

Exam Questions from Exam 1 – Basic Genetic Tests, Setting up and Analyzing Crosses, and Genetic Mapping

1. You are studying three autosomal recessive mutations in the fruit fly *Drosophila melanogaster*. Flies that are homozygous for the hb^- mutation are “humpbacked” (wild-type flies are straight-backed). Flies that are homozygous for the bl^- mutation are “blistery-winged” (wild-type flies are smooth-winged). Flies that are homozygous for the st^- mutation are “stubby-legged” (wild-type flies are long-legged).

You mate flies from two true-breeding strains, and the resulting F1 flies are all straight-backed, smooth-winged, and long-legged. F1 females are then mated to males that are humpbacked, blistery-winged, and stubby-legged. In the F2 generation, among 1000 progeny resulting from this cross, you observe the following phenotypes:

<u>Phenotype</u>	<u>Number</u>
humpbacked, blistery-winged, and stubby-legged	(26 flies)
humpbacked, blistery-winged, and long-legged	(455 flies)
humpbacked, smooth-winged, and long-legged	(24 flies)
straight-backed, blistery-winged, and stubby-legged	(27 flies)
straight-backed, blistery-winged, and long-legged	(4 flies)
straight-backed, smooth-winged, and stubby-legged	(442 flies)
straight-backed, smooth-winged, and long-legged	(22 flies)

(a) The male flies that were bred to the F1 generation in order to produce the F2 generation were humpbacked, blistery-winged, and stubby-legged. On each of their chromosomes, they have the alleles $hb^- bl^- st^-$. Using this notation, **state the genotype** of each of the two true-breeding parental strains (i.e. the two strains in the **P generation**).

Genotype of one parental strain:

Genotype of the other parental strain:

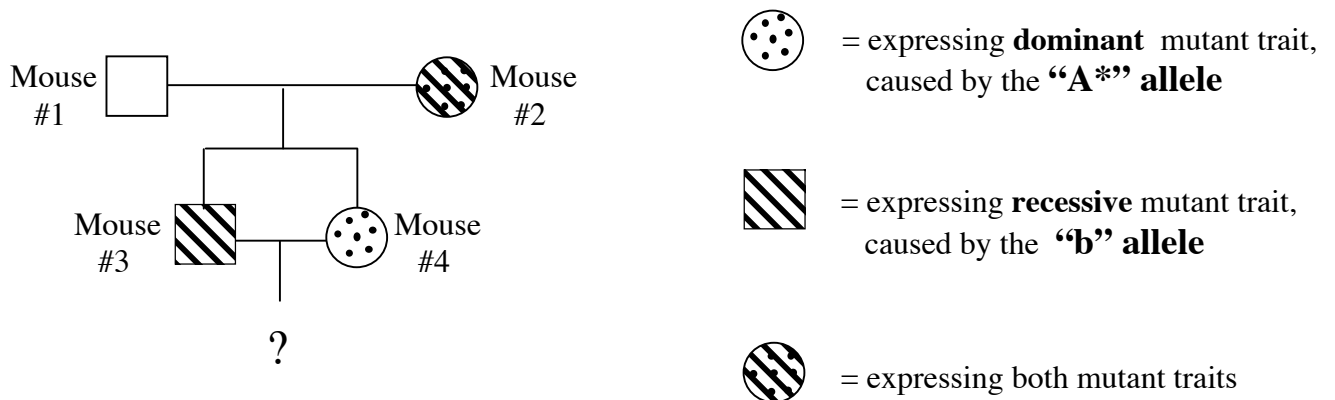
(b) How many flies are found in the class that is the reciprocal class of the humpbacked, blister-winged, and stubby-legged flies?

(c) What is the genetic distance between the **hb** and **bl** loci? (Label your answer with the proper units.)

(d) What is the genetic distance between the **bl** and **st** loci? (Label your answer with the proper units.)

(e) Draw a genetic map showing the correct order of the **hb**, **bl**, and **st** loci.

2. The following mouse pedigree shows the segregation of two different mutant traits. The mutant trait indicated by the dots is dominant, whereas the mutant trait indicated by the stripes is recessive. Assume 100% penetrance and no new mutations. (Squares = males, circles = females.)

