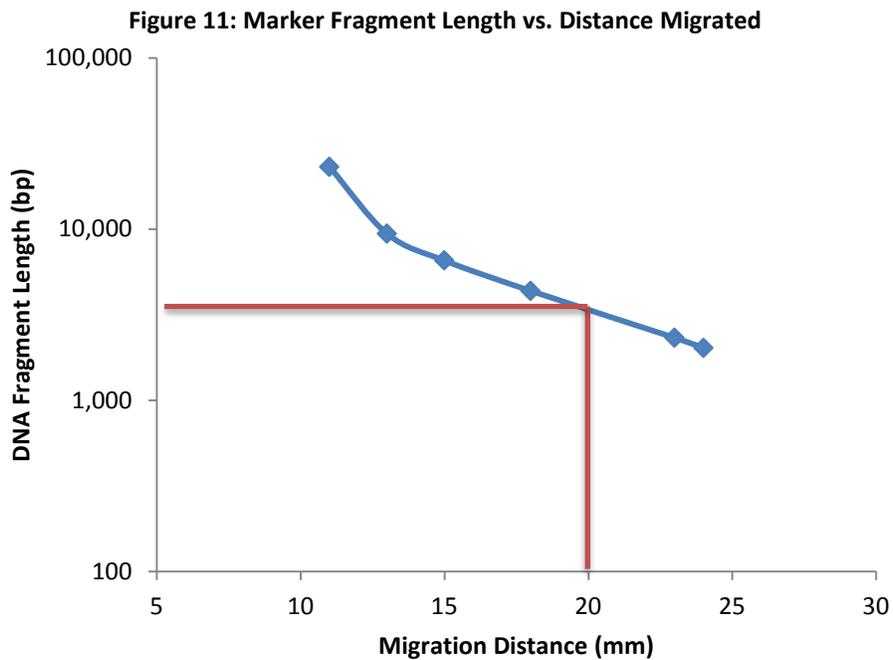
The scientists also estimated the value of the unknown protein concentration from the regression line itself, as illustrated by the red lines drawn on the graph in **Figure 12**. To determine this estimate, they located the absorbance of 0.921 on the  $y$ -axis and traced it horizontally to its intersection with the regression line. A vertical line from the intersection will cross the  $x$ -axis at the corresponding protein concentration.

### **Application in Biology—Example 2: DNA Fragment Size Analysis**

In RFLP (restriction fragment length polymorphism) analysis, the fragment sizes of unknown DNA samples can be determined from the standard curve of DNA markers of known fragment lengths. First, scientists measured the distance traveled by each of the marker fragments in a gel plate and plotted it as a function of size. This provides a standard for comparison to interpolate the size of the unknown fragments (**Table 19**).

**Table 19. Distance in Millimeters That Various DNA Fragments of Different Known Lengths Migrate Because of Gel Electrophoresis**

Distance Migrated (mm)	Fragment Length (no. of base pairs)
11	23,130
13	9,416
15	6,557
18	4,361
23	2,322
24	2,027



**Note:** The standard curve in Figure 13 was plotted on a logarithmic y-axis scale, because the relationship between fragment length and distance migrated is exponential, or nonlinear.

Scientists estimated the length of an unknown DNA fragment that migrated 20 millimeters by using the graph in **Figure 13**, as illustrated by the red lines. To estimate the unknown length, they located the distance of 20 millimeters on the x-axis and traced a vertical line to the line of best fit. A horizontal line from the point of intersection will cross the y-axis at the corresponding fragment length. In this case, they estimated the fragment length to be 3,100 base pairs.

**Authors:**

Written by Paul Strode, PhD, Fairview High School, CO, and Ann Brokaw, Rocky River High School, OH.

Edited by Laura Bonetta, PhD, HHMI

Reviewed by Brad Williamson; Sandra Blumenrath, PhD, and Satoshi Amagai, PhD, HHMI

Copyedited by Barbara Resch

Graphics by Heather McDonald, PhD, and Bill Pietsch

For a supplementary discussion of statistical methods and additional classroom examples, refer to the College Board's *AP Biology Quantitative Skills: A Guide for Teachers*, [http://apcentral.collegeboard.com/apc/public/repository/AP\\_Bio\\_Quantitative\\_Skills\\_Guide-2012.pdf](http://apcentral.collegeboard.com/apc/public/repository/AP_Bio_Quantitative_Skills_Guide-2012.pdf).

