HOMEWORK SET #4

Due: Thursday, December 6

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
R_0	0.535	0.037	0.605
A	0.158	0.246	0.147
Hb^s	0.043	0	0.061

   R_0 and A are alleles at the Rh and ABO loci while Hb^s 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. One interpretation of Wahlund's effect is that population mixing via migration can create correlations between alleles within loci (i.e., increase homozygosity). Likewise, migration can create associations between alleles at *different* loci. To see this, consider two diallelic loci and two populations. Locus A has alleles A and a and locus B has alleles B and b. Let p_i = the frequency of A in subpopulation i and q_i = the corresponding frequency of B, i = 1, 2. Assume both populations are in linkage equilibrium and consider the effects of a one-time migration event.

   (a) After the migration event, the two subpopulations are mixed in respective proportions 1–m resident and m immigrant. Let D be the disequilibrium created in subpopulation 1 immediately after migration but before reproduction. Show that $D = m(1-m)(p_1 - p_2)(q_1 - q_2)$. (Hint: use the formula $D = \overline{P}_{AB} - \overline{p}\overline{q}$ where $\overline{P}_{AB}$ is the frequency of the AB gamete, $\overline{p}$ is the frequency of A, and $\overline{q}$ is the frequency of B in the mixed subpopulation before reproduction. Note that $\overline{P}_{AB} = (1-m)p_1q_1 + mp_2q_2$, $\overline{p} = (1-m)p_1 + mp_2$, and $\overline{q} = (1-m)q_1 + mq_2$.)

(b) Let $\text{var}(p) = (1-m)p_1^2 + mp_2^2 - \overline{p}^2$ be the spatial (i.e., among population) variance in the frequency of allele *A* before immigration. Show that $\text{var}(p) = m(1-m)(p_1 - p_2)^2$. Similarly, show that the spatial variance in the frequency of *B* is $\text{var}(q) = m(1-m)(q_1 - q_2)^2$.

(c) Use (a) and (b) to conclude that $D = \pm\sqrt{\text{var}(p)\,\text{var}(q)}$ where $D > 0$ if $\text{sign}(p_1 - p_2) = \text{sign}(q_1 - q_2)$ and $D < 0$ otherwise. Why is this formula is equivalent to $D = \pm F_{ST}\sqrt{\overline{p}(1-\overline{p})\overline{q}(1-\overline{q})}$? When will migration *fail* to generate disequilibrium in a subpopulation?

(d) Is the following statement true or false? Any disequilibrium created by migration will be reduced by a factor (1–*r*) after random mating in the mixed subpopulation, where *r* is the rate of recombination between the A and B loci. Explain your choice.

3. Hedrick, p. 597 #13

4. Hedrick, p. 597, #15

5. Hedrick, p. 597, #17