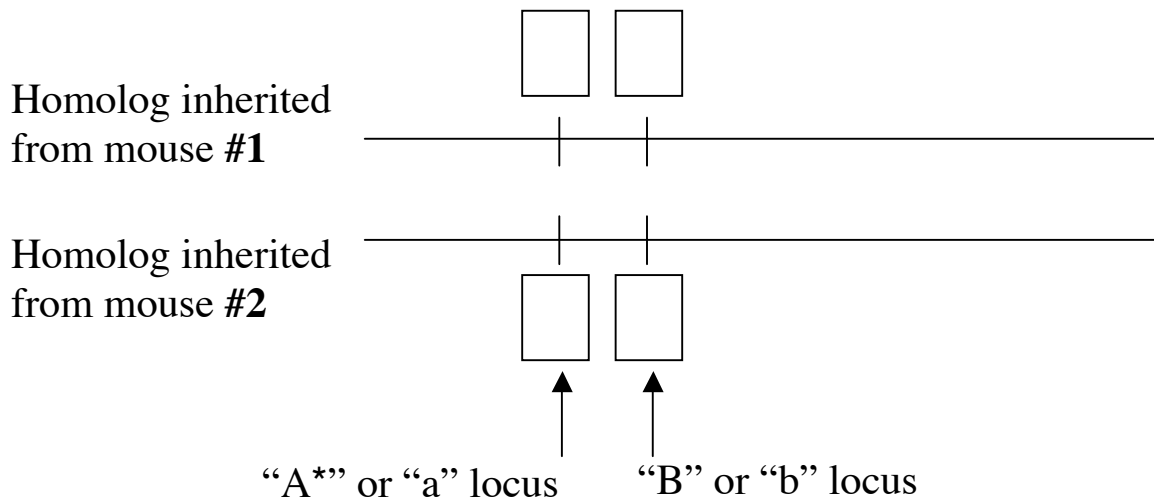


(a) Assuming that both mutant traits are due to linked autosomal genes that are 6 cM apart, **fill in** the following chart using the allele notation indicated by the key above. Blocks in the chart that cannot be filled in conclusively should be indicated as *“inconclusive.”*

NOTE: One line of the chart is already filled in correctly for you.

	Number of “A*” alleles	Number of “a” alleles	Number of “B” alleles	Number of “b” alleles
Mouse #1				
Mouse #2				
Mouse #3	0	2	0	2
Mouse #4				

(b) Assuming that both mutant traits are due to linked autosomal genes that are 6 cM apart, fill in the boxes with the alleles possessed by mouse #4 on each of the two homologs of this autosome that are depicted in the diagram below.



(c) Assuming that both mutant traits are due to linked autosomal genes that are 6 cM apart, what is the probability that the mouse indicated by a question mark will show **both** mutant traits (the trait encoded by “A*” **and** the trait encoded by “b”)?

(d) Assuming that the **recessive** mutant trait is caused by a gene on an autosome and the **dominant** mutant trait is caused by a gene on the X chromosome, **fill in** the following chart using the allele notation indicated by the key above. Blocks in the chart that cannot be filled in conclusively should be indicated as “*inconclusive*.”

	X-linked		autosomal	
	Number of “A*” alleles	Number of “a” alleles	Number of “B” alleles	Number of “b” alleles
Mouse #1				
Mouse #2				
Mouse #3				
Mouse #4				

(e) Assuming that the **recessive** mutant trait is caused by a gene on an autosome and the **dominant** mutant trait is caused by a gene on the X chromosome, what is the probability that the mouse indicated by a question mark will show **only** the recessive mutant trait **assuming that the mouse is born female**?

3. You are working with a mutant strain of yeast that is dark tan (wild-type yeast are white). The “dark tan” phenotype of the haploid cells you are working with is caused by two different mutations in the same strain. The two mutations are designated $drk1^-$ and $drk2^-$.

(a) Mating of the $drk1^- drk2^-$ double mutant to **wild-type** yeast produces diploids that are white. Sporulation of these diploids yields 50 tetrads. 4 of these tetrads (called “Type One”) contain four light tan spores. 37 of these tetrads (called “Type Two”) contain two dark tan spores and two white spores. 9 of these tetrads (called “Type Three”) contain one dark tan spore, two light tan spores, and one white spore. Categorize **each** of the tetrad types as parental ditype (PD), tetratype (TT), or nonparental ditype (NPD).

(b) Are the $drk1^-$ and $drk2^-$ mutations linked? **If so**, give the distance between them. (Label your answer with the proper units.)

(c) In yeast, 1 cM of genetic distance corresponds to 3,500 base pairs of physical distance. An average yeast gene is about 1,400 base pairs long, and the longest yeast gene is 14,700 base pairs. Keeping this information in mind, you select a “Type Three” tetrad from part **(a)** and mate the two light tan spores from that tetrad to each other. Can you deduce the color of the resulting diploids? **If so**, what color would the diploids be?

Next you isolate a mutant strain of yeast that cannot grow on medium lacking leucine. This strain contains a single mutation you call $leu1^-$. The $leu1^-$ mutation is near to $drk1^-$ on the same chromosome. When the $leu1^-$ mutant is mated to wild-type yeast, the resulting diploids cannot grow on medium lacking leucine.

(d) You mate $leu1^-$ yeast to $drk1^-$ yeast and sporulate the resulting diploid. You grow the resulting spores on medium containing leucine. You then test for growth on medium lacking leucine. It is apparent that you have isolated only two types of tetrads, 10 tetrads of Type A and 10 tetrads of Type B. On medium lacking leucine, only two spores from each Type A tetrad can grow; both are light tan in color. Complete the chart below so as to indicate: **How many** spores from each Type B tetrad can grow on medium lacking leucine, **and what color** is each spore that can grow?

	# of spores that can grow on medium lacking leucine	color of each spore that can grow on medium lacking leucine
Type A tetrad	2	both are light tan
Type B tetrad		

(e) What are the genotypes at the *leu1* and *drk1* loci of each of the two light tan spores from the Type A tetrads that grew on medium lacking leucine?

