

EXERCISES FOR CHAPTER 10

Exercise 10.1. In the article by C. Clark Cockerham, 1963, "Estimation of Genetic Variances" in Statistical Genetics and Plant Breeding, National Academy of Sciences-National Research Council, Publication 982, he has the subtitle "Mating Designs with Unrelated Mates".

- What is the true meaning or consequence of the subtitle?
- Why do you think that Cockerham uses the subtitle?

Exercise 10.2. Give an example of a one-factor mating design. Show the analysis of variance for such a mating design. Given the fact that only one variance component or covariance of relative can be estimated, what kind of covariance of relative would probably be most useful to estimate?

Exercise 10.3. In mating designs used to estimate genetic variance components, why is it advantageous to use parents which are inbred?

Exercise 10.4. Years ago and still to some extent today, corn or maize (*Zea mays*) breeders would go into an indigenous open-pollinated population of maize, take a random sample of ears, shell each individual ear, and plant the seed from each in a single row in possibly two or more blocks of a randomized complete block design (called ear-to-row method of progeny testing).

- In more formal genetic terminology what would such a family from a single plant be called? Why?
- For a family to be designated by such terminology means that any two random individuals in that family bear the same relationship. What does that imply about the pollination pattern of maize?
- What is the family variance component generally set equal to in terms of genetic variance components?
- What assumptions are being made in doing that?

Exercise 10.5.

- In a diallel cross, under what conditions would

$$\sigma_g^2 = \frac{1}{2}\sigma_A^2 + \frac{1}{4}\sigma_{AA}^2 + \frac{1}{8}\sigma_{AAA}^2 + \dots$$

and

$$\sigma_s^2 = \sigma_D^2 + \frac{1}{2}\sigma_{AA}^2 + \sigma_{AD}^2 + \sigma_{DD}^2 + \frac{3}{4}\sigma_{AAA}^2 + \sigma_{AAD}^2 + \sigma_{ADD}^2 + \sigma_{DDD}^2 + \dots ?$$

- Suppose that in testing the general and specific combining ability sources an experimenter found both σ_g^2 and σ_s^2 to be present, can the experimenter be certain of obtaining an unbiased estimate of σ_A^2 ? What assumptions would have to be made to obtain an unbiased estimate of the additive variance? In that case, how would one obtain an unbiased estimate of the additive variance?

- Suppose that an experimenter found σ_g^2 to be present and σ_s^2 to be absent, can the experimenter be certain of obtaining an unbiased estimate of σ_A^2 ? Why or why not?

Exercise 10.6.

For the following diallel model, given in equation (10.14),

$$Y_{ijk} = \mu + g_i + g_j + m_i - m_j + s_{ij} + r_{ij} + e_{ijk}$$

and its associated restrictions

$$g_i = g_j \quad \text{for } i = j$$

$$m_i = -m_j \quad \text{for } i = j$$

$$s_{ij} = s_{ji}$$

$$r_{ij} = -r_{ji}$$

derive equation (10.15) (2) which is equal to the covariance between reciprocal full sibs, namely,

$$C_{rf} = 2\sigma_g^2 - 2\sigma_m^2 + \sigma_s^2 - \sigma_r^2$$

Show the derivation in *complete* detail. Do not omit any important steps.

Exercise 10.7. Suppose that a breeder had a large random-mating population of a given species and that the population had been random mating without selection for many generations. In addition, the breeder had developed a large number of random inbred lines, say m lines, with coefficient of inbreeding $F = 1$ from the population. The breeder desired to obtain some notion of the amount of genetic variability for yield in the population. To do so he used a nested mating design in which he used the inbred lines as male parents and m random sets of n individuals each, i.e., a total of mn individuals, as female parents, from the random-mating population. He randomized the mn full-sib families in a randomized complete block design and estimated the experimental design variance components due to males, σ_M^2 , and that due to females, σ_F^2 .

