Allman Ch 6.1 Ex 4,9,10,12,14,16 and Ch 6.2 Ex 6,12,14,15,16 and Ch 6.4 Ex 1,3,5,7,9 11,12

6.1.4. a. Since the probability of having the allele is 1/31 for the male and also 1/31 for the female, assuming these are independent the probability is $(1/31)^2 \approx .00104$.
b. Since the child must inherit the recessive allele from each parent, the probability is $(1/2)(1/2) = 1/4$.
c. $(1/31)^2(1/4) \approx .0002601$.

6.1.9. a. Genotype $WwGg$, with round yellow seed phenotype.
b. If the genes assort independently, F_2 should be: 1/16 with wrinkled green seeds, 3/16 with wrinkled yellow seeds, 3/16 with round green seeds, and 9/16 with round yellow seeds.
c. If Mendel's data did not exactly match these proportions, he should not necessarily doubt the independent assortment hypothesis. After all, these proportions are really probabilities, so only for very large amounts of data should the fit be very close. The more data he collected, the closer he should expect his data to match these proportions if the hypothesis is valid. Deciding how close is close enough for a match, taking into account the amount of data collected, will be discussed in the next section.

6.1.10. The cross is $Y^l y \times Y^l y$. Embryo genotype ratios will be Y^lY^l:Y^ly:yy=1:2:1, but only the last two genotypes will be born. Thus the viable progeny will have genotypes Y^ly or yy, with respective phenotypes yellow and agouti, in proportions 2/3 and 1/3.

6.1.12. a. The trait is dominant. If it were recessive, all children of the parents would exhibit brachydactyly. The parents must each be heterozygotes, since one child has normal length fingers. The child with normal length fingers is a homozygous recessive. The child with short fingers is either homozygous dominant or heterozygous.
b. The probability that one child has normal fingers is 1/4, and since the two children's phenotypes are independent, the probability that both have normal length fingers is $(1/4)^2 = 1/16$.

6.1.14. F_1 has genotype Ww only, with pink flower phenotype. F_2 has genotypes WW, Ww, and ww in proportions 1/4, 1/2, and 1/4, with red flower, pink flower, and white flower phenotypes, respectively.

6.1.16. a. Type A: I^AI^A, I^AI^O; Type B: I^BI^B, I^BI^O; Type AB: I^AI^B; Type O: I^OI^O

b. $I^AI^A \times I^BI^O$ produces offspring with genotypes I^AI^B and I^AI^O with equal probability. Thus type AB and type A blood occur with relative frequencies 1/2 and 1/2.

c. From $I^AI^O \times I^BI^O$ we expect 1/4 of the progeny to have type O blood (genotype I^OI^O). So out of four children, we would expect one to have type O blood. However, any number might have this blood type. The probability of any one child having it is 1/4, and it is really only in a very large number of trials (much greater than 4) that we can be reasonably confident that close to 1/4 of the trials will produce this outcome. For instance, there is a probability of $(1/4)^4 = 1/256$ that all four children will have type O blood, and of $(3/4)^4 = 81/256$ that none of them will. (See the next section for a more careful definition of the word 'expect'.)

6.2.6. a. $\binom{6}{4}(\frac{1}{2})^4(\frac{1}{2})^2 = 15\frac{1}{64} = \frac{15}{64} \approx .2344$

b. $\mathcal{P}(\text{exactly } i \text{ boys in 6 children}) = \binom{6}{i}(\frac{1}{2})^6$, so for $i = 0, 1, 2, \ldots 6$, the values are: .0156, .0938, .2344, .3125, .2344, .0938, .0156.

$\mathcal{P}(\text{exactly } i \text{ girls in 6 children})$ has exactly the same values.

c. The expected number of boys is $\sum_{i=0}^{6} i\mathcal{P}(\text{exactly } i \text{ boys in 6 children}) = 0(.0156) + 1(.0938) + 2(.2344) + 3(.3125) + 4(.2344) + 5(.0938) + 6(.0156) = 3$. Alternately, for a binomial distribution, the expected value is $n \cdot p = 6 \cdot \frac{1}{2} = 3$.

d. $\mathcal{P}(4 \text{ or more girls of 6 children}) = \mathcal{P}(4 \text{ girls}) + \mathcal{P}(5 \text{ girls}) + \mathcal{P}(6 \text{ girls}) = .2344 + .0938 + .0156 = .3438$.