Genotype of one light tan spore:

Genotype of the other light tan spore:

4. Wild-type humbugs have brown bodies and brown eyes, and are not spotted. You have isolated mutations in three new autosomal humbug genes. The mutation **sp** gives a dominant phenotype of spotted bodies. The mutation **gr** gives a recessive phenotype of green bodies. The mutation **bl** gives the recessive phenotype of black eyes.

You cross two true-breeding mutant strains to produce F1 females heterozygous for **sp**, **gr**, and **bl**. These F1 females are then test-crossed to true-breeding black-eyed, green-bodied non-spotted males. The phenotypes of 3000 progeny are scored as shown below:

<u>Phenotypes</u>	<u>Number of flies in each class</u>		
not spotted	black eyes	brown bodies	4
not spotted	brown eyes	green bodies	1347
spotted bodies	black eyes	green bodies	53
spotted bodies	black eyes	brown bodies	1390
spotted bodies	brown eyes	green bodies	2
not spotted	black eyes	green bodies	74
not spotted	brown eyes	brown bodies	61
spotted bodies	brown eyes	brown bodies	70

(a) What are the genotypes of the two true-breeding parents of the F1 females?

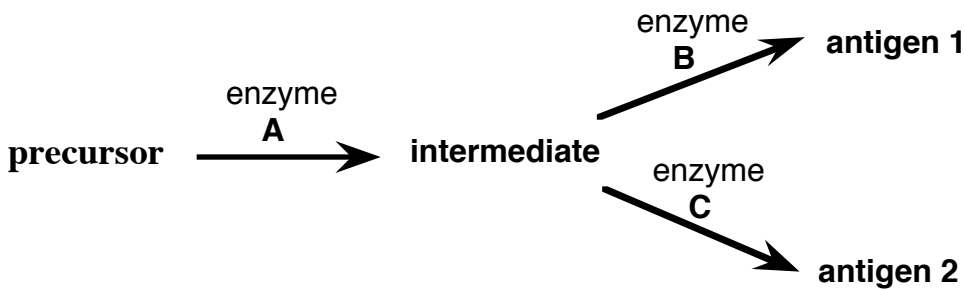
(b) Draw a map showing the order and all pair-wise distances between the **sp**, **gr**, and **bl** genes.

A mutation called eyeless (**ey**) is identified, which gives the autosomal dominant phenotype of having no eyes. You want to map **ey** relative to **bl**, but your colleague claims this can't be done since you obviously can't score the presence of black or brown eyes in an eyeless bug. You don't agree that it can't be done, and you cross a true-breeding single mutant eyeless bug to a true-breeding black-eyed bug. An F1 female that results is then crossed to a true-breeding black-eyed male. The following phenotypes are observed in 100 progeny:

eyeless	51
black-eyed	39
brown-eyed	10

(c) What is the map distance between **bl** and **ey**?

5. Consider two different antigen molecules produced on the surface of blood cells of wild-type mice, according to the biosynthetic pathway below.



Mice homozygous for alleles that block the production of enzyme A (genotype *a/a*) do not make either antigen 1 or antigen 2. Mice homozygous for defects in the gene encoding enzyme B (genotype *b/b*) do not make antigen 1. Mice homozygous for defects in the gene encoding enzyme C (genotype *c/c*) do not make antigen 2. All three of these phenotypes of absences of antigen are autosomal recessive phenotypes.

(a) Two different true-breeding strains of mice have been isolated that do not make either antigen 1 or antigen 2. When an individual from one strain is crossed with an individual from the other strain, all of the F1 mice produce both antigens. Write out the genotypes for both strains. (Use "A," "B," and "C" to designate the wild-type alleles and "a," "b," and "c" to designate the defective alleles of the three genes that encode these enzymes.) Assume that these three genes are unlinked.

(b) Two of the F1 mice are crossed to one another. The possible phenotypes for the F2 progeny are shown below. What proportion of the F2 will be represented by each phenotype on average?

Fraction of F2

antigen 1⁺, antigen 2⁺

antigen 1⁺, antigen 2⁻

antigen 1⁻, antigen 2⁻

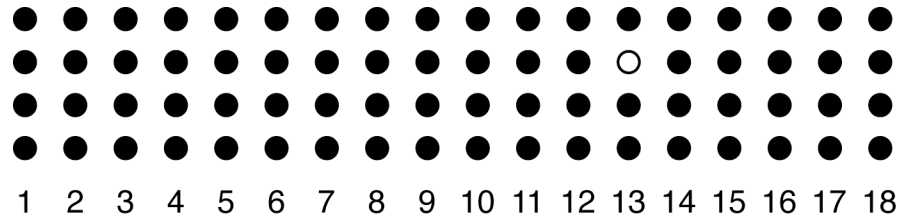
antigen 1⁻, antigen 2⁺

(c) Among the F2 progeny, there will be mice of several different genotypes that are phenotypically antigen 1⁻ and antigen 2⁻. Suppose you wanted to use a test cross in order to test whether a given F2 mouse that does not express either antigen is defective in production of enzyme A. What genotype would you choose for a mouse to be used for such a test cross of the F2 mouse? Describe the possible outcomes of this cross and how you would interpret them.

