

7.03 Exam 1

Name: _____

TA (circle one):

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Section time: _____

Exam starts at 11:05 and ends at 11:55

There are eight pages including this cover page.

Please write your name on each page.

Please...

- Look over the entire exam so you don't spend too much time on hard questions leaving easy questions unanswered.
- Check your answers to make sure that they make sense.
- To help us give partial credit, show your work and state any assumptions that you make.

Question 1 26 points

Question 2 36 points

Question 3 38 points

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1. Consider the following autosomal *Drosophila* traits caused by recessive alleles: bent wings (**bn**⁻), short legs (**sh**⁻), and orange eyes (**or**⁻). You cross two true breeding lines to produce F1 flies, all of which have the wild type phenotype (strait wings, long legs, and red eyes). F1 females are then mated to triply homozygous males with bent wings, short legs, and orange eyes. Among 100 progeny from this cross you observe the following phenotypes:

<u>Phenotype</u>	<u>Number</u>
strait wings, long legs, and red eyes	10
bent wings, short legs, and orange eyes	14
strait wings, short legs, and red eyes	26
bent wings, long legs, and orange eyes	30
strait wings, long legs, and orange eyes	8
bent wings, short legs, and red eyes	6
strait wings, short legs, and orange eyes	2
bent wings, long legs, and red eyes	4

(a 6 points) What were the genotypes of the two true breeding parental lines that were crossed?

We can determine the genotypes of the parental flies by looking at the two highest classes of progeny in the F2. These classes are the Parental Classes. Based on these classes, we can determine that the original true-breeding strains were

$bn^{-}/bn^{-} \ sh^{+}/sh^{+} \ or^{-}/or^{-}$ and $bn^{+}/bn^{+} \ sh^{-}/sh^{-} \ or^{+}/or^{+}$

(b 12 points) Draw a genetic map showing the order and relevant distances in cM of the **bn**, **sh**, and **or** markers.

There are three possible orders for these genes along the chromosome.

or bn sh or sh bn sh or bn

Since we know what the parental genotypes are, we can draw the three possible F1 chromosome arrangements.

$$\begin{array}{ccc} \frac{or^- \quad bn^- \quad sh^+}{or^+ \quad bn^+ \quad sh^-} & \frac{or^- \quad sh^+ \quad bn^-}{or^+ \quad sh^- \quad bn^+} & \frac{sh^+ \quad or^- \quad bn^-}{sh^- \quad or^+ \quad bn^+} \end{array}$$

The smallest class of F2 progeny represents the Double-Crossover class. These progeny resulted from a double crossover event during meiosis of the F1 parent.

Double Crossover Class 1 Straight wings, short legs, orange eyes
 Double Crossover Class 2 Bent wings, long legs, red eyes

Only the following order can generate these classes via a double crossover event.

$$\begin{array}{ccc} \frac{sh^+ \quad or^- \quad bn^-}{sh^- \quad or^+ \quad bn^+} & & \frac{sh^+ \quad or^+ \quad bn^-}{sh^- \quad or^- \quad bn^+} \end{array}$$

To calculate the distance between each of the markers we must add up the total number of recombinant progeny for that interval and divide by the total number of progeny.

The distance between sh and or is:

$$(10 + 14 + 4 + 2) / 100 \times 100 = 30 \text{ cM}$$

The distance between or and bn is:

$$(8 + 6 + 4 + 2) / 100 \times 100 = 20 \text{ cM}$$

The cumulative map distance between sh and bn is 50 cM

HOWEVER, if you were to calculate the distance between sh and bn by ignoring the "or" locus, you would end up with:

$$(10 + 14 + 8 + 6) / 100 \times 100 = 38 \text{ cM}$$

The correct map should be the following:

$$sh \text{ } \underline{\hspace{1cm}} \text{ } 30cM \text{ } \underline{\hspace{1cm}} \text{ } or \text{ } \underline{\hspace{1cm}} \text{ } 20cM \text{ } \underline{\hspace{1cm}} \text{ } bn$$

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(c 8 points) A colleague calls to tell you she plans to carry out the following two-factor cross. A true breeding line with bent wings will be crossed to a true breeding line with short legs (unless specified other traits appear normal). F1 flies will then be crossed to a true breeding strain with bent wings and short legs. Your colleague wants to know what proportion of the progeny from this cross will have bent wings and short legs. What would you tell her?

It is very important to realize that this question is dealing with a two-factor cross and not a three-factor cross. Although we have shown the cumulative map distance between "bn" and "sh" is 50 cM via a three-factor cross, the observable map distance in a two-factor cross will only be 38 cM.

This means that 38% of the F2 progeny will be recombinant progeny. One half of these progeny will inherit the sh- bn- chromosome.

Therefore, $38 / 2 = 19\%$ of the F2 progeny will have short wings and bent legs.