6.2.12. a. 1/2

b. $(1/2)(1/2) = 1/4$

c. $\binom{2}{1}(1/2)(1/2) = 1/2$

d. $\binom{2}{1}(1/2)(1/2) + \binom{2}{2}(1/2)^2(1/2)^0 = 3/4$, or, computing the probability that it is not the case that no children are albinos, $1 - \binom{2}{0}(1/2)^0(1/2)^2 = 3/4$.

e. Using the formula for the expected value of a binomial random variable, $2(1/2) = 1$, or, using the definition of expected value, $0 \cdot \binom{2}{0}(1/2)^0(1/2)^2 + 1 \cdot \binom{2}{1}(1/2)^1(1/2)^1 + 2 \cdot \binom{2}{2}(1/2)^0(1/2)^2 = 1$.

6.2.14. a. $\mathcal{P}(\text{age at death} = 0) = 1/2$;
$\mathcal{P}(\text{age at death} = 1) = (1/2)(3/4) = 3/8$;
$\mathcal{P}(\text{age at death} = 2) = (1/2)(1/4)(3/4) = 3/32$;
$\mathcal{P}(\text{age at death} = 3) = (1/2)(1/4)(1/4)(1) = 1/32$.
These probabilities add to 1 since the events are disjoint and exhaust all possibilities.

b. $0(1/2) + 1(3/8) + 2(3/32) + 3(1/32) = .65625$

6.2.15. a. Recall from problem 6.1.10, that the probability an offspring is yellow is 2/3 Then the probability 5 of 12 have normal coloring is $\binom{12}{5}(1/3)^5(2/3)^7 \approx .1908$
b. $\sum_{i=10}^{12}\binom{12}{i}(2/3)^i(1/3)^{12-i} \approx .1811$
c. $\sum_{i=0}^{3}\binom{12}{i}(2/3)^i(1/3)^{12-i} \approx .0039$

6.2.16. a. Since the probability that any given child in the family will develop Huntington disease is 1/2, the probability that none of 4 do is $\binom{4}{0}(1/2)^0(1/2)^4 = 1/16$
b. The probability that at least one of the 4 develops the disease is $1 - \mathcal{P}(\text{none of 4}) = 1 - 1/16 = 15/16$.
c. The probability that 3 or more develop the disease is $\binom{4}{3}(1/2)^3(1/2)^1 + \binom{4}{4}(1/2)^4(1/2)^0 = 5/16$.

6.4.1. a. Let p be the frequency of ct in the population. Then $p^2 = 9/450$, so $p \approx .1414$.
b. The percentage of the population heterozygous for the gene is $2p(1-p) \approx .2428$.

6.4.3. a. $2p(1-p) = .4$ implies $p^2 - p + .2 = 0$, so $p = (1 \pm \sqrt{1-.8})/2 = (1 \pm \sqrt{.2})/2 \approx .2764$ or $.7236$, with q being the other value.
For $2p(1-p) = H$, the values of p and q are $(1 \pm \sqrt{1-2H})/2$.
b. $H = 2p(1-p)$ is maximized when $p = 1/2$, $q = 1/2$. This can be seen either by graphing the parabola, or by using calculus.