- What does each of the variance components estimate in terms of the genic factorial model?
- Suppose that the inbred lines used as male parents were not a random sample of inbred lines, but tended to represent the two tails of the distribution of all possible inbred lines. What effect would this have on the magnitude and meaning of the variance components?

Exercise 10.8.

Part I.

Assume a single random-mating population with one locus and two alleles. Suppose each of 200 random individuals from the population was randomly crossed or mass mated to the population (i.e., each of the individual offspring from any individual has a different random parent from the population as is possible with certain organisms such as maize), and that each of the 200 random individuals produced a *very large number* of individuals (say, infinite) -- all of which were measured with *no environmental error variance*.

- In terms of genetic effects show algebraically what the expected variance of the family means (or

among the means), i.e., $E(\bar{Y} - \mu)^2 = E \frac{\sum_{i=1}^{200} (\bar{Y}_i - \bar{Y})^2}{199}$, is equal to. What is it equal to in terms of additive and dominance variances?

- What is the relationship between any two individuals selected at random from among the offspring of any one family of the 200 random individuals? What do you think the expected variance of the families means in (a) is equal to in terms of kind(s) of covariances of relatives and genetic variance component(s)? Is your answer in agreement with other reported results?

- Set up the algebraic expression for the expected variance of individuals within the families in terms of genetic effects. Use the definition formula for the variance in all cases. You do not have to do all of the algebra to verify that it equals $\frac{3}{2}\sigma_\alpha^2 + \sigma_\delta^2 = \frac{3}{4}\sigma_A^2 + \sigma_D^2$, unless you have the time and desire to do it. (If you do attempt to do the algebra, it would be a good test of your algebraic ability.)

- Give the expected variance of individuals within the families in terms of kind(s) of covariances of relatives. Evaluate the expression and show that it equals the expression in (c) above.

e. Complete an analysis of variance table, giving the sources, degrees of freedom, and the expected mean squares. Use the symbol n to denote the number of progeny from each of the 200 random individuals. Give the expected mean squares in terms of both design variance components and covariances of relatives. State what each design variance component is equal to in terms of covariances of relatives, genic variances (σ_{α}^2 and σ_{δ}^2) and additive and dominance variances. What must be done to the expected mean square for among families, so that it equals (a) above? Show that this is also true in terms of the definition mean square for among families which is equal to the definition of the sum of squares divided by the degrees of freedom, i.e., (definition mean square) =

$$(\text{definition sum of squares})/\text{degrees of freedom} = n \sum_{i=1}^{200} (\bar{Y}_i - \bar{Y}_{..})^2 / 199 .$$

Suppose that each of the 200 random individuals produced 100 *individuals* instead of a "very large number of individuals". All other conditions stated above for items (a) to (e) hold.

f. Is the expected variance of the family means (or among the means), i.e.,

$$E(\bar{Y} - \mu)^2 = E \frac{\sum_{i=1}^{200} (\bar{Y}_i - \bar{Y}_{..})^2}{199} , \text{ different from that in (a) above? If so, why and what is it equal to in terms of}$$

design variance components? What is it equal to in terms of additive and dominance variances?

Part II.

Assuming the same conditions as in Part I, (a) to (e) above, except that one is unable to mass mate or does not mate each of the 200 individuals to the population as a whole. Instead, each of the 200 individuals is mated at random to a different set of 15 random individuals from the population. Each of the 3000 crosses produced a *very large number* of individuals (say, infinite) all of which were measured with *no environmental error variance*.

a. What is the relationship between any two individuals selected at random from within the offspring of any one of the 3000 random crosses? Between two individuals each selected from different random crosses, but within the 15 crosses from one of the 200 individuals?

b. Complete an analysis of variance table, giving the sources, degrees of freedom, and the expected mean squares. Again, use the symbol n to denote the number of progeny from each of the 3000 crosses. Give the expected mean squares in terms of both design variance components and covariances of relatives. State what each variance component is equal to in terms of covariances of relatives, genic variances (σ_{α}^2 and σ_{δ}^2), and additive and dominance variances. What is the expected variance of the 200 group means, averaged over the progenies of the 15 crosses within each of the 200 groups, equal to? How does it differ, if any, from that in Part I (a) above? If it does differ, explain why.

