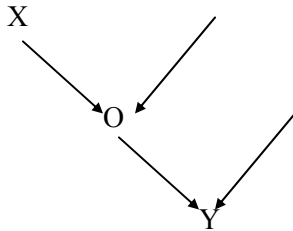


EXERCISES FOR CHAPTER 9

**Exercise 9.1.** Derive the covariance between a random parent  $X$  (i.e., grandparent) and its random grandoffspring  $Y$  in a population in Hardy-Weinberg equilibrium with only two alleles at one locus, using

- algebraic method,
- expectation method, and
- general, identity-by-descent method by use of equation (9.63).

Also, derive  $\theta_{XY}$  by some method presented in Chapter 4. The pedigree involved is



**Exercise 9.2.** State, in words, why the genotypic covariance between a random parent in the population and a random single offspring *individual* is equal to that of a random parent and the *mean* of two or more (up to an infinite number) of offspring individuals?

**Exercise 9.3.**

- Define what we mean when we talk about two-gene, three-gene, and four-gene identical-by-descent probability functions.
- How many different states of identity-by-descent are there for each of the three cases above?
- Show why you need only one new additional parameter to define the probability of each state of identity-by-descent for the three-gene probability functions.
- Similarly show why you need only four new additional parameters to define the probability of each state of identity-by-descent for the four-gene probability functions.
- Define the coefficient of dominance coancestry.
- What kinds of two-locus identical-by-descent probability functions have we talked about?

**Exercise 9.4.** In the following expression obtained from the expectation of one of the terms in  $E(7_X)(7_Y)$  (see equation (9.135)) in the derivation of the covariance of relatives we have

$$\begin{aligned} & \sum_i \sum_j \sum_k p_{a_i} p_{a_j} p_{b_k} \left[ (\delta\alpha)_{a_i a_j b_k}^{mfm} \right]^2 \left[ P(a_X^m \equiv a_Y^m; a_X^f \equiv a_Y^f) + P(a_X^m \equiv a_Y^f; a_X^f \equiv a_Y^m) \right] P(b_X^m \equiv b_Y^m) \\ &= \sigma_{(\delta\alpha)_{ab}}^2 (\delta_{mm,ff} + \delta_{mf,fm}) P(b_X^m \equiv b_Y^m) \\ &= \frac{\sigma_{DA_{ab}}^2}{2} \delta_{dXY} P(b_X^m \equiv b_Y^m) \end{aligned}$$

What specific basic assumption stated in genetic terms permits one to write each of the following:

- $\delta_{mm,ff} + \delta_{mf,fm}$ , i.e., why can this be written as a sum?
- $p_{a_i} p_{a_j}$ , i.e., why can this be written as a product?
- $\delta_{dXY} P(b_X^m \equiv b_Y^m)$ , i.e., why can this be written as a product, namely,  $\delta_{dXY}$  times  $P(b_X^m \equiv b_Y^m)$ ?
- $p_{a_i} p_{b_k}$ , i.e., why can this be written as a product?
- $\sigma_{(\delta\alpha)_{ab}}^2 = \frac{\sigma_{DA_{ab}}^2}{2}$ , i.e., why is  $\sigma_{(\delta\alpha)_{ab}}^2$  equal to one-half of  $\sigma_{DA}^2$ ?

**Exercise 9.5.**

In the general, identity-by-descent method for the covariance between relatives, what condition(s) must exist with respect to identity-by-descent for a nonzero term to arise in the covariance for effects involving one pair, two pairs, three pairs, and four pairs of genes, respectively.

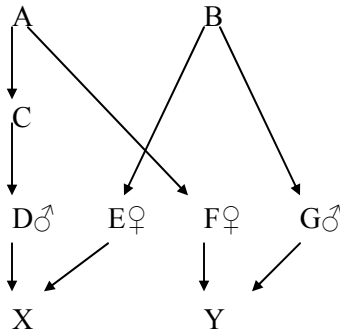
**Exercise 9.6.**

The general formulation of the covariance of relatives is

$$Cov(G_X, G_Y) = \sum_{\substack{r=0, s=0 \\ i \leq (r+s) \leq n}}^n (2\theta_{XY})^r (\delta_{dXY})^s \sigma_{A^r D^s}^2$$

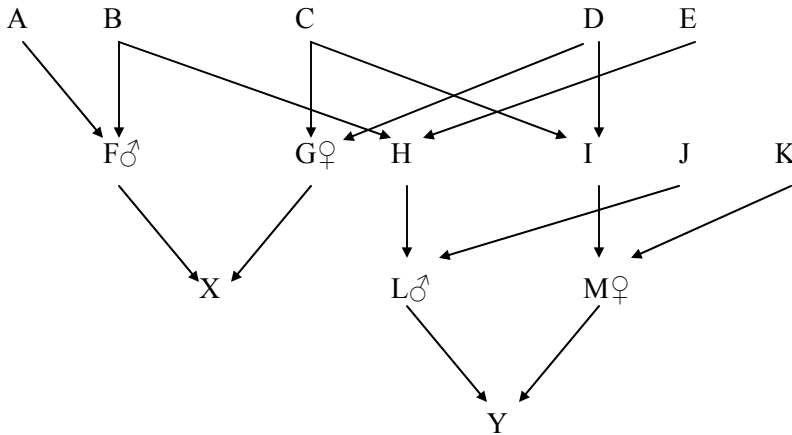
List the conditions assumed or implied in its proper use, and the assumptions made in its derivation.