6. Some yeast mutants with defects in enzymes in the pathway for adenine biosynthesis form red colonies because of the accumulation of an intermediate in the pathway, which is a red pigment.

(a) You have isolated two different red-colored mutants in haploid yeast strains of different mating types, which you call *ade1*⁻ and *ade2*⁻. When either the *ade1*⁻ or *ade2*⁻ haploid mutant is mated to wild-type haploid yeast, the resulting diploid forms white colonies like those of wild-type yeast. When the *ade1*⁻ haploid mutant is mated to the *ade2*⁻ haploid mutant, the resulting diploid makes red colonies. From these observations, describe as much as you can about the *ade1*⁻ and *ade2*⁻ mutations and the relationship between them.

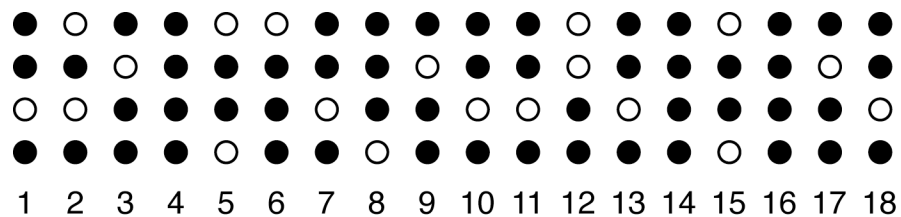
(b) Next, you induce sporulation of the diploid that was formed by mating the *ade1⁻* and *ade2⁻* haploid strains. From the resulting 18 tetrads shown below, you determine that only one spore clone is white, and the rest are red.



What does this result tell you about the distance between the *ade1* and *ade2* loci?

(c) Next, you isolate a new red-colored mutant, which you call *ade3⁻*. When the *ade3⁻* haploid mutant is mated to wild-type haploid yeast, the resulting diploid is red. You mate the *ade3⁻* haploid mutant to an *ade1⁻* haploid mutant, and the resulting diploid is red also. What do these results tell you about the *ade3⁻* mutant and the relationship between the *ade3⁻* and *ade1⁻* mutations?

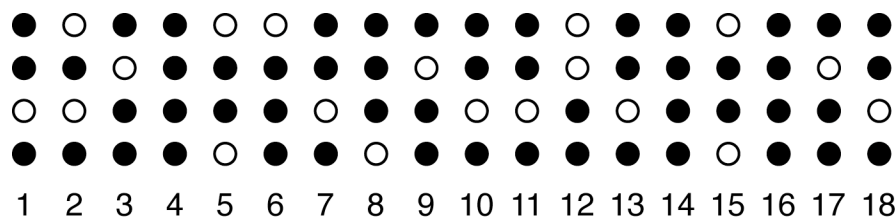
(d) When you induce sporulation of the diploid that was formed by mating the *ade3⁻* and *ade1⁻* haploid strains, you obtain the results shown below:



Of the 18 dissected tetrads shown, how many tetrads of each type (PD, NPD or TT) are there?

(e) What do the results from this tetrad analysis tell you about the relationship between the *ade3*⁻ and *ade1*⁻ mutations? Mention in your answer whether these mutations can be in the same gene.

(f) Suppose that you wanted to do some experiments with an *ade3*⁻*ade1*⁻ double mutant haploid yeast strain. Below is the same image from above of the tetrads formed from inducing sporulation of the diploid formed by mating *ade3*⁻ and *ade1*⁻ haploid mutants. On this image, **circle each spore clone** that you can be sure is double mutant haploid strain, without any further testing.



(g) You mate an *ade3*⁻ haploid mutant to an *ade2*⁻ haploid mutant. You then induce sporulation of the resulting diploid, and dissect 18 tetrads. How many Tetratype (TT) tetrads would you expect to see?

7. You are studying the genetics of a new insect species and have identified three different autosomal recessive traits -- apricot eyes, black body, and curly wings. These phenotypes are caused by alleles in three different genes -- **a**, **b**, and **c** respectively. Wild-type flies have red eyes, brown body, and straight wings, and are genotypically **a+**, **b+**, and **c+**. Two different true-breeding lines are crossed and the F₁ progeny all appear as wild-type. These F₁ progeny are then crossed to individuals from a true-breeding line that has all three recessive traits, and 100 progeny from this cross are analyzed. The phenotypes and numbers are as follows:

<u>Phenotype</u>	<u>Number</u>
wild-type (red eyes, brown body, straight wings)	3
apricot eyes, black body, curly wings	7
apricot eyes, brown body, curly wings	34
red eyes, black body, straight wings	36
red eyes, black body, curly wings	8
apricot eyes, brown body, straight wings	12

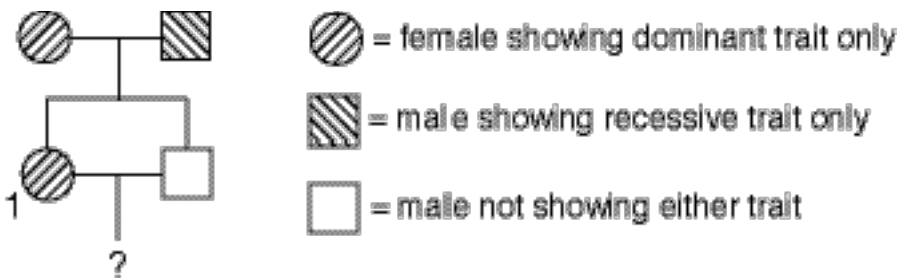
(a) What are the genotypes of the two parental true-breeding lines? Use the notation in the introduction to this question.

