S1. The narrow sense heritability for potato weight in a starting population of potatoes is 0.42, and the mean weight is 1.4 lb. If a breeder crosses two individuals with average potato weights of 1.9 and 2.1 lb, respectively, what is the predicted average weight of potatoes in the offspring?

Answer: The mean weight of the parents is 2.0 lb. To solve for the mean weight of the offspring:

$$h_N^2 = \frac{\bar{X}_O - \bar{X}}{\bar{X}_P - \bar{X}}$$

$$0.42 = \frac{\bar{X}_O - 1.4}{2.0 - 1.4}$$

$$\bar{X}_O = 1.65 \text{ lbs.}$$

S2. A farmer wants to increase the average body weight in a herd of cattle. She begins with a herd having a mean weight of 595 kg and chooses individuals to breed that have a mean weight of 625 kg. Twenty offspring were obtained, having the following weights in kilograms: 612, 587, 604, 589, 615, 641, 575, 611, 610, 598, 589, 620, 617, 577, 609, 633, 588, 599, 601, and 611. Calculate the realized heritability in this herd with regard to body weight.

Answer:

$$h_N^2 = \frac{R}{S}$$

$$= \frac{\bar{X}_O - \bar{X}}{\bar{X}_P - \bar{X}}$$

We already know the mean weight of the starting herd (595 kg) and the mean weights of the parents (625 kg). First, we need to calculate the mean weights of the offspring.

$$\bar{X}_O = \frac{\text{Sum of the offspring's weights}}{\text{Number of offspring}}$$

$$\bar{X}_O = 604 \text{ kg}$$

$$h_N^2 = \frac{604 - 595}{625 - 595}$$

$$= 0.3$$

S3. The following are data that describe the 6-week weights of mice and their offspring of the same sex:

Parent (g)	Offspring (g)
24	26
21	24
24	22
27	25
23	21
25	26
22	24
25	24
22	24
27	24

Calculate the correlation coefficient.

Answer: To calculate the correlation coefficient, we first need to calculate the means and standard deviations for each group:

$$\bar{X}_{parents=} = \frac{24 + 21 + 24 + 27 + 23 + 25 + 22 + 25 + 22 + 27}{10} = 24$$

$$\bar{X}_{offspring} = \frac{26 + 24 + 22 + 25 + 21 + 26 + 24 + 24 + 24 + 24}{10} = 24$$

$$SD_{parents} = \sqrt{\frac{0 + 9 + 0 + 9 + 1 + 1 + 4 + 1 + 4 + 9}{9}}$$

$$= 2.1$$

$$SD_{offspring} = \sqrt{\frac{4 + 0 + 4 + 1 + 9 + 4 + 0 + 0 + 0 + 0}{9}}$$

$$= 1.6$$

Next, we need to calculate the covariance.

$$CoV_{(parents,\ offspring)} = \frac{\Sigma[X_p - \bar{X}_p)(X_o - \bar{X}_o)]}{N - 1}$$

$$= \frac{0 + 0 + 0 + 3 + 3 + 2 + 0 + 0 + 0 + 0}{9}$$

$$= 0.9$$

Finally, we calculate the correlation coefficient.

$$r_{(parent,\ offspring)} = \frac{CoV_{(p,o)}}{SD_p SD_o}$$

$$r_{(parent,\ offspring)} = \frac{0.9}{(2.1)(1.6)}$$

$$r_{(parent,\ offspring)} = 0.27$$

S4. As described in chapter 24, the correlation coefficient provides a way to determine the strength of association between two variables. When the variables are related due to cause and effect (i.e., one variable affects the outcome of another variable), it is valid to use
a regression analysis to predict how much one variable will change in response to the other variable. This is easier to understand if we plot the data for two variables. The graph shown here compares mothers' and offspring's body weights in cattle. The line running through the data points is called a **regression line.** It is the straight line that is closest to all the data points. It is the minimal distance away from the squared vertical distance of all the points.
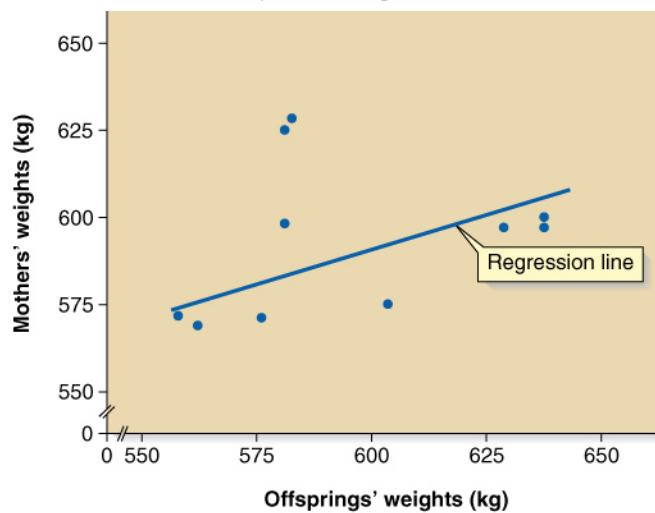
For many types of data, particularly those involving quantitative traits, the regression line can be represented by the equation

