PROBLEM SET 2 EVOLUTIONARY BIOLOGY FALL 2017

Mutation, Selection, Migration, Drift (20 pts total)

1)   In class we discussed some prion diseases including the infamous Kuru. There are many other prion diseases found in wildlife and livestock that occasionally are transferred to humans. One alarming prion disease known as Chronic Wasting Disease (CWD) has been found in a number of North American deer populations and can be transfer to humans via the consumption of infected animals. In some deer populations resistance seems to be due to the presence of an allele, **R** at a single locus in which the normal nonresistant allele may be denoted **N**. In the **absence** of CWD, the scaled fitnesses of the **NN**, **NR**, and **RR** genotypes have been estimated as 1.00, 0.61, and 0.28 respectively. In the **presence** of CWD, the scaled fitnesses have been estimated as 0.23, 1.00, and 0.78 respectively. (5 pts total)

a)   Calculate the selection coefficient (s) against the **RR** homozygous genotype when CWD is not present. Calculate the dominance coefficient (h). (2 pts)

b)   Calculate the equilibrium frequency of **R** in the presence of CWD. (1 pt)

c)   In the absence of selection from CWD, the effects of the **R** allele on fitness is negative and its frequency in a population would be determined by the balance between mutation and selection. Given the probability that **N** mutates to **R** at a rate of 4×10^{-5}, what are the frequencies of **N** and **R** at mutation-selection equilibrium? How does this equilibrium value compare to the equilibrium values under CWD selection? (1 pt)

d)   A small amount of dominance can have a major effect in reducing the equilibrium frequency of a harmful allele when there is a mutation-selection balance. To confirm this for yourself, imagine the **R** allele is completely recessive to the **N** allele when no CWD is present. In this case, the scaled fitness values of the **NN**, **NR**, and **RR** genotypes are 1.00, 1.00, and 0.28 respectively. How does the equilibrium value of the two alleles change when R is completely recessive? (1 pt)

2)   Conservation managers are concerned about the CWD susceptibility in a deer population that has a very low frequency of the R allele so they are considering introducing individuals from another population with a higher frequency of this allele. Before they start mixing these populations they want to estimate the level of gene flow between them. They gather data from a single allozyme locus with 2 alleles and determine the frequency of these 2 alleles in each population. The data are shown below. (5 pts total)

a)   Using these data, and assuming that no selection operates on this allozyme locus, and the populations are in Hardy-Weinberg equilibrium, calculate F_{ST}. (2 pts)

	p	**q**
Population 1	0.9	0.1
Population 2	0.3	0.7

b)   Assuming the necessary assumptions are met, what is the effective number of migrants(N_m) among these populations each generation? (2 pts)

c)   Assuming other genes in these populations related to local adaptation have a similar F_{ST} as this allozyme locus, do you think it is a good idea to mix these populations? Why or why not? (1 pt)

3)   Declines in available habitat due to deforestation have led to dramatic population declines in many Malaysian primate species including Orangutans. To provide a demographic buffer, a conservation organization in Sumatra maintains a captive colony of 80 Orangutans. (4 pts total)

a)   If there are 60 female and 20 male Orangutans in this colony, what is the effective population size (N_e)? (2 pts)

b)	One big concern in any captive breeding program is that genetic variation will be lost over time via random genetic drift and that this loss will cause a decrease in fitness. If the original heterozygosity in the colony was 0.60, what proportion of the original heterozygosity would be lost after 15 generations? Assume the colony is kept at its current size and sex-ratio. (2 pts)

4)	In class we discussed some nice examples of coloration being under selection including peppered moths in Kettlewell's experiments on industrial melanism and King & Lawson's water snakes. Often these color patterns or color intensities are under selection from predation. Another nice example of this phenomenon is found in lizards that live in the White Sands National Monument in New Mexico. Lighter individuals are more cryptic in this environment. To investigate how selection is operating on coloration in these lizards, graduate students from Notre Dame conducted a mark-recapture experiment similar to Kettlewell's (1973) classic study. Use the data from this mark-recapture experiment (given below) to answer the following questions. Assume that lizard skin coloration is controlled by a single locus with two alleles (L & D) and that you can directly infer the underlying genotype of an individual by its skin color. In this wild population, there is incomplete dominance so that all three genotypes can be distinguished based on skin color. (6 points total)

Dark skin color= DD homozygote
Medium skin color= LD heterozytgote
Light skin color= LL homozygote

Genotype	Marked Sample	Recaptured sample
DD	200	50
DL	900	250
LL	400	200
Total (N)	1500	500

a)	What is the survival rate for each genotype? (2 pts)

b)	What form of selection is operating on this locus? (1 pt)

c)	What are the selection (**s**) and the dominance (**h**) coefficients? (2 pts)

d)	Assuming the frequency of the light-skinned allele (L) in this population is Freq(L) = p = 0.70 what is the population mean fitness ($\overline{W}$)? (1 pt)