6.4.5. a. Let p, q, and r denote the frequencies of the alleles I^A, I^B, and I^O. Assuming random mating in the population,

$$p^2 + 2pr = .32,\ q^2 + 2qr = .15,\ 2pq = .04,\ r^2 = .49.$$

Solving these gives $r = .7$, $p = .2$, and $q = .1$. Note that even though there are 4 equations in only 3 unknowns here, these values makes all equations hold.
b. The equations to be solved are

$$p^2 + 2pr = .40,\ q^2 + 2qr = .11,\ 2pq = .05,\ r^2 = .44.$$

From the last we find $r = .6633$. Then the first gives $p = .2532$, and the second gives $q = .0783$. With these values $2pq = .0396$, so the third equation is *not* satisfied. (Also, $p + q + r \neq 1$.) Thus the system has no exact solution.
It could be that the population is not in a Hardy-Weinberg equilibrium, or that the data is flawed. Given the relative ease of collecting bloodtype data, and the doubtfulness of the random mating assumption applying to the U.S. population, the first is more likely.

6.4.7. a. $p = (2Np_1 + 2Np_2)/(4N) = (p_1 + p_2)/2$
b.After the flood, a^+a^+ has frequency $(p_1^2 + p_2^2)/2$, a^+a has frequency $p_1(1-p_1) + p_2(1-p_2)$, and aa has frequency $((1-p_1)^2 + (1-p_2)^2)/2$.
A Hardy-Weinberg equilibrium would predict the three frequencies were $(p_1 + p_2)^2/4$, $(p_1 + p_2)(2 - p_1 - p_2)/2$, and $(2 - p_1 - p_2)^2/4$.
These disagree (for most values of p_1, p_2) since the population has not yet undergone random mating. There is no reason to expect a Hardy-Weinberg equilibrium.

6.4.9. a. The model shows a gradual increase in frequency of A, toward fixation at $p = 1$. Thus a is eliminated ultimately. It appears that $p = 1$ is a stable equilibrium, and $p = 0$ an unstable one.

b. The model shows a gradual decrease in frequency of A, toward elimination at $p = 0$. Thus A is eliminated ultimately. It appears that $p = 0$ is a stable equilibrium, and $p = 1$ an unstable one.

c. If $p_0 > .5$, the frequency of A increases, toward $p = 1$; if $p_0 < .5$, the frequency of A decreases, toward $p = 0$. Thus the model shows a gradual increase in the frequency of whichever allele is initially more common. Eventually that allele is fixed in the population, while the other dies out. There are stable equilibria at $p = 0$ and 1, and an unstable one at $p = .5$.

d. If $p_0 > .5$, the frequency of A decreases, toward $p = .5$; if $p_0 < .5$, the frequency of A increases, toward $p = .5$. Thus the model shows movement toward an equal proportion of both alleles. While $p = .5$ is a stable equilibria, there are unstable ones at $p = 0$ and 1.

6.4.11. a. The parameters indicate homozygous dominants do not reproduce, while heterozygotes have no selective disadvantage relative the homozygous recessives. (See problem 6.4.10.)

b. $p_{t+1} = \dfrac{p_t q_t}{2p_t q_t + q_t^2} = \dfrac{p_t}{2p_t + q_t} = \dfrac{p_t}{p_t + 1}$, if $q_t \neq 0$ (or $p_t \neq 1$).

c. $p_1 = \dfrac{p_0}{p_0 + 1}$, so $p_2 = \dfrac{\frac{p_0}{p_0+1}}{\frac{p_0}{p_0+1} + 1} = \dfrac{p_0}{p_0 + (p_0 + 1)} = \dfrac{p_0}{2p_0 + 1}$. In general, if $p_t = \dfrac{p_0}{tp_0 + 1}$, then $p_{t+1} = \dfrac{\frac{p_0}{tp_0+1}}{\frac{p_0}{tp_0+1} + 1} = \dfrac{p_0}{p_0 + (tp_0 + 1)} = \dfrac{p_0}{(t+1)p_0 + 1}$.

Note that this shows that as $t \to \infty$, $p_t \to 0$ so such an allele will die out under random mating.

6.4.12. a. The homozygous recessives have no progeny, while heterozygotes are at no relative advantage to homozygous dominants.

b. $p_{t+1} = 1/(2 - p_t)$

c. $p_t = (t - (t-1)p_0)/((t+1) - tp_0)$, thus as $t \to \infty$, $p_t \to 1$ and the dominant allele becomes fixed.