(b) Why are there only six phenotypic classes, rather than eight?

(c) Give as much information as you can about the chromosomal positions of the three loci **a**, **b**, and **c**. Include in your answer any relevant map distances in cM.

(d) Given the map distances in part (c), if F_1 insects are crossed to one another, what frequency of the resulting F_2 progeny would have all three recessive traits?

8. The following mouse pedigree shows the segregation of both a dominant and a recessive trait. (Assume all phenotypes are completely penetrant and that no new mutations arise).



(a) What is the genotype of mouse 1 if the two traits are X-linked? For your answer use X^D to designate the allele for the dominant trait (with X^d representing the corresponding wild-type allele) and X^r to designate the allele for the recessive trait (with X^R representing the corresponding wild-type allele).

(b) If the genes for both traits are 30 cM apart on the X chromosome, what is the probability that a progeny mouse indicated by the ? will show both traits if she is born female?

(c) If the genes for both traits are 30 cM apart on the X chromosome, what is the probability that a progeny mouse indicated by the ? will show both traits if he is born male?

(d) What is the genotype of mouse 1 if the two traits are autosomal? For your answer use **D** to designate the allele for the dominant trait (with **d** representing the corresponding wild-type allele) and **r** to designate the allele for the recessive trait (with **R** representing the corresponding wild-type allele).

(e) If the genes for both traits are 30 cM apart on the same autosome, what is the probability that a progeny mouse indicated by the ? will show both traits?

9. You have isolated two different mutants of phage λ that make fuzzy plaques, which you name **fz-1⁻** and **fz-2⁻**. These two mutations are in a single gene, the “**fz**” gene. You cross **fz-1⁻** phage with **fz-2⁻** phage by coinfecting *E. coli* with phage of both types. You plate out the resulting phage lysate, and examine 1000 plaques that result from the cross. 15 of these plaques are NOT fuzzy.

(a) What is the distance between the **fz-1** and the **fz-2** loci in map units?

Mutations in the **cl** gene of phage λ give clear plaques, whereas wild-type phage have turbid plaques.

(b) You cross a **cl⁻ fz-1⁻** double mutant to a **fz-2⁻** mutant by coinfecting *E. coli* with both types of mutant phage. You plate the resulting lysate and examine a total of 1000 plaques. Among the 15 plaques that are NOT fuzzy, 12 are clear and 3 are turbid. Draw a genetic map showing the order of the **cl**, **fz-1**, and **fz-2** mutations.

10. You have obtained a strain of *Drosophila*, which is homozygous for the cn^- mutation (and thus has cinnabar colored eyes) and is homozygous for the $shi-1^-$ mutation (and thus becomes paralyzed at high temperature). You mate this strain to a true-breeding wild-type fly and obtain F1 flies, all of which have the wild type phenotype (red eyes, not paralyzed). F1 females are then mated to males of the starting strain (homozygous cn^- and $shi-1^-$). Among 100 progeny from this cross you observe the following phenotypes:

<u>Phenotype</u>	<u>Number</u>
wild-type (not paralyzed, red eyes)	44
paralyzed, cinnabar eyes	41
not paralyzed, cinnabar eyes	7
paralyzed, red eyes	8

(a) From this data, what is the distance between the **cn** and **shi** genes?

(b) You isolate a second allele of the *shibire* gene designated $shi-2^-$, which also causes the recessive phenotype of paralysis at high temperature. Flies from a true-breeding $shi-2^-$ strain are crossed to flies from the true-breeding cn^- , $shi-1^-$ strain described above.

What is the phenotype of the resulting F1 female flies?

F1 females are then mated to males from the true-breeding cn^- , $shi-1^-$ strain. You collect 10,000 progeny from this cross and note that, although almost all the flies are paralyzed at high temperature, there are 10 that are not paralyzed.

(c) What is the distance between the $shi-1$ and $shi-2$ loci?

(d) Among the 10 progeny flies that are not paralyzed that result from the cross described in part **(b)**, 8 have cinnabar eyes and 2 have normal red eyes. On the basis of this information as well as the results from parts **(a)** and **(b)**, draw a genetic map showing the order of the cn , $shi-1$, and $shi-2$ loci.

11. You have isolated a new His⁻ yeast mutant.

(a) When you mate this haploid mutant to a wild-type haploid yeast strain (that is His⁺), you find that the resulting diploids are His⁺. What does this tell you about the mutant that you isolated?

