

(1) **[10 points]** You are using marker loci to look for a linked QTL and have a single large full-sib family. Three marker loci are considered, A, B, and C. The father has genotype  $A_1A_2B_1B_2C_2C_2$ , while the mother is  $A_3A_2B_1B_2C_1C_1$ .

(a) Can all of these markers can be used to detect potential linkage? If some loci cannot be used, why is this so?

**A and B can, but C cannot, as must be a heterozygote**

(b) Suppose the mean value of the trait of interest in the offspring genotyped for marker A are as follows:

$$A_1A_3 \quad 15, \quad A_1A_2 \quad 25, \quad A_2A_2 \quad 45, \quad A_2A_3 \quad 55.$$

Is there evidence that the marker is linked to a QTL? If a QTL found, is it segregating (i.e., a heterozygote) in the father? The Mother? Both?

**A1 father = (15+25)/2 = 20, A2 father = (45 +55)/2 = 50 Linked QTL segregating in father**

**A3 mother = (15+55)/2 = ,35 A2 = (25+45)/2 = 35**

**linked QTL, heterozygous in father, not segregating in mother**

(3) **[10 points]** Under random mating, you have the following allele frequencies  $A_1 = 0.3$ ,  $A_2 = 0.5$ . There are also other alleles present.

a) What is the frequency of an  $A_1A_2$  heterozygote?

$$2*0.3*0.5 = 0.30$$

b) What is the frequency all heterozygotes involving allele  $A_1$ ?

$$2*0.3*0.7 = 0.442$$

c) What is the frequency of matings between an  $A_1A_2$  individual and an  $A_1A_1$  individual?

$$2*freq(A_1A_2)*freq(A_1A_1) = 2*0.30*0.09 = 0.054$$

(1) **[5 points]** You are trying to estimate when a mutation arose, and have the following information. You have a marker (alleles M1, M2, and M3) at recombination frequency  $c = 0.00005$  from the mutation of interest, and you observe that 95% of all mutation-bearing chromosomes carrying marker allele M3. For normal chromosomes, 35% of the these carry marker allele M3. Based on this information, when did the mutation arise?

$$(1-0.00005)^t = 0.95. \quad \text{Solving by taking logs gives}$$

$$t \quad \text{Log}(1-0.00005) = \text{log}(0.95), \quad \text{or}$$

$$t = \text{log}(0.95)/\text{Log}(1-0.00005) = 1026 \quad \text{generations.}$$

(4) [25 Points] Consider two linked loci (A with alleles **A** and **a**, B with alleles **B** and **b**) with recombination frequency 0.1. In a random-mating population you observe the following gamete frequencies

<b>AB</b>	<b>Ab</b>	<b>aB</b>	<b>ab</b>
0.3	0.2	0.1	0.4

a) What is Freq(A)? Freq(B)?

$$\begin{aligned} \text{freq(A)} &= \text{freq(AB)} + \text{freq(Ab)} = 0.5 \\ \text{freq(B)} &= 0.3 + 0.1 = 0.4 \end{aligned}$$

b) What is the expected frequency of the genotypes **AA**? **BB**? **AABB**?

$$\begin{aligned} \text{freq(AA)} &= 0.5^2 = 0.25, \text{freq(BB)} = 0.4^2 = 0.16 \\ \text{freq(AABB)} &= \text{freq(AB)}^2 = 0.3^2 = 0.09 \end{aligned}$$

c) What is the linkage-equilibrium value of the **AB** gamete?

$$\text{freq(AB)} = \text{freq(A)} * \text{freq(B)} = 0.5 * 0.4 = 0.2$$

d) What is the linkage disequilibrium value in this initial generation for **AB**?

$$D(\text{AB}) = \text{freq(AB)} - \text{freq(A)} * \text{freq(B)} = 0.3 - 0.2 = 0.1$$

e) What is the expected frequency of the **AB** gamete following 10 generations of recombination and random mating?

$$D(\text{AB, gen 10}) = (1 - 0.1)^{10} * D(\text{AB, gen 0}) = 0.035$$

$$\begin{aligned} \text{freq(AB, gen 10)} &= D(\text{AB, gen 10}) + \text{freq(A)} * \text{freq(B)} \\ &= 0.035 + 0.2 = 0.235 \end{aligned}$$

f) What is the expected frequency getting any genotype EXCEPT **AABB** by random mating the gametes from Example e?

$$\begin{aligned} 1 - \text{freq(AABB)} &= \text{freq(AB)}^2 = 0.235^2 \\ &= 1 - 0.055 = 0.945 \end{aligned}$$