c. Suppose that you are a breeder who is interested in progeny testing each of 200 random individuals from the population. You wonder how large the random sample of individuals, say, size f , i.e., more or less than 15, should be to which an individual (one of the 200 individuals) to be progeny tested should be crossed. You will bulk equal amounts of seed from each of the crosses for the progeny test of a single individual. Derive a general expression for this number f , as a function of σ_A^2 , σ_D^2 , and E , so that you do not increase the variance of the 200 progeny or group means by more than the proportion E , in contrast to testing 200 half-sib families. Note that the group is not a half-sib family; it is composed of a mixture of half and full sibs. Assume that you are able to test a *very large number* of individuals in each progeny and that *no environment error variance* exists.

d. Suppose that $\sigma_A^2 = 100$, $\sigma_D^2 = 20$, and $E = 0.05$, i.e., you do not want to increase the variance by more than 5%, how large would f have to be?

Suppose that each of the 3000 crosses produced 100 *individuals* instead of a "very large number of individuals". All other conditions hold as stated in Part II, (a) and (b).

e. Is the expected variance of the group means, i.e., $E(\bar{Y} - \mu)^2 = E \frac{\sum_{i=1}^{200} (\bar{Y}_{i..} - \bar{Y}_{...})^2}{199}$, different from that in

Part II (b) above? If so, why and what is it equal to in terms of design variance components? What is it equal to in terms of additive and dominance variances?

Exercise 10.9. A three-factor mating design which Cockerham gives in his 1963 paper, "Estimation of Genetic Variances" in *Statistical Genetics and Plant Breeding*, National Academy of Sciences-National Research Council, Publication 982, pp. 60-61, is one designated $(A(BC))$. Cockerham's description of the design is given herein.

Factorial matings—design $(A(BC))$ —For this design, let an additional group of individuals which are to be used in the matings be designated as C. First, mate each C_l ($l = 1, 2, \dots, m$) individual to each B_j ($j = 1, 2, \dots, n$) individual. Next, mate each A_i ($i = 1, 2, \dots, p$) individual to a single offspring of each mating ($B_j C_l$). This gives altogether pnm progenies, one for each mating ($A_i(B_j C_l)$). The order in which the matings are made is from right to left in the designation $(A(BC))$. The types of relatives in this mating pattern and their designations are put in Table 9. The expectations of mean squares for a replicated experiment are given in Table 10. The analysis of variance is the usual one for a three factor factorial and the expectations of the mean squares are the usual ones for an all random model of effects. Altogether, seven components of variance and covariances of relatives are estimable when the inbreeding

TABLE 9.—DESCRIPTION OF COVARIANCES OF RELATIVES FOR DESIGN $(A(BC))$.

Relationship of relatives	Designation of covariance
Full sib, parent from mating CB and parent A both common	$C_{fA(BC)}$
Three quarter sibs, both parent A and grandparent B common	C_{sAcB}
Half sibs, parent A common	C_{sA}
Half sibs, parent from mating BC common	C_{sBC}
Cousins, grandparent B common	C_{cB}

TABLE 10.—EXPECTATIONS OF MEAN SQUARES FOR DESIGN $(A(BC))$.

Source	df	Expectations of mean squares
Replications.....	$k-1$	
A parents.....	$p-1$	$\sigma^2 + k\sigma^2_{ABC} + kn\sigma^2_{AC} + km\sigma^2_{AB} + knm\sigma^2_A$
B grandparents.....	$n-1$	$\sigma^2 + k\sigma^2_{ABC} + kp\sigma^2_{BC} + km\sigma^2_{AB} + kmp\sigma^2_B$
C grandparents.....	$m-1$	$\sigma^2 + k\sigma^2_{ABC} + kp\sigma^2_{BC} + kn\sigma^2_{AC} + knp\sigma^2_C$
A x B.....	$(p-1)(n-1)$	$\sigma^2 + k\sigma^2_{ABC} + km\sigma^2_{AB}$
A x C.....	$(p-1)(m-1)$	$\sigma^2 + k\sigma^2_{ABC} + kn\sigma^2_{AC}$
B x C.....	$(n-1)(m-1)$	$\sigma^2 + k\sigma^2_{ABC} + kp\sigma^2_{BC}$
A x B x C.....	$(p-1)(n-1)(m-1)$	$\sigma^2 + k\sigma^2_{ABC}$
Error.....	$(k-1)(pnm-1)$	σ^2