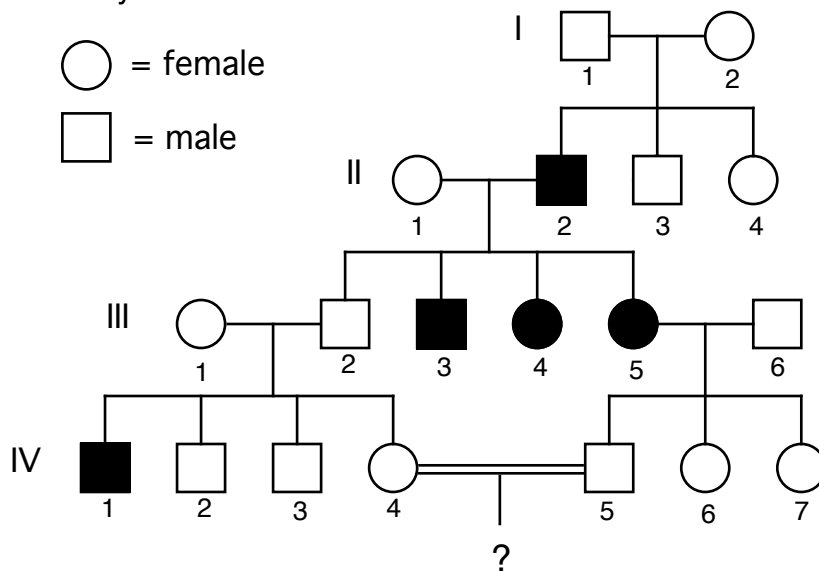
(b) When you induce sporulation in the His⁺ diploid from part (a), you find that tetrads of three types are produced. From a total of 100 tetrads, the following tetrad types are seen:

Type:	2 His ⁻ : 2 His ⁺ spores	3 His ⁻ : 1 His ⁺ spores	4 His ⁻ spores
Number:	65	30	5

What does this result tell you about the original His⁻ strain? Give any relevant genetic distances (in cM) that you can calculate.

(c) There are a total of 240 His⁻ spore clones in the 100 tetrads from part (b). If you picked two of these His⁻ clones (of opposite mating type) at random and mated them, what is the probability that the resulting diploid would be His⁺? (You may find it helpful to consider the genotypes of the His⁻ spores in each tetrad type).

12. In the following human pedigree, individuals exhibiting a **common** inherited allergy to milk are shown by shaded-in symbols, and unaffected individuals are shown by unshaded symbols.



(a) Assuming complete penetrance and no new mutations, what is the mode of inheritance of the milk allergy (your choices are: autosomal dominant, autosomal recessive, and X-linked recessive)?

(b) Give the genotypes of the following individuals, using **+** to indicate the allele that does not cause the allergy, and **m** to indicate the allele specifying the milk allergy. In ambiguous cases, indicate all possible genotypes.

<u>Genotype</u>	<u>Genotype</u>
II-1	III-2
II-2	III-5
II-3	

(c) If cousins **IV-4** and **IV-5** have a child together, what is the probability that the child will have the milk allergy? (Give separate probabilities for sons and daughters if their chances of acquiring the allergy differ.)

13. Wild-type yeast form white colonies. You have isolated two mutants that make red colonies that you call **red3** and **red4**.

(a) When a **red3** haploid mutant is mated to a **red4** haploid mutant of the opposite mating type, the resulting diploid makes white colonies. What does this observation tell us about **red3** and **red4**?

(b) When the diploids from part (a) are induced to sporulate, three types of tetrads are found. Type I have 4 red spores. Type II have 1 white spore and 3 red spores. Type III have 2 white spores and 2 red spores

Classify each tetrad type as PD, NPD or TT.

(c) When the number of each tetrad type is tallied, you find that the cross produces 30 Type I tetrads, 16 Type II tetrads, and 4 Type III tetrads.

Are the **red3** and **red4** loci linked? If so, how far apart are they in cM?

(d) One of the Type II tetrads from above is selected for further analysis and you designate the four spore clones **a**, **b**, **c**, and **d**. Clone **a** is white, whereas clones **b**, **c**, and **d** are red. Each clone is mated to either a **red3** haploid mutant or a **red4** haploid mutant, and the color of the resulting diploid is noted.

Clone **a** (white) x **red3** haploid → white diploid

x **red4** haploid → white diploid

Clone **b** (red) x **red3** haploid → red diploid

x **red4** haploid → white diploid

Clone **c** (red) x **red3** haploid → red diploid

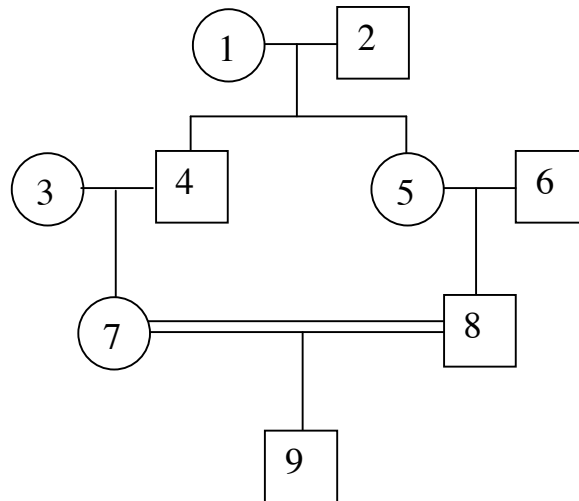
x **red4** haploid → red diploid

Clone **d** (red) x **red3** haploid → white diploid

x **red4** haploid → red diploid

Give the genotypes of each of the four spore clones with respect to **red3** and to **red4**.

