

General Instructions: For all problems, show how you determined your answer. Be sure to define all variables that you use and justify your logic. If you have used software to obtain answers, output should be attached, but this is not a substitute for showing the steps of your analysis! The required data sets are available from the course web-site.

- 3.1 Consider the children of a pair of monozygotic twins that are married to unrelated spouses.
- Calculate the coefficient of kinship between the children.
 - Calculate the genetic covariance between the trait values of the two children.
- 3.2 Consider a trait that is affected by two LINKED diallelic loci such that there is no gametic phase disequilibrium. For each of the following relationships, give the genetic covariance and describe the effect of linkage on this covariance.
- Parent-offspring
 - Full sibs
 - Monozygotic twins
 - Half-sibs
- 3.3 Conditional on marker genotypes for the parents and offspring, derive the likelihood for the trait vector, $[Z_1, Z_2, Z_m, Z_f]$, that includes the parent and children trait values for a nuclear family with two children. Assume:
- a completely dominant QTL that is in HWE and
 - that the likelihood, conditional on QTL genotype, is normally distributed.
- Be sure to specify any assumptions that are made.
- 3.4 For example 6.1 of the lecture notes:
- Complete the derivation by incorporating linkage disequilibrium, D_{AB} , between alleles A and B.
 - If $D_{AB} = 0$, to what does $\Pr(Q_o = Bb | M_o, M_M, M_F, Q_M, Q_F)$ reduce? Provide an interpretation of your answer.
 - Would your conclusions in part b change if there are multiple offspring?
- 3.5 Our derivation for the variance components method of linkage analysis assumed a QTL without evidence for dominance. Suppose that we would like to now add in a dominance component for the QTL in addition to the additive component for the QTL, additive polygenic background and residual error. You can assume that environmental factors have been taken into account and that there is no epistasis. Provide the following for this extended model:
- Model for the trait mean
 - The variance/covariance matrix for the trait
 - Assuming multivariate normality for a family's vector of trait values, $\underline{y}$, provide the likelihood for $\underline{y}$.