$$Y = bX + a$$

where

b is the regression coefficient

a is a constant

In this example, X is the value of an offspring's weight and Y is the value of its mother's weight.

In the equation shown, the value of b, known as the **regression coefficient,** represents the slope of the regression line. The value of a is the y-intercept (i.e., the value of Y when X equals zero). The equation shown is very useful because it allows us to predict the value of X at any given value of Y, and vice versa. To do so, we first need to determine the values of b and a. This can be accomplished in the following manner:

$$b = \frac{CoV_{(X,Y)}}{V_x}$$

$$a = \bar{Y} - b\bar{X}$$

Once the values of a and b have been computed, we can use them to predict the values of X or Y by using the equation

$$Y = bX + a$$

For example, if $b = 0.5$, $a = 2$, and $Y = 31$, this equation can be used to compute a value of X that equals 58. It is important to keep in mind that this equation predicts the average value of X. As we see in the preceding figure, the data points tend to be scattered around the regression line; there are significant deviations between the data points and the line. The equation predicts the values that are the most likely to occur. In an actual experiment, however, there will be some deviation between the predicted values and the experimental values due to random sampling error.

Now here is the question: using the data found in chapter 24 regarding weight in cattle, what is the predicted weight of an offspring if its mother weighed 660 lb?

Answer: We first need to calculate a and b.

$$b = \frac{CoV_{(X,Y)}}{V_x}$$

We need to use the data on page 669 to calculate V_X, which is the variance for the mothers' weights. The variance equals 445.1. The covariance is already calculated on page 669; it equals 152.6.

$$b = \frac{152.6}{445.1}$$

$$b = 0.34$$

$$a = \bar{Y} - b\bar{X}$$

$$a = 598 - (0.34)(596) = 395.4$$

Now we are ready to calculate the predicted weight of the offspring using the equation

$$Y = bX + a$$

In this problem, $X = 660$ pounds

$$Y = 0.34(660) + 395.4$$

$$Y = 619.8 \text{ lb}$$

The average weight of the offspring is predicted to be 619.8 lb.

S5. Genetic variance can be used to estimate the number of genes affecting a quantitative trait by using the following equation:

$$n = \frac{D^2}{8V_G}$$

where

n is the number of genes affecting the trait

D is the difference between the mean values of the trait in two strains that have allelic differences at every gene that influences the trait

V_G is the genetic variance for the trait; it is calculated using data from both strains

For this method to be valid, several assumptions must be met. In particular, the alleles of each gene must be additive, each gene contributes equally to the trait, all the genes assort independently, and the two strains are homozygous for alternative alleles of each gene. For example, if three genes affecting a quantitative trait exist in two alleles each, one strain could be *AA bb CC* and the other would be *aa BB cc.* In addition, the strains must be raised under the same environmental conditions. Unfortunately, these assumptions are not typically met with regard to most quantitative traits. Even so, when one or more assumptions are invalid, the calculated value of *n* is smaller than the actual number. Therefore, this calculation can be used to estimate the minimum number of genes that affect a quantitative trait.

Now here is the question. The average bristle numbers in two strains of flies were 35 and 42. The genetic variance for bristle number calculated for both strains was 0.8. What is the minimum number of genes that affect bristle number?

Answer: We apply the equation described previously.

$$n = \frac{D^2}{8V_G}$$

$$n = \frac{(35-42)^2}{8(0.8)}$$

$$n = 7.7 \text{ genes}$$

Because genes must come in whole numbers, and because this calculation is a minimum estimate, one would conclude that there must be at least eight genes that affect bristle number.

S6. Are the following statements regarding heritability true or false?

A. Heritability applies to a specific population raised in a particular environment.

B. Heritability in the narrow sense takes into account all types of genetic variance.

C. Heritability is a measure of the amount that genetics contributes to the outcome of a trait.

Answer:

A. True.

B. False. Narrow sense heritability considers only the effects of additive alleles.

C. False. Heritability is a measure of the amount of phenotypic *variation* that is due to genetic variation; it applies to the variation of a specific population raised in a particular environment.