HOMEWORK SET #3

Due: Tuesday, November 8

1. We saw in lecture that if the pattern of migration and initial allele frequencies in a population are known, the frequencies after migration can be predicted. We can make inferences in the reverse direction too. That is, if we know the allele frequencies before and after migration, we can estimate the rate of gene flow.

(a) Rearrange the equation for the change in allele frequency from the one-island model of migration (with no selection) to show that the migration rate, *m*, in terms of the allele frequencies on the island before migration (*p*), after migration and reproduction (*p*'), and on the continent (p_c) is given by the following expression:

$$m = \frac{p' - p}{p_c - p}$$

(b) Use this expression and the following data to estimate the proportion of nuclear genes that originated in Africa. Make a separate estimate for each allele. (Important hint: think gene flow, not geography!)

Allele	Blacks (Georgia)	Caucasians (Georgia)	West Africans
Ro	0.535	0.037	0.605
A	0.158	0.246	0.147
Hbs	0.043	0	0.061

R0 and A are alleles at the Rh and ABO loci while Hbs is the sickle cell allele.

(c) Do your three estimates agree? What are some plausible explanations for any discrepancies? What assumptions are needed for the estimation formula in part (a)?

2. Nielsen & Slatkin, p. 75 #4.6 modified:

(a) Note that equation (4.19) on p. 69 connects F_{ST} to the per individual rate of migration *m* for Wright's island model assuming a <u>finite</u> number *d* of populations. Use (4.19) with $d = 2$ and $2N = 10{,}000$ to solve for *m* from the value of F_{ST} computed from the data in Exercise 4.1.

(b) Suppose the two populations described in Exercise 4.1 are instead a subsample of a very large number of populations that are coupled by gene flow. Use the equation we discussed in class that connects F_{ST} to the per individual rate of gene flow, m_T, for Wright's infinite island model (i.e., equation 4.20 on p. 69) with $2N = 10{,}000$ to estimate m_T from the same value of F_{ST} you used for part (a).

(c) Compare the two gene flow estimates *m* and m_T that you computed in parts (a) and (b). Discuss.

3. Consider the following scenarios of one-locus selection with two alleles, *A* and *a* and selection coefficient $s = 0.1$ against *a*. The genetic basis of fitness is given for each scenario. In each case, compute $\Delta p = p' - p$, the between-generation change in the frequency of *A* for each of two initial frequencies: $p = 0.05$ and $p = 0.9$.

(a) haploid ($w_A = 1$, $w_a = 1 - s$)
(b) diploid; *A* dominant advantageous/*a* recessive deleterious
(c) diploid; *A* recessive advantageous/*a* dominant deleterious
(d) diploid; *A* advantageous and partially dominant with $h = 0.4$
(e) Using your results, briefly discuss how the individual and population genetic architectures of fitness affect rates of adaptive evolution.

4. Nielsen & Slatkin, p. 150 #7.5

5. Nielsen & Slatkin, p. 150 #7.6

6. Nielsen & Slatkin, p. 150 #7.7