14. Consider the following family pedigree where two first cousins have a son. Each individual is numbered for reference in this problem. PLEASE NOTE that, in this pedigree, the phenotypes of the family members are NOT denoted. They will be described in the text of the question instead. In this problem, assume complete penetrance and no new mutations.



(a) Say that female #1 exhibits a rare recessive X-linked trait, and that male #2 does not exhibit the trait. Because the trait is rare, assume that the individuals #3 and #6 neither have nor are carriers of the trait.

What is the probability that male #4 will have the trait?

What is the probability that female #5 will have the trait?

What is the probability that female #7 will have the trait?

What is the probability that male #8 will have the trait?

What is the probability that male #9 will have the trait?

(b) Now say that female #1 exhibits two different rare recessive X-linked traits that are each caused by a single gene. The two genes causing these two traits are found 10 cM apart on the X chromosome. (We will refer to the two traits as trait A and trait B). Male #2 does not exhibit either trait. Assume that individuals #3 and #6 neither have nor are carriers of either trait.

What is the probability that male #4 will have both traits?

What is the probability that male #8 will have both traits?

What is the probability that male #9 will have trait A only?

What is the probability that male #9 will have both traits?

What is the probability that male #9 will have neither trait?

15. Consider two autosomal recessive *Drosophila* mutant phenotypes -- curly-wings (caused by the **cr** allele) and humpback (caused by the **hb-1** allele). The **cr** and **hb** genes are on the same autosome. A wild-type female is crossed to a curly-winged, humpbacked male to produce F₁ flies that all look normal. An F₁ female is then crossed to a curly-winged humpbacked male and 100 progeny from this cross are examined.

<u>Phenotype</u>	<u>Number of flies</u>
Wild-type	41
curly-wings, straight back	12
straight wings, humpback	9
curly-wings, humpback	38

(a) What is the distance between the **cr** and the **hb-1** loci in cM?

Next you isolate a second mutation in a different gene (**hb-2**) that also causes the recessive phenotype of humpback. A female from a true-breeding **hb-2** strain is crossed to a male from a true breeding **cr, hb-1** strain. An F₁ female from this cross is then crossed to a true-breeding **cr hb-1 hb-2** male (who has curly wings and a humpback) and 500 progeny are examined.

<u>Phenotype</u>	<u>Number of flies</u>
straight-wings, straight back	5
straight wings, humpback	240
curly-wings, humpback	255

(b) What is the phenotype of the F₁ females in this cross?

(c) What is the distance between the **hb-1** and **hb-2** loci in cM?

(d) Draw a genetic map showing the relative order of the **cr**, **hb-1**, and **hb-2** loci.

16. A true-breeding mouse strain exhibits two different rare traits. When a male from this true-breeding strain is crossed to a wild-type female, all of the female F₁ progeny exhibit both traits, whereas all of the male F₁ progeny look wild-type. Assume complete penetrance and no new mutations.

(a) What is the mode of inheritance of the two traits?

(b) The male and female F₁ mice described above are crossed to one another to produce F₂ progeny. Of the male F₂ progeny, 40% have both traits (the rest of the F₂ males either appear wild-type or have only one trait or the other). What fraction of the female F₂ progeny would you expect to have both traits?

(c) What is the map distance (in cM) between the genes for the two traits?

17. You have isolated a yeast mutant that makes small colonies. When you mate your haploid mutant to a haploid wild-type strain, the resulting diploids look like wild-type.

(a) What does this observation tell you about your mutant?

(b) When the diploids from part **(a)** are induced to sporulate, all of the tetrads appear to be PDs. What does this observation tell us about your mutant?

(c) What is the phenotype of each of the four spores from a PD tetrad described in part **(b)**?

(d) You isolate a second haploid mutant that also makes small colonies. When a haploid of one small mutant is mated to a haploid of the other small mutant, the resulting diploids appear normal. What is the relationship between the two “small” mutations?

When the diploids from part **(d)** are induced to sporulate, three types of tetrads are found.

Type I have 4 small spores

Type II have 1 normal and 3 small spores

Type III have 2 normal and 2 small spores

The cross produces 24 type I tetrads, 24 type II tetrads, and 2 type III tetrads.

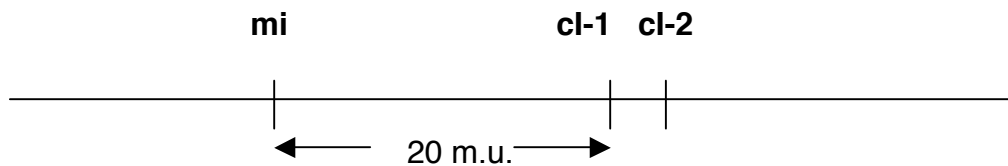
(e) What is the map distance between the two “small” loci?

(f) Give your best estimate for the number of tetrads (out of 50 total) described in part **(d)** that resulted from two crossovers in the interval between the two “small” loci.