## Part 4: BioInteractive’s Mathematics and Statistics Classroom Resources

<p style="text-align: center;"><b>BioInteractive Resource Name (Links to Classroom-Ready Resources)</b></p>	Mean	Median	Mode	Range	Frequency	Rate	Variance and Standard Deviation	Standard Error and 95% Confidence Interval	Chi-Square Analysis	Student’s <i>t</i> -Test	Linear Regression and Pearson’s Correlation	Hardy-Weinberg	Probability	Standard Curves
<p><a href="#"><u>Diet and the Evolution of Salivary Amylase</u></a> Students analyze data obtained from two different research studies in order to draw conclusions between <i>AMY1</i> gene copy number and amylase production, and also between <i>AMY1</i> gene copy number and dietary starch consumption. The activity involves graphing, analyzing research data utilizing statistics, making claims, and supporting the claims with scientific reasoning.</p>	X						X	X		X	X			
<p><a href="#"><u>Evolution in Action: Data Analysis</u></a> Students analyze frequency distributions of beak depth data from Peter and Rosemary Grant’s Galápagos finch study and suggest hypotheses to explain the trends illustrated in the graphs. Students then investigate the effect of sample size on descriptive statistics and notice that the means and standard deviations vary for each subsample. Finally, students use wing length and body mass data to construct bar graphs, and they are asked to propose explanations for how and why some characteristics are more adaptive than others in given environments.</p>	X						X							
<p><a href="#"><u>Evolution in Action: Statistical Analysis</u></a> Students calculate descriptive statistics (mean, standard deviation, and 95% confidence interval) for eight sets of data from Peter and Rosemary Grant’s Galápagos finch study. Students construct bar graphs with 95% confidence intervals and analyze the means of finch body measurements with <i>t</i>-tests. Students also graph two of the finch measurements against each other to investigate a possible association.</p>	X							X		X				

<p align="center"><b>BiInteractive Resource Name (Hyperlinked Titles)</b></p>	Mean	Median	Mode	Range	Frequency	Rate	Variance and Standard Deviation	Standard Error and 95% Confidence Interval	Chi-Square Analysis	Student's t-Test	Linear Regression and Pearson's Correlation	Hardy-Weinberg	Probability	Standard Curves
<p><a href="#"><b>The Stickleback Evolution Virtual Lab</b></a> This virtual lab is appropriate for the high school biology classroom as an excellent companion to an evolution unit. Because the trait under study is fish pelvic morphology, the lab can be used for lessons on vertebrate form and function. In an ecology unit, the lab can be used to illustrate predator-prey relationships and environmental selection pressures. The sections on graphing, data analysis, and statistical significance make the lab a good fit for addressing the “science as a process” or “nature of science” aspects of the curriculum.</p>						<b>X</b>			<b>X</b>					
<p><a href="#"><b>Battling Beetles</b></a> This series of activities complements the HHMI DVD <i>Evolution: Constant Change and Common Threads</i> and requires simple materials such as M&amp;Ms, food storage bags, colored pencils, and paper cups. An extension of this activity allows students to model the Hardy-Weinberg principle and selection using a spreadsheet. The overall goal of “Battling Beetles” is to engage students in thinking about the mechanism of natural selection through data collection, analysis, and pattern recognition.</p>					<b>X</b>							<b>X</b>		
<p><a href="#"><b>Lizard Evolution Virtual Lab</b></a> The virtual lab includes four modules that investigate different concepts in evolutionary biology, including adaptation, convergent evolution, phylogenetic analysis, reproductive isolation, and speciation. Each module involves data collection, calculations, analysis and answering questions. The “Educators” tab includes lists of key concepts and learning objectives and detailed suggestions for incorporating the lab in your instruction.</p>	<b>X</b>				<b>X</b>		<b>X</b>	<b>X</b>						

<p style="text-align: center;"><b>BiInteractive Resource Name (Hyperlinked Titles)</b></p>	Mean	Median	Mode	Range	Frequency	Rate	Variance and Standard Deviation	Standard Error and 95% Confidence Interval	Chi-Square Analysis	Student's t-Test	Linear Regression and Pearson's Correlation	Hardy-Weinberg	Probability	Standard Curves
<p><a href="#"><b>Population Genetics, Selection, and Evolution</b></a> This hands-on activity, teaches students about population genetics, the Hardy-Weinberg principle, and how natural selection alters the frequency distribution of heritable traits. It uses simple simulations to illustrate these complex concepts and includes exercises such as calculating allele and genotype frequencies, graphing and interpretation of data, and designing experiments to reinforce key concepts in population genetics.</p>					X							X		
<p><a href="#"><b>Mendelian Genetics, Probability, Pedigree, and Chi-Square Statistics</b></a> This lesson requires students to work through a series of questions pertaining to the genetics of sickle cell disease and its relationship to malaria. These questions will probe students' understanding of Mendelian genetics, probability, pedigree analysis, and chi-square statistics.</p>													X	
<p><a href="#"><b>Using Genetic Crosses to Analyze a Stickleback Trait</b></a> This hands-on activity involves students in applying the principles of Mendelian genetics to analyze the results of genetic crosses between stickleback fish with different traits. Students use photos of actual research specimens (the F1 and F2 cards) to obtain their data; they then analyze the data they collected along with additional data from the scientific literature. In the extension activity, students use chi-square analysis to determine the significance of genetic data.</p>								X					X	
<p><a href="#"><b>Allele and Phenotype Frequencies in Rock Pocket Mouse Populations</b></a> - A lesson that uses real rock pocket mouse data collected by Dr. Michael Nachman and his colleagues to illustrate the Hardy-Weinberg principle.</p>					X							X		