

POPULATION GENETICS

Fall 1999

Homework Problems

1. A total of 782 *Zoarcetes viviparus* are caught while pregnant. The genotype of the mother and of one randomly chosen offspring is determined at an esterase locus. The results are as follows:

Maternal genotype	Offspring genotype		
	A_1A_1	A_1A_2	A_2A_2
A_1A_1	41	70	—
A_1A_2	65	173	119
A_2A_2	—	127	187

- a. Find the frequency of A_1 among males that fertilized A_1A_1 females; that fertilized A_1A_2 females; that fertilized A_2A_2 females.
- b. Find the allele frequencies among the breeding males, averaged across *all* female genotypes.
2. A population survey resulted in the following numbers of different genotypes:

A_1A_1	A_1A_2	A_1A_3	A_2A_2	A_2A_3	A_3A_3
8	38	121	27	252	401

Calculate the frequency of all the alleles and test whether the genotype frequencies differ significantly from Hardy-Weinberg proportions.

3. Sometimes in electrophoretic surveys a null allele (an allele that does not code for an enzymatically active protein) is detected. Suppose A_1 codes for the fast migrating allele, A_2 for the slow migrating allele, and A_3 for the null allele. Then the phenotypes are as follows:

A_1A_1	A_1A_2	A_1A_3	A_2A_2	A_2A_3	A_3A_3
F	FS	F	S	S	N

In other words, there are four phenotypic classes: F, FS, S, and N. Suppose the number in each of these classes is N_F , N_{FS} , N_S , and N_N , respectively, and the total sample size is N .

- a. Using either the E-M algorithm or WinBUGS, estimate p_1 , p_2 , and p_3 from the following data (Hint: The relationship between genotype and phenotype in this problem is identical to the relationship between genotype and phenotype in the ABO blood group system that we looked at last Friday.):

Phenotype	F	FS	S	N
Number	30	90	20	10

- b. Use a goodness-of-fit test (χ^2 or G-test) to determine whether the genotype frequencies differ significantly from Hardy-Weinberg proportions. (If you're really ambitious,

you could try applying the EM-algorithm assuming an inbreeding coefficient of f in the population, but you won't be able to put confidence limits on f . You could also try WinBUGS. If you use $\mathbf{f} \sim \text{dunif}(-1,1)$ for your prior, you can produce a 95% credible interval for f . If this interval includes zero, you have no evidence for a departure from Hardy-Weinberg.)

- c. Suppose you were unaware of the presence of a null allele. Then your data would be:

Phenotype	F	FS	S
Number	30	90	20

and you would assume a biallelic polymorphism. Re-estimate the allele frequencies, test for goodness-of-fit to Hardy-Weinberg proportions (assuming only two alleles), and see what effect it has on your conclusions.