Homework Set #1 Key

See Nielsen & Slatkin for solutions to problems 2, 3, 5, 8, 9, & 11

1. (a) $p' = P_{AA} + \left(\frac{1}{2}\right)P_{Aa} = p_m p_f + \left(\frac{1}{2}\right)\left[p_m\left(1-p_f\right) + p_f\left(1-p_m\right)\right] = \left(\frac{1}{2}\right)\left(p_m + p_f\right)$, the even average of the parental allele frequencies. This makes sense because mothers and fathers contribute equally to autosomal genotypes of their offspring.
   (b) No. For example, if $p_f = 0$ and $p_m = 1$, then $P_{AA} = P_{aa} = 0$ and $P_{Aa} = 1$, which are not Hardy-Weinberg proportions. (Why?)
   (c) Because <u>all</u> the Hardy-Weinberg conditions hold for the offspring generation, the frequency of A will remain at $p = (p_f + p_m)/2$ in their descendants with genotype frequencies in Hardy-Weinberg proportions AA p^2: Aa $2p(1\text{-}p)$: aa $(1\text{-}p)^2$.

4. Nielsen & Slatkin, p. 19 #1.4
   Let q be the frequency of the recessive allele. Because the population is in HWE, $q = \sqrt{\text{frequency of the disease}} = \sqrt{0.0002}$ =0.0141. The frequency of heterozygote carriers is then $2pq = 2 \cdot (1 - 0.0141) \cdot 0.0141$=0.0279

6. Nielsen & Slatkin, p. 20 #1.8
   1st Locus:
   Frequency of allele C = $\frac{2\cdot 42+16}{2(42+16+32)} = 5/9$;
   Frequency of allele T = 1 – 5/9 = 4/9
   Frequency of genotype CT = $2 \cdot 5/9 \cdot 4/9$ = 0.494

   2nd Locus:
   Frequency of allele A = $\frac{2\cdot 10+10+5}{2(10+10+5+20+5+20)} = 1/4$;
   Frequency of allele C = $\frac{2\cdot 20+10+5}{2(10+10+5+20+5+20)} = 11/28$
   Frequency of genotype CT = $2 \cdot \frac{1}{4} \cdot \frac{11}{28}$=0.196

   Frequency of the two locus genotype (CT, AC) = $0.494 \cdot 0.196 = 0.0968$

7. Nielsen & Slatkin, p. 126 #6.2
   Assume two diallelic loci, the 4 haplotypes are AB, Ab, aB, and ab with respective haplotype frequencies P_{AB}, P_{Ab}, P_{aB}, and P_{ab}.

   There are 6 scenarios with 2 haplotypes missing:

i) AB & Ab missing: $P_{AB} = P_{Ab} = 0$. Allele frequencies are then $p_A = P_{AB} + P_{Ab} = 0 + 0 = 0$ and, since $p_B = P_{AB} + P_{aB}$, $0 \le p_B \le 1$

ii) aB & ab missing: $P_{aB} = P_{ab} = 0$. Allele frequencies are then $p_A = P_{AB} + P_{Ab} = 1$ and, since $p_B = P_{AB} + P_{aB}$, $0 \le p_B \le 1$

iii and iv) Similar reasoning applies to the cases AB & aB missing, and Ab & ab missing.

v) AB & ab missing: $P_{AB} = P_{ab} = 0$. Since $p_A = P_{AB} + P_{Ab} = 0 + P_{Ab} = P_{Ab}$ and $p_B = P_{AB} + P_{aB} = 0 + P_{aB} = P_{aB}$, then $0 \le p_A \le 1$ and $0 \le p_B \le 1$.

vi) Similar reasoning to case v.

10. Nielsen & Slatkin, p. 127 #6.6

(b) $D0 = P_{AB} P_{ab} - P_{Ab} P_{aB} = (30/1000)(330/1000) - (27/1000)(370/1000) = -0.00009$

(c) *The following is the question I meant to ask: Assuming the recombination rate is 0.001, how many generations of random mating will be necessary until the LD is 1% of its original value?*

Ans: We know that under these assumptions, $D_T = (1 - r)^T D_0$. At what time T is $D_T = 0.01 \cdot D_0$? It's the solution T of $D_T = 0.01 \cdot D_0 = (1 - 0.001)^T D_0$. Canceling D_0 from both sides gives the equivalent equation $0.01 = .999^T$. Solving for T gives $T = \frac{\log 0.01}{\log .999} = 4602$ generations.