Homework Set #3 Key

See Nielsen & Slatkin for solutions to problems 4 & 6

1. (a) Start with $p' = (1-m)p + mp_c$. Rearrange as $p' = p + m(p_c - p)$. Subtracting p from both sides and dividing by $(p_c - p)$ gives the final formula.

   (b) p' is obviously the allele frequency in Blacks of Georgia, who descended from a mixture of African (Black) and Caucasian (White) ancestry. There are two ways to interpret this mixture in terms of the continent-island model: 1. Black alleles (p_c) flowing into a White population (p) or 2. White alleles (p_c) flowing into a Black population (p). Interpretation 2 is better since the descendants of White-Black mating are typically identified in the US as Black.

   R_0: $m = (.535 - .605)/(.037 - .605) = 0.123$
   A: $m = (.158 - .147)/(.246 - .147) = 0.111$
   Hbs: $m = (.043 - .061)/(0 - .061) = 0.295$

   (c) The estimates from R_0 and A are similar but quite distinct from Hbs. The estimation formula depends on a number of assumptions including the constancy of p_c and the absence of selection of the locus in question. In addition, we are assuming that the ancestral frequencies p are well-represented in the contemporary West African sample. The latter assumption especially is suspect for Hbs since modern medical care has probably caused a significant change in the overdominant selection that maintains the sickle cell allele compared to when Africans were forcibly brought to America. Also, the lower frequency of Hbs in Georgia Blacks is probably as much a consequence of locally purifying selection as gene flow from Caucasians due to the relative absence of malaria in the US.

2. Note from Exercise 4.1 that $F_{ST} = 0.016$

   (a) With $d = 2$, eq. 4.19 is $F_{ST} = 1/(1 + 8M) = 1/(1 + 16Nm)$. Solving for m shows that $m = (1 - F_{ST})/(16NF_{ST})$. Substituting $F_{ST} = 0.016$ gives the estimate and $2N = 10{,}000$ gives the estimate $m = 7.69 \times 10^{-4}$

   (b) $m_T = (1 - F_{ST})/(4NF_{ST}) = 3.1 \times 10^{-3}$

   (c) Note for the same values of F_{ST} and $2N$ that $m_T/m = [(1 - F_{ST})/(4NF_{ST})]/ [(1 - F_{ST})/(16NF_{ST})] = 4$. That m_T is larger than m is perhaps not surprising since the former value assume immigrants can arrive from an infinite number of sites rather than from just one site. Given that, the fact that m_T is only 4 times as large of m is remarkable.

3. (a) $\Delta p = pq\dfrac{s}{1-qs}$ = .0052, .0091

   (b) $\Delta p = pq\dfrac{qs}{1-q^2s}$ = .0050, .0009

(c) $\Delta p = pq\dfrac{ps}{1-\left(1-p^2\right)s}$ = .0002, .0083

(d) $\Delta p = pq\dfrac{\left[h(p-q)+q\right]s}{1-q(2ph+q)s}$ = .0031, .0038

(e) *Population genetic architecture (allele frequency)*: Has greatest impact on evolutionary rates in recessive and dominance cases. Rates are high (low) for a rare (common) dominant favorable allele. The opposite is true for a recessive favorable allele. Evolutionary rates are comparatively similar at high and low frequencies for haploids and partial dominance.

Individual genetic architecture (genetic basis): Haploids had the overall highest rates of evolution for the same strength of selection. In diploids, the rate of evolution at a particular frequency was strongly dependent on whether the favored allele was dominant, recessive, or partially dominant in its effects on individual fitness.

5. The data show w_{BB} = 1/5, w_{Bb} = 1/6, and w_{bb} = 1/10. Let p = frequency of B. If p = 1/4 and seeds are in HW equilibrium, then $\overline{w} = \left(\frac{1}{4}\right)^2\left(\frac{1}{5}\right) + 2\left(\frac{1}{4}\right)\left(\frac{3}{4}\right)\left(\frac{1}{6}\right) + \left(\frac{3}{4}\right)^2\left(\frac{1}{10}\right) = 0.131$ and $\overline{w}_B = \left(\frac{1}{4}\right)\left(\frac{1}{5}\right) + \left(\frac{3}{4}\right)\left(\frac{1}{6}\right)$ = 0.175. This gives $p' = p\,\frac{\overline{w}_B}{\overline{w}} = \left(\frac{1}{4}\right)\left(\frac{0.175}{0.131}\right)$= 0.33.