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 all 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 $AA p^2$: $Aa 2p(1-p)$: $aa (1-p)^2$.

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 = $\frac{2 \cdot 42 + 16}{2 \cdot (42 + 16 + 32)} = \frac{5}{9}$;
Frequency of allele T = $1 - \frac{5}{9} = \frac{4}{9}$
Frequency of genotype CT = $2 \cdot \frac{5}{9} \cdot \frac{4}{9} = 0.494$

2nd Locus:
Frequency of allele A = $\frac{2 \cdot 10 + 10 + 5}{2 \cdot (10 + 10 + 5 + 20 + 5 + 20)} = \frac{1}{4}$;
Frequency of allele C = $\frac{2 \cdot 20 + 10 + 5}{2 \cdot (10 + 10 + 5 + 20 + 5 + 20)} = \frac{11}{28}$
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 $p_B = P_{AB} + P_{aB}, 0 \leq p_B \leq 1$

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

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 $0 \leq p_A \leq 1$ and $0 \leq p_B \leq 1$.

vi) Similar reasoning to case v.

10. Nielsen & Slatkin, p. 127 #6.6

(b) $D_0 = P_{AB} P_{ab} - P_{Ab} P_{aB} = (30/1000)(330/1000) - (27/1000)(370/1000) = -0.00009$

(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.