$\sigma^2_A = C_{sA}, \quad \sigma^2_B = C_{cB}, \quad \sigma^2_C = C_{cC}, \quad \sigma^2_{AB} = C_{sAcB} - C_{sA} - C_{cB}$
 $\sigma^2_{AC} = C_{sAcC} - C_{sA} - C_{cC}, \quad \sigma^2_{BC} = C_{sBC} - C_{cB} - C_{cC}$
 $\sigma^2_{ABC} = C_{fA(CB)} - C_{sAcC} - C_{sAcB} - C_{sBC} + C_{sA} + C_{cB} + C_{cC}$

coefficients are different in the three groups of parents. If parents B and parents C are equally inbred, then

$$\sigma_B^2 = \sigma_C^2, \quad \sigma_{AC}^2 = \sigma_{AB}^2, \quad C_{cB} = C_{cC}, \text{ and } C_{sAcB} = C_{sAcC}.$$

If, in addition, the same number of parents is used in groups B and C, i.e., $n = m$, the mean squares for B and C may be pooled together, and the mean squares $A \times B$ and $B \times C$ may be pooled together, since, in each case, the two have the same expectations. This gives five components of variance or covariances of relatives that are estimable.

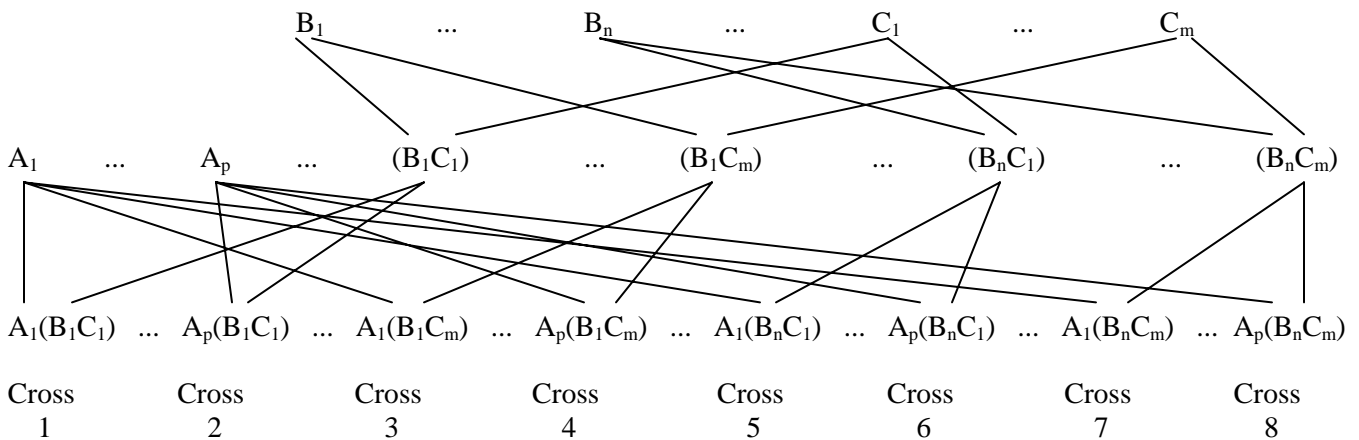
When none of the parents are inbred there are only four distinct covariances of relatives because $C_{sA} = C_{sBC}$ since C_{sBC} is the covariance between half sibs from a non-inbred parent, BC.

