# BSCI 410 Homework 1 Answer Key

1. **A** **(1 point)**

2. a. Parental Ditype (PD) = 170; Non-parental Ditype (NPD) = 2;

   Tetrads (T) = 28

   RF = (NPD + 0.5T) / Total Tetrads = (2 + 0.5 * 28) / (170 + 2 + 28) = 16/200

   = **0.08** or **8%** **(1 point)**

   b. Option 1: Perkins equation (more accurate > 50 cM)

   map distance = (3 * NPD + ( 1 / 2 ) * T) / Total Tetrads

   (3 * 2 + 0.5 * 28) / (1000) = 0.10 or **10 cM (10 m.u.)**

   Option 2:

   When the actual distance between two genes is very small, only then are the values for RF and the values for map distance very similar. In this specific case, you could argue that map distance = RF = .08 or **8 cM** but only if you used the reasoning above.

   Preferred Option: Mapping function

   w = -1/2*ln(1-2(RF)) = -1/2ln(1-2(.08))

   = .087 or **8.7 cM** (also accepted) **(1 point)**

Note that RF and map distance are different. The RF is observed, so 8% is exactly right (16/200 spores were recombinant; that is the data). By contrast, map distance values are both estimates. RF should never be larger than 50%, but the map distance between the ends of some human chromosomes could be close to 300 cM.

3. RF = 0.5(1 – $e^{-2w}$), where w = map distance in "Morgans" (lecture 4)

RF = 0.5(1 – $e^{-2*0.6}$), RF = 0.35

RF = (NPD + 0.5T ) / Total Tetrads = 0.35 Equation I

w = 0.6 = ( 3 * NPD + ( 1 / 2 ) * T ) / Total Tetrads (Perkins) Eqn. II

Total Tetrads = PD + NPD + T = 1000 Eqn. III

Solve equation I for NPD in terms of T (or vice versa), plug into Eqn II.

Solve III, **PD = 425, NPD = 125, T = 450** **(2 points)**

Variations based on rounding differences were accepted.

4. a. The probability of CF children is 1/4, so the probability of normal children is 3/4. According to binomial distribution, the probability of having 0 CF children and 3 normal children is:

$(3!/(0!*3!)) \times (1/4)^0 \times (3/4)^3$ = **27/64** or **42%** **(1 point)**

Or 3/4 * 3/4 * 3/4 if you want to calculate it directly

b. It is more complicated if you want to calculate this probability directly, because there are three different orders in which the CF child can be born (first, second or last), and you will have to calculate the probability of each situation and sum them up. Using the binomial distribution, however:

$(3!/(1!*2!)) \times (1/4)^1 \times (3/4)^2$ = **27/64** or **42%** **(1 point)**

c. $(3!/(2!*1!)) \times (1/4)^2 \times (3/4)^1$ = **9/64** or **14%** **(1 point)**

d. $(3!/(3!*0!)) \times (1/4)^3 \times (3/4)^0$ = **1/64** or **1.5%** **(1 point)**

5. Two ways to consider the problem:

As discussed in lecture Probability (A|B) = P (AB)/P(B) where A = affected

B = family with at least 1 affected child

P(AB) = 1/4

P(B) = 1 – P(no affected children) = 1 – 27/64 (from 4a) = 37/64

P(no affected children) is the fraction of families with two parents who are carriers that have no affected children. These families are not part of the study. These families are part of the sample space to which Mendel's ratio applies, but they are not part of the study sample. It is because these families could have had affected children but did not that more than 1/4 of the children in the study group are affected.

6. a. The expected rate is 1/1000. According to the binomial distribution, the probability of getting exactly 4 recombinant spores is:

$(500!/(4!*496!)) \times (1/250)^4 \times (249/250)^{496}$ = **9.02% (1 point)**

Using 2000 in place of 500 and 1/1000 instead of 1/250, etc. was accepted as the difference in the final percentage is negligible. However, there are truly 500 events (each event produces 4 spores), not 2000 (considering each spore separately).

b. Remember that all possibilities sum up to 1. Therefore:

$1 - Prob_0 - Prob_1 - Prob_2 - Prob_3 = Prob_{\text{greater or = 4}}$

where $Prob_0$ = probability of getting 0 spores, $Prob_1$ = probability of getting 1 spore, etc.

NOTE: Prob1 and Prob3 != 0, different from the question in lecture.

$Prob_{\text{greater or = to 4}}$ = **14.3%** **(1 point)**

c. $P[4] = (2^4/4!)*e^{-2}$ = **9.02%** **(1 point)**

d. You will see one (ABC1, ABC2) spore every 1,000 spores. For every thousand spores, the recombination event that creates the recombinant (ABC1, ABC2) spore will also result in a recombinant (abc1, abc2) spore. Therefore, the recombination rate is actually 2/1,000 or 0.002, and ABC1 and ABC2 are

$0.002 \times 100$ = **0.2 cM apart** **(1 point)**

7. a. **Complete dominance** (red dominant to white) **(1 point)**

**X-linked dominance** was also accepted. Autosomal dominance was accepted; however, it is not technically correct as X-linked inheritance is possible.

b. Considering complete dominance, only a mating between a heterozygous male and a heterozygous female could generate some white-eyed progeny. 2/3 of red-eyed F2 male beetles are heterozygous (1/3 are homozygous dominant), and 2/3 of red-eyed F2 female beetles are heterozygous. So the probability of the required mating is (2/3)*(2/3) = **4/9** or **0.44** **(1 point)**

If you wrote X-linked recessive, you must cross a red eyed male with a heterozygous female. The probability of a red eyed male is 1/2, while the probability of a heterozygote female is 1/2, so the probability of the required mating is **1/4**.

8. The frequency of homozygotes for allele 1 is 9%. That is $p^2$ (p = frequency of allele 1), so p = 0.3. Frequency of allele 1 + allele 2 is 96% or 0.96, therefore frequency of allele 2 = 0.66 and the frequency of homozygotes for allele 2 is $(0.6)^2$ = **43.56%**

   **(1 point)**

9. There is 1 allele of the X-linked gene in a male diploid cell (G1 is before DNA is replicated), i.e. 1 copy per cell, so you need **1 picomole of cells** or $10^{-12} * 6\times10^{23}$ = $\mathbf{6\times10^{11}}$. In this question, only the copy number matters, not the size of the gene or the genome. **(1 point, no partial credit)**