F1

$$\begin{array}{c} \text{sh}^+ \\ \hline \text{sh}^- \end{array} \begin{array}{c} \text{bn}^- \\ \hline \text{bn}^+ \end{array} \quad \times \quad \begin{array}{c} \text{sh}^- \\ \hline \text{sh}^- \end{array} \begin{array}{c} \text{bn}^- \\ \hline \text{bn}^- \end{array}$$

F2

$$\begin{array}{c} \text{sh}^+ \\ \hline \text{sh}^- \end{array} \begin{array}{c} \text{bn}^- \\ \hline \text{bn}^- \end{array} \quad 62 / 2 = 31\% \text{ Bent wings}$$

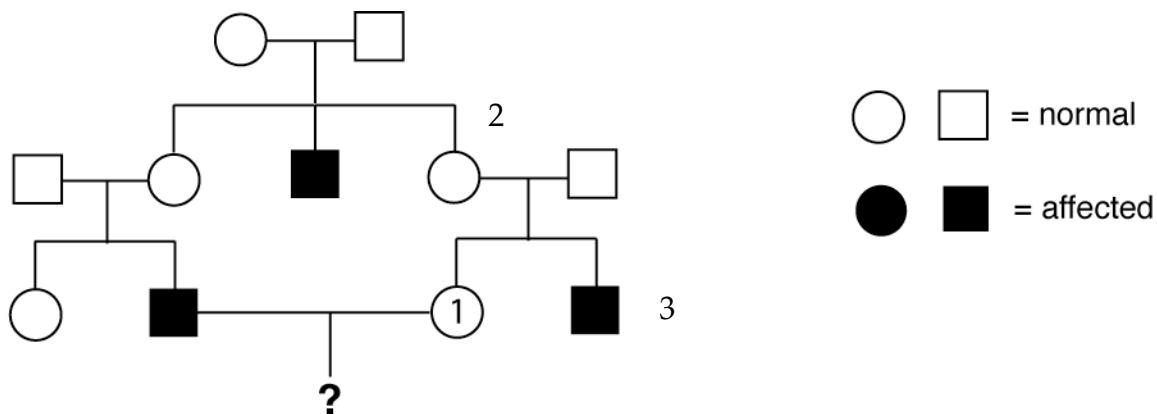
$$\begin{array}{c} \text{sh}^- \\ \hline \text{sh}^- \end{array} \begin{array}{c} \text{bn}^+ \\ \hline \text{bn}^- \end{array} \quad 62 / 2 = 31\% \text{ Short legs}$$

$$\begin{array}{c} \text{sh}^+ \\ \hline \text{sh}^- \end{array} \begin{array}{c} \text{bn}^+ \\ \hline \text{bn}^- \end{array} \quad 38 / 2 = 19\% \text{ Wild-type}$$

$$\begin{array}{c} \text{sh}^- \\ \hline \text{sh}^- \end{array} \begin{array}{c} \text{bn}^- \\ \hline \text{bn}^- \end{array} \quad 38 / 2 = 19\% \text{ Short legs and Bent wings}$$

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2. The pedigree shows inheritance of an X-linked recessive trait. (Assume the trait is completely penetrant).



(a 4 pts.) What is the probability that the female designated **1** is a carrier for the trait?

Given that male #3 is affected, female #2 must be a carrier. As a result, the probability that female #1 is a carrier is $\frac{1}{2}$.

(b 6 pts.) If the child indicated by **?** is a boy, what is the probability he will be affected by the trait?

$$P(\text{boy ? affected}) = P(\text{\#1 is a carrier}) \times P(\text{boy ? receives } X^{\text{rec}} \text{ from mom})$$

$$= \frac{1}{2} \times \frac{1}{2} = \frac{1}{4}$$

(c 6 pts.) If the child indicated by **?** is a girl, what is the probability she will be affected by the trait?

$$P(\text{girl ? affected}) = P(\text{\#1 is a carrier}) \times P(\text{girl ? receives } X^{\text{rec}} \text{ from mom}) \times P(\text{girl ? receives } X^{\text{rec}} \text{ from dad})$$

$$= \frac{1}{2} \times \frac{1}{2} \times 1 = 1/4$$

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(d 8 pts.) If the child indicated by ? is affected by the trait, what is the probability that the couple's next child will be affected by the trait?

If the child indicated by ? is affected, then female #1 must be a carrier. Thus, the probability that the next child is affected is $\frac{1}{2}$.

(e 12 pts.) If the child indicated by ? is not affected by the trait, calculate the new probability that the female designated **1** is a carrier for the trait.

Bayes Theorem can be used to compute this conditional probability.

X = #1 is a carrier

Y = the child isn't affected

$$P(Y|X) = \frac{1}{2}$$

$$P(X) = \frac{1}{2}$$

$$P(Y|\text{not } X) = 1$$

$$P(\text{not } X) = 1/2$$

$$P(X|Y) = \frac{p(Y|X) \cdot p(X)}{[p(Y|X) \cdot p(X) + p(Y|\text{not } X) \cdot p(\text{not } X)]}$$

$$P(X|Y) = \frac{(1/2 \times 1/2)}{[(1/2 \times 1/2) + (1 \times 1/2)]}$$

$$P(X|Y) = 1/3$$

After the birth of a child without the trait, the probability that female #1 is a carrier is reduced from 50% to 33.33%.