In a three-factor mating design there are three sets of parents designated A, B, and C. In this design we first mate each C_l individual, $l = 1, 2, \dots, m$, to each B_j individual, $j = 1, 2, \dots, n$. Then mate each A_i individual, $i = 1, 2, \dots, p$, to a single offspring of each mating (B_jC_l). This gives altogether pnm progenies, one for each mating ($A_i(B_jC_l)$), which are measured (no parents are measured). B and C are unrelated, so $F_{BC} = 0$.

a. In this design there is a maximum of seven distinct covariances of relatives. Why? Cockerham describes five covariances of relatives as follows:

Relationship of relatives	Designation of covariance
Full sib, parent from mating BC and parent A both common	$C_{fA(BC)}$
Three-quarter sibs, both parent A and grandparent B common	C_{sAcB}
Half sibs, parent from mating BC common	C_{sBC}
Half sibs, parent A common	C_{sA}
Cousins, grandparent B common	C_{cB}

Describe the additional two kinds of relatives and designate the corresponding covariance. Give the conditions in terms of equality or inequality of subscripts for each of the three subscript positions which identifies each of the seven kinds of relatives and their corresponding covariances. Illustrate each of the seven kinds of relatives by denoting from which of the eight progeny crosses specifically given in the pedigree diagram below, each of the random relatives X and Y may be drawn.



b. Derive the precise expressions for two times the coefficient of coancestry ($2\theta_{XY}$) and the coefficient of dominance coancestry (δ_{dXY}) for each of the seven distinct covariances of relatives.

c. Which covariances are the same if parents B and C are equally inbred? Why?

d. Suppose that parents B and C are equally inbred ($F_B = F_C$) and $F_A > 0$, how many distinct covariances of relatives exist?

- e. Suppose that all three sets of parents are noninbred ($F_A = F_B = F_C = 0$), how many distinct covariances of relatives exist? Why?
- f. By extension of techniques and procedures which we have discussed, derive what each of the seven distinct covariances of relatives is equal to in terms of design variance components.
- g. Derive what each variance component is equal to in terms of covariances of relatives.
- h. Assume that the coefficients of inbreeding are different in the three groups of parents. In addition, assume a restrictive genetic model consisting of only the following variances: $\sigma_A^2, \sigma_D^2, \sigma_{AA}^2, \sigma_{AD}^2, \sigma_{DD}^2, \sigma_{AAA}^2, \sigma_{AAD}^2$. Express each of the variance components as a function of the above genetic variances and the inbreeding coefficients.
- i. Calculate what the numerical values for all the coefficients of the genetic variances in (h) would be if $F_A = 1, F_B = 1/2, F_C = 0$.

Exercise 10.10. Prior to the rediscovery of Mendel's laws in 1900, Francis Galton studied the inheritance of human stature. Galton collected data on the heights of adult children and their parents in 205 families. After multiplying the female heights by 1.08 to make them comparable with male heights, he considered the relationship between the mean height of the children and the average height of their parents (their midparent). He found that there was a strong association between the heights of parents and children, but that the average deviation from the mean among the children was less than the corresponding deviation in their midparents. Galton expressed this by saying that the children showed "a regression towards mediocrity", and he estimated this filial regression as $2/3$. By a chain of rather dubious arguments from this regression towards the mean he inferred his law of ancestral inheritance. He stated his law as follows: "The two parents contribute between them an average one-half of the total heritage of the offspring, the four grandparents one-quarter, the eight great grandparents one-eighth, and so on."

- a. In present-day understanding what is the real reason for this regression being less than one? Explain. Could the regression coefficient ever be equal to one? If so, state the conditions.
- b. In what way does it involve genetics, and in what way does it not involve genetics, i.e., genetic values or parameters?
- c. Suppose Galton had observed height of individual parent plants in a highly heterogeneous population, i.e., a population composed of many, many genotypes, but that each plant was fully homozygous (the population was a mixture of pure lines), and that he also observed the mean height of selfed progeny from a large random sample of plants from the population. What would he have very likely found with respect to the regression of the mean plant height of the progenies on the parental height? Explain.

