

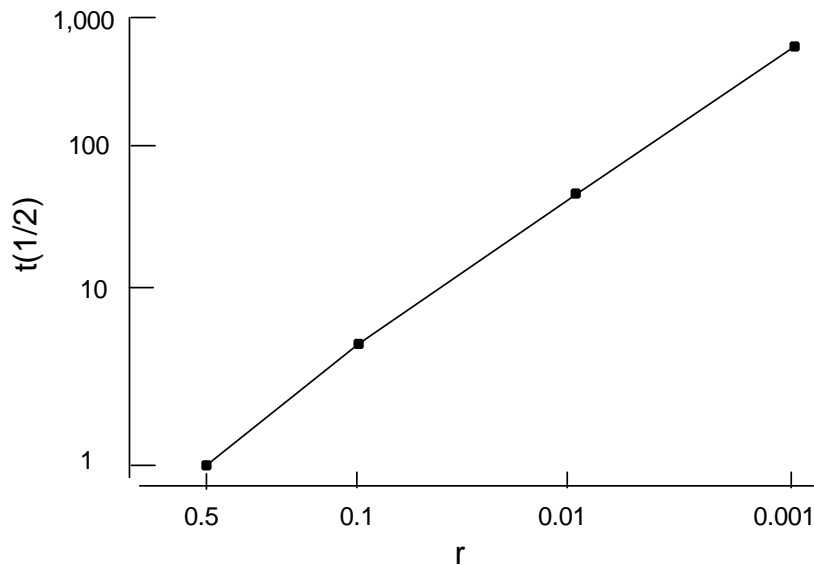
## CHAPTER 10 Answers to Problems

**Problem 10.1.** Genetic hitchhiking occurs when selection at one locus affects allele frequencies at another locus. This will occur only when genotypes at the two loci are nonrandomly associated (i.e., in gametic disequilibrium). As we saw in Section 10.2, a bottleneck will generate gametic disequilibrium between loci.

**Problem 10.2.** No. The amount of recombination between two loci can only be estimated by examining the gamete frequencies produced by individuals that are segregating at two loci. However, linkage between loci will increase the probability that the loci will be in gametic disequilibrium. Therefore, loci that are found to be in gametic disequilibrium in one or more populations are candidates to be closely linked. See Guest Box 10.

**Problem 10.3.** -0.25.

**Problem 10.4.**



**Problem 10.5.** There is no real threshold for a “small” amount of recombination. Nevertheless, in general gametic disequilibrium will decay rather quickly if  $r$  is more than 0.1.

**Problem 10.6.** In this case, only two gametes will occur  $AB$  and  $ab$ . That is,  $G_1 = G_4 = 0.5$  and  $G_2 = G_3 = 0.0$ . Therefore, the genotype frequencies in a random mating population will be

$AABB$	$AaBb$	$aabb$
0.25	0.50	0.25

Therefore, the marginal fitnesses at locus  $B$  will be 0.8, 1.0, and 0.8 for  $BB$ ,  $Bb$ , and  $bb$ , respectively because all heterozygotes at the  $B$  locus will also be heterozygous at the  $A$  locus.

The marginal fitnesses will be the same as above when  $D = -0.25$ .

**Problem 10.8.** See Example 10.2.

**Problem 10.9.** Note: There are actually 12 (not 11) individuals at the  $pUC5$  locus that are  $FF$ .

Locus	$FF$	$FP$	$PP$	$F_{IS}$	Chi-sq	Prob
$pUC5$	12	6	7	0.50	6.25	0.012
$pUC279$	11	10	4	0.13	0.44	0.51
$pUC351$	10	2	7	0.78	11.67	0.001

These results do support the authors’ conclusions of assortative mating. There is an excess of  $FF$  and  $PP$  individuals at all loci, and this departure from Hardy-Weinberg proportions is significant at two of the three loci.

**Problem 10.10.** Yes, this population appears to be mating at random because there is no indication of departure from H-W populations at either *LDH-A2* or *ME-4*.

There are 16 out of 28 individuals in the sample for which we can unambiguously determine their two gamete types. For example, each *AABB* individual carries two copies of the *AB* gamete, and each *AABb* individual carries one copy of the *AB* gamete and one copy of the *Ab* gamete. Therefore, the estimated frequency of the *AB* gamete ( $G_1$ ) is  $(2 \times 7) + 3 / (2 \times 16) = 17/32 = 0.531$ . Similarly,  $G_2$  is  $4/32=0.125$ ,  $G_3$  is zero, and  $G_4$  is  $11/32=0.344$ . Therefore, our estimate of  $D$  is  $(0.531 \times 0.125) - (0.125 \times 0) = 0.183$ .

This is close to the EM estimate from these same data of 0.213.