Practice Problems 5

1. Calculate H for each of the following genes from the allele frequencies:

(a) f(A1) = 0.5 f(A2)= 0.5
(b) f(B1) = 0.99 f(B2) = 0.01
(c) f(C1) = 0.2 f(C2) = 0.2 f(C3) = 0.2 f(C4) = 0.2 f(C5) = 0.2
(d) f(D1) = 0.90 f(D2) = 0.04 f(D3) = 0.03 f(D4) = 0.02 f(D5) = 0.01

Do you see any general patterns in these numbers?

2. The *c* coat color gene was sequenced from 335 individuals from a population of unicorns. Four different alleles were found, called c^1, c^2, c^3, and c^4. Four genotypes were found, with numbers as follows:

c^1/c^1 309
c^1/c^4 24
c^1/c^2 1
c^1/c^3 1

(a) Calculate the frequencies of each allele, to four decimal places/

(b) Calculate the expected heterozygosity to four decimal places:

(c) Is this population of unicorns inbred, outbred, or random mating?

3. Suppose that you measure the nucleotide diversity in the open reading frame of the human cytochrome oxidase subunit 3 gene, using restriction enzymes. The diversity turns out to be 0.001.

(a) Consider the third base pair in the second codon of the open reading frame. What is the probability that it is identical in your cytochrome oxidase 3 gene and mine?
(b) Consider the first base pair in the open reading frame: what is the probability that it is identical in our genes?

4. On a scale where the selection coefficient of a mutant allele can range from –1 to +1, what would be the selection coefficient of each of the following mutant alleles? Answers could be -1, > -1 and < 0, 0, > 0 and < 1, or 1.

(a) A mutation in the first codon position of a processed pseudogene in the mouse?
(b) In bacteria, an erythromycin-resistance mutation in culture medium containing the antibiotic.
(c) In bacteria, an erythromycin-resistance mutation in culture medium with no antibiotic.

5. For each of the following populations, indicate whether you would predict that the observed heterozygosity be equal to (=), greater than (>), or less than (<) the expected heterozygosity:

(a) a random mating population of one million human beings
(b) the gorillas in the Columbus, Ohio zoo

6. How much expected heterozygosity would you expect to see under the neutral hypothesis, if you looked for electrophoretic variants for α-globin in a large sample of rabbits from a population, assuming that the rabbit population is in mutation-drift equilibrium? Calculate the expected heterozygosity, assuming that the mutation rate is 5×10^{-5} mutations per gene per generation and the effective population size is (a) 10^3, (b) 10^5, and (c) 10^7. (Note that you can't use the approximate formula in this case.) (d) Assuming that this mutation rate is approximately correct for electrophoretic variants of α-globin, and that α-globin is a fairly typical protein, which of the preceding effective population sizes do you think is closer to correct for this population of rabbits? Hint: look at the expected heterozygosities.

7. A genetic engineer introduces a modified globin gene in an unfertilized mouse egg, replacing the normal allele by transformation. The egg is fertilized in vitro and implanted in a foster mother who rears it to maturity. Then the modified (heterozygous) mouse is illegally released from captivity by animal rights activists who believe that it is suffering. Actually it is very healthy: the modified globin gene has the same fitness as the wild type. The mouse joins a wild population of 50 individuals.

(a) The modified mouse has 20 offspring by wild fathers and then dies, what is the probability that the engineered globin gene will be lost in the first generation? Note that you can use basic Mendelian genetics to answer this question, as opposed to what we learned about population genetics.
(b) What is the probability that the engineered globin allele will be lost from the population sometime, without ever being fixed?

8. Which of the following is the most accurate explanation of why functionally important sequences such as promoters can be recognized by their sequence conservation? Explain why you did, or did not, choose each one.

(a) They have a lower mutation rate than other sequences.
(b) They have more synonymous substitutions than other sequences.
(c) They are transcribed more often than other sequences.
(d) They have a higher ratio of detrimental to neutral mutations than do other sequences.