Exercise 10.11. A quantitative geneticist often writes the model

$$\text{Model 1: } Y_{ij} = \mu + G_i + E_{ij}$$

where G_i = i th genotypic value,

E_{ij} = environmental deviation of the j th individual of the i th genotype.

The same quantitative geneticist may also write

$$\text{Model 2: } Y_{ijkl} = \mu + G_i + L_j + GL_{ij} + Y_k + GY_{ik} + LY_{jk} + GLY_{ijk} + E_{ijkl}$$

- a. If he were a plant geneticist and wrote model 2 for a typically conducted, replicated field experiment involving plot yields of homozygous lines, criticize the model. State what Y_{ijkl} represents and clarify what he may have meant by the term E_{ijkl} in model 2. Interrelate it to E_{ij} in Model 1. Rewrite what you would regard as possibly a better model if you think a better one exists, defining all terms and interrelating them to those in Models 1 and 2.
- b. Reconsider part (a) if the genotypes represented half-sib families.
- c. Suppose you were an animal geneticist and genotypes represented different strains within a breed of farm animals. Answer part (a) for this case.

Exercise 10.12. Suppose that in a monoecious species one has two random samples of individuals from a noninbred, random-mating, linkage equilibrium population -- one set of individuals was designated A and the other set designated B . Every individual in set A used as a male was crossed to every individual in set B used as a female. This was designated Set 1. Then every individual in set B was used as a male and was crossed reciprocally to every individual in set A used as a female. This was designated Set 2. In both sets observations were observed on individuals.

a. Do the following for Set 1 ($A \times B$):

i. Write the model for the mating design itself, i.e., write a model which partitions the total genotypic value G itself.

ii. Derive what each of the possible kinds of covariances between relatives is equal to in terms of variance components, including the genotypic value of an individual with itself. Clearly show your work for one kind of covariance between relatives.

b. Repeat (a) for Set 2 ($B \times A$).

Suppose that all full-sib families from both sets were randomized in a randomized complete block design, the environmental design, with r blocks assumed to be random, and that n individuals were observed separately within each plot or experimental unit. The inference space was limited to one location and one year.

c. Do the following for Set 1:

i. Write the model for the individual observation Y , identifying separate genetic and environmental terms even if they are confounded.

ii. Write out the analysis of variance table, including the source, degrees of freedom, and expected mean squares in terms of variance components.

iii. State what each variance component is equal to in terms of genetic covariances between relatives. If a variance component has no genetic component, state it.

d. Repeat (c) for Set 2.

e. Since corresponding cells in Sets 1 and 2 represent reciprocal crosses, consider the genetic covariances between the terms in the genetic model for Set 1 (see your answer in a(i)) and that for Set 2 (see your answer in b(i)). Derive what each of the possible kinds of covariances between relatives is equal to in terms of covariance components.

f. Write out the analysis of covariance table including the source, degrees of freedom, and expected cross products in terms of covariance components, using cell or plot means in Sets 1 and 2 within individual blocks.

g. State what each covariance component is equal to in terms of genetic covariances between relatives.

Exercise 10.13.

Part I.

An experimenter chose 200 different sets of three different random individuals each from a random-mating, linkage equilibrium, noninbred population with independence between loci. Then the experimenter made two different three-way crosses within each set (see Figure 4.27A, pp. 4.112 to 4.115). Assume that one would evaluate each of the 400 three-way crosses in a randomized complete block design, with r blocks, say two blocks, where each plot or experimental unit consisted of a large number of individuals.

a. i. Write the model, giving the range of each subscript.

ii. Show how one would partition the 399 degrees of freedom by setting up the analysis of variance table.