**Exercise 9.7.** Assume that the pedigree for  $X$  and  $Y$  is



Assume  $\theta_{AB} = 0$ . Calculate or express  $\theta_{mm}, \theta_{mf}, \theta_{fm}, \theta_{ff}$ , for  $X$  and  $Y$ , and  $\delta_{dXY}$ , as the case may be, as functions of the coefficient of inbreeding of individuals  $A$  and  $B$ .

**Exercise 9.8.** Suppose that you are given the following pedigree where  $B$ ,  $C$ , and  $D$  are random members *arbitrarily* inbred ( $0 \leq F \leq 1$ ) from a random-mating population in linkage equilibrium with no linkage between loci. ( $A$ ,  $E$ ,  $J$ , and  $K$  are also random noninbred individuals in the population.)



- Calculate the coefficient of coancestry between  $X$  and  $Y$  by any method in Chapter 4.
- Calculate the coefficient of dominance coancestry between  $X$  and  $Y$ ,  $\delta_{dXY} = \Delta_5$ , by the simplified method. What is the basic idea behind the simplified method?
- What is the covariance between  $X$  and  $Y$  equal to in terms of  $\sigma_A^2, \sigma_D^2, \sigma_{AA}^2, \sigma_{AD}^2, \sigma_{DA}^2, \sigma_{DD}^2, \sigma_{AAA}^2, \sigma_{AAD}^2, \dots$  when  $F_B = F_C = F_D = 0$ . When  $F_B = 0, F_C = \frac{1}{2}, F_D = 1$ ? Write in expanded form.

**Exercise 9.9.** Discuss the role of linkage disequilibrium in population and quantitative genetics by considering the following:

- Define two-locus and three-locus linkage equilibria. Can you have one without the other?
- Distinguish between linkage disequilibrium and genetic linkage. Can you have linkage disequilibrium between genes at two loci on separate chromosomes?
- In what way does genetic linkage relate to linkage disequilibrium?
- Discuss the role of linkage disequilibrium upon the population mean in the absence and presence of epistasis.
- Discuss the role of linkage disequilibrium upon the genetic variance as it affects the gametic genetic variance in the absence and presence of epistasis.
- Define gametic genetic variance.

**Exercise 9.10.**

Consider all of the same conditions which exist in Example 8.6, pp. 8.118 and 8.119. All individuals in the population are noninbred.

a. Suppose that random individuals were chosen in the population and randomly mated to the population to produce half-sib families. Assuming that the linkage relation between the two loci was independent, namely,  $\rho_1 = 0.5$  or  $\lambda_1 = 0.0$ , calculate the covariance between half-sibs in the population. Note that the genetic variance components are given in the *second* column labeled “Value” on p. 8.119.

b. Repeat part (a) for  $\rho_1 = 0.2$  or  $\lambda_1 = 0.6$ . What is the percentage change on the variance component(s)? What is the percentage change on the half-sib covariance?

c. Suppose that random pairs of individuals in the population were chosen and mated to produce full-sib families. Calculate the covariance between full sibs in the population, assuming  $\rho_1 = 0.5$  or  $\lambda_1 = 0.0$ .

d. Repeat part (c) for  $\rho_1 = 0.2$  or  $\lambda_1 = 0.6$ . What are the percentages of change on their corresponding variance component? What is the percentage change on the full-sib covariance?

e. Suppose that random individuals in the population were each mated to a random individual in the population to produce a single offspring. Calculate the parent-offspring covariance, assuming  $\rho_1 = 0.5$  or  $\lambda_1 = 0.0$ .

f. Repeat part (e) for  $\rho_1 = 0.2$  or  $\lambda_1 = 0.6$ . What is the percentage change on the variance component(s)? What is the percentage change on the parent-offspring covariance?

g. Suppose that every single offspring was mated to another random individual in the population to produce a grandoffspring. Calculate the grandparent-grandoffspring covariance, assuming  $\rho_1 = 0.5$  or  $\lambda_1 = 0.0$ .

h. Repeat part (g) for  $\rho_1 = 0.2$  or  $\lambda_1 = 0.6$ . What is the percentage change for the variance component(s)? What is the percentage change on the grandparent-grandoffspring covariance?

**Exercise 9.11.** What assumptions must be made so that the variance components in the mating designs may be equated to

$$\sum_{\substack{r=0,s=0 \\ 1 \leq (r+s) \leq n}} (2\theta_{XY})^r (\delta_{dXY})^s \sigma_{A^r D^s}^2$$

Indicate the reason or discuss why each assumption is important or the role that each assumption plays in the derivation of the above expression. If appropriate, be as specific as possible by indicating the exact place where the assumption enters or is considered in the derivation. (You may cite an equation number in notes and *discuss* the role of the assumption in the equation.)