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3. You have isolated two different yeast mutants called *cys1*⁻ and *cys2*⁻ that cannot synthesize the amino acid cysteine and therefore require cysteine added to the medium for growth (i.e. they are Cys⁻).

(a 4 points) You mate a *cys1*⁻ mutant to a *cys2*⁻ mutant. The resulting diploids don't require cysteine (i.e. they are Cys⁺). What does this tell you about the *cys1*⁻ and *cys2*⁻ mutations?

This result is indicative of complementation between *cys1* and *cys2*. Therefore, the mutations are in different genes.

Next, you sporulate the diploid from part (a). Among the 50 tetrads analyzed three different tetrad types are found

Type:	4 Cys ⁻	3 Cys ⁻ : 1 Cys ⁺	2 Cys ⁻ : 2 Cys ⁺
Number:	39	10	1

(b 6 points) Say that you want a *cys1*⁻*cys2*⁻ double mutant. What is the easiest way to obtain such a mutant without further analysis?

The double crossover event creating the NPD tetrad resulted in the production of two Cys⁻ and two Cys⁺ spores. The two Cys⁻ spores (*cys1*⁻*cys2*⁻) are double mutants.

(c 6 points) You choose one of the tetrads for further analysis and the four spores have the following properties: Spore 1 = MAT α Cys⁺, Spore 2 = MAT α Cys⁻, Spore 3 = MAT α Cys⁻, and Spore 4 = MAT α Cys⁻. You carry out the matings that are possible and find that the diploid produced by mating Spore 2 to Spore 3 is Cys⁻, while the diploid produced by mating Spore 2 to Spore 4 is Cys⁺. Which spore is the double mutant? Explain your reasoning.

Spore 3 is the double mutant. The cross between spore 2 (Cys⁻) and spore 4 (Cys⁻) generated a Cys⁺ diploid. This is complementation and indicates that spores 2 and 4 are single mutants carrying mutations in different genes. Since we know spore 1 is Cys⁺, it is not a mutant. This leaves spore 3 as the double mutant.

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(d 6 points) Given the number of tetrads of each type, what is the distance between the *cys1⁻* and *cys2⁻* mutations?

$$\text{Map Distance (cM)} = 100 \times \frac{\text{TT} + 6 \text{ (NPD)}}{2 \sum \text{TETRADS}}$$

$$= 100 \times [16 / 100]$$

$$= 16 \text{ cM}$$

You have isolated a mutation that you call *cysX⁻* that activates an alternative pathway for cysteine synthesis. A *cysX⁻* mutation on its own is Cys⁺, and when a *cysX⁻* mutation is combined with a *cys1⁻* mutation, the double mutant is Cys⁺.

(e 8 points) Describe the cross you would perform and the interpretation of the outcome that you would use to determine whether *cysX⁻* is dominant or recessive?

cysX⁻ cys1⁻ (haploid) × *cysX⁺ cys1⁻* (haploid) > *cysX⁻ cysX⁺; cys1⁻ cys1⁻* (diploid)

If diploid is *cys⁺*, then *cysX⁻* is dominant to *cysX⁺*

If diploid is *cys⁻*, then *cysX⁻* is recessive to *cysX⁺*

(f 8 points) Say that *cysX⁻* is 5 cM away from *cys1⁻*. In a cross of a MAT^a *cysX⁻* mutant to a MAT^α *cys1⁻* mutant what types of tetrads (in terms of the proportion of Cys⁻ : Cys⁺) would you expect to find and how many of each type would you expect from a total of 50 tetrads?

PD(45)	NPD(0)	TT(5)
<i>cysX⁻ cys1⁺</i>	<i>cysX⁻ cys1⁻</i>	<i>cysX⁻ cys1⁻</i>
<i>cysX⁻ cys1⁺</i>	<i>cysX⁻ cys1⁻</i>	<i>cysX⁻ cys1⁺</i>
<i>cysX⁺ cys1⁻</i>	<i>cysX⁺ cys1⁺</i>	<i>cysX⁺ cys1⁺</i>
<i>cysX⁺ cys1⁻</i>	<i>cysX⁺ cys1⁺</i>	<i>cysX⁺ cys1⁻</i>
2 <i>cys⁺</i> : 2 <i>cys⁻</i>	4 <i>cys⁺</i>	3 <i>cys⁺</i> : 1 <i>cys⁻</i>

Out of 50 tetrads, 0 NPD would be expected. The frequency of a double crossover is .05 × .05 = 0.0025. Of these double crossovers, only ¼ represent NPDs. Thus, only one in 1600 tetrads would be expected to be NPD.