iii. Give the expected mean squares for the analysis. *For simplicity*, we assume that the two three-way crosses made are the only possible three-way crosses within each set of three parental individuals (actually there is another possible two-way cross, namely, $(AC)B$, but we ignore that fact). What parallelism can you draw with the following expectations given by Griffing 1956, Concept of general and specific combining ability in relation to diallel crossing systems, Aust. J. Biol. Sc. 9:463-493, for Method 3 (one set of F_1 's and reciprocals are included but not the parents), Model II (random model) as:

<u>Source of variation</u>	<u>df</u>	<u>Expected mean squares</u>
General combining ability	$p - 1$	$\sigma^2 + 2\sigma_s^2 + 2(p - 2)\sigma_g^2$
Specific combining ability	$p(p - 3)/2$	$\sigma^2 + 2\sigma_s^2$
Reciprocal effects	$p(p - 1)/2$	$\sigma^2 + 2\sigma_r^2$
Error		σ^2

Think particularly about the relation between expected mean squares for the specific combining ability and reciprocal effects. Also think about the general form of the degrees of freedom for reciprocal effects. What assumptions or restrictions are being made in the model with respect to the two different three-way crosses, *assuming* that there are only two such crosses possible?

iv. What design variance component would be equal to $2\theta_{XY}\sigma_A^2 + (2\theta_{XY})^2\sigma_{AA}^2 + \dots$, where θ_{XY} equals $5/32$ (see p. 4.115 since $F_A = F_B = F_C = 0$)? How would you estimate that component?

b. i. Write the model for an alternative analysis for estimating one of the same variance components as in Part I (a).

ii. Give the analysis of variance table.

iii. Give the expected mean squares for that analysis of variance table.

iv. What design variance component would be the same as that in Part I(a)iv? How would you estimate that component?

Part II.

Since this same experimenter had a lot of individuals (seeds) in reserve of both single crosses made for the two-way crosses in each of the 200 sets, he decided to include the 400 single crosses in another randomized complete block design with r blocks, say two blocks.

a. i. Write the model, giving the range of each subscript.

ii. Show how one would partition the 399 degrees of freedom by setting up the analysis of variance table.

iii. Give the expected mean squares for this analysis. What kind of mating design is this? Do you think similar restrictions apply here as in Part I(a)iii?

iv. What do the design variance components estimate in terms of covariances of relatives?

b. i. Write the model for an alternative analysis for estimating at least one of the variance components in Part II(a).

ii. Give the analysis of variance table.

iii. Give the expected mean squares for that analysis of variance table.

iv. What design variance component would be the same as that in (iv) in Part II(a).

Exercise 10.14. In Example 8.5, pp. 8.105 to 8.117, we obtained the additive, dominance, additive-by-additive, additive-by-dominance, and dominance-by-dominance variances for a 9:7 F_2 ratio, which assumed independence between loci. The variances were:

$$\sigma_A^2 = \frac{9}{16}, \sigma_D^2 = \frac{9}{32}, \sigma_{AA}^2 = \frac{1}{16}, \sigma_{AD}^2 = \frac{1}{16}, \text{ and } \sigma_{DD}^2 = \frac{1}{64}$$

a. If one created half-sib families in such a population, measured their performance, and estimated the half-sib variance component from a one-factor mating design, what would be the expected value of that component? Include all appropriate variance components that are involved in Example 8.5.

b. Repeat (a) for full-sib families.

c. Assume that the two loci are linked with a recombination value $\rho_1 = 0.20$ or

$\lambda_1 = 1 - 2\rho_1 = 1 - 2(0.20) = 0.6$. Linkage equilibrium was assumed in Example 8.5 and is assumed here also.

What are the variance components in both (a) and (b) now equal to? Evaluate the total effect of the linkage per se or percentage change upon both the half-sib and full-sib covariance components, as well as upon each genetic variance component separately.

d. In Example 8.5, where independence between loci was assumed, linkage equilibrium was assumed. If the F_2 population had resulted from the cross between two homozygous lines, would the F_2 population be in linkage equilibrium? If so, why? If not, why?

e. Repeat (d) above, if $\rho_1 = 0.20$.