18. You have isolated two different mutants of phage lambda in the repressor gene (**cl**); these mutations cause clear plaques rather than the normal turbid plaques. These mutants are called **cl-1⁻** and **cl-2⁻**. You cross **cl-1⁻** phage with **cl-2⁻** phage by coinfecting *E. coli* with phage of both types. Of 1000 plaques that result from the cross, 980 plaques are clear (whereas the rest are turbid).

(a) What is the distance between the **cl-1** and the **cl-2** loci in map units?



Phage mutants that are **mi⁻** are easily detected because they form small plaques. The distance between the **mi** gene and the **cl** gene is about 20 map units. Assume that the genetic order of the loci is as follows:



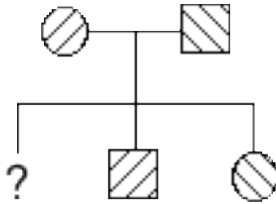
(b) For a cross of a **mi⁻ cl-1⁻** double mutant to a **cl-2⁻** mutant, a total of 1000 plaques are examined. In the table below, fill in the expected number of plaques of each phenotypic type.

Phenotype	# of Plaques in this class	Genotype(s) of Plaques in this class
Clear, large		
Clear, small		
Turbid, large		
Turbid, small		

19. The genes for two rare human autosomal dominant traits are 10 cM apart (as determined by meiosis in females). In the following pedigrees the traits are indicated as follows. Assume no new mutations arise and complete penetrance in this problem.

 = individual with trait 1
  = individual with trait 2
  = individual with trait 1 and trait 2

(a) For each of the pedigrees shown below, calculate the probability that the individual designated by “?” will have either dominant trait 1, dominant trait 2, or both traits.



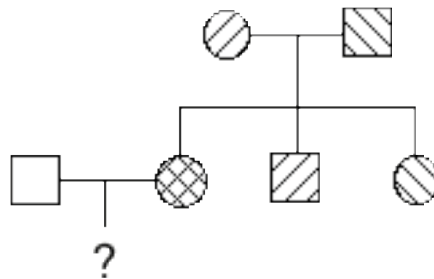
Probability

Dominant trait 1 only

Dominant trait 2 only

Both dominant trait 1 and trait 2

(b)



Probability

Dominant trait 1 only

Dominant trait 2 only

Both dominant trait 1 and trait 2

20. Mutations in the **w** gene on the X chromosome of *Drosophila* give white eyes instead of the normal red. You have isolated both a white-eyed mutation (designated **w-1**) that gives a dominant phenotype, and a white-eyed mutation (designated **w-2**) that gives a recessive phenotype.

(a) A white-eyed male from the **w-1** line is crossed to a wild-type female. What color eyes will the female progeny from this cross have?

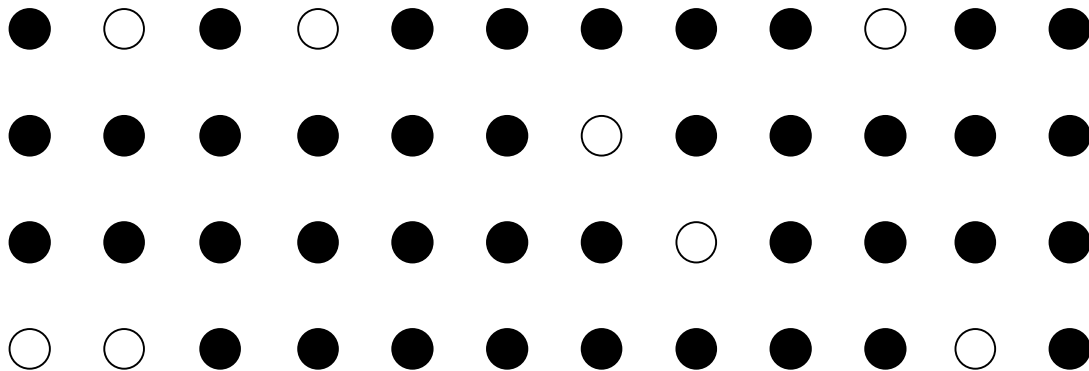
(b) What color eyes will the male progeny from the cross in part **(a)** have?

(c) One of the female progeny from the cross in part **(a)** is mated to a white-eyed male from the **w-2** line. What fraction of the white-eyed progeny from this cross will be female?

(d) A white-eyed female resulting from the cross described in part **(c)** is crossed to a wild-type male. Among 50,000 male progeny produced by this cross, there are 5 that have red eyes. What is the distance between **w-1** and **w-2** in cM?

(e) You have isolated a mutation that is called (**hw**) and gives hairy-wings. The **hw** gene is also on the X chromosome and is linked to the **w** gene. A female fly from a line that is true-breeding for both hairy wings and the **w-2** allele is crossed to a male fly that has normal wings and the **w-1** allele. An F₁ female from this cross is mated to a wild-type male and a very large number of male progeny from this cross are examined. Three of the male progeny have red eyes, and all of these red-eyed males have hairy wings. Draw a genetic map showing the most likely order of **hw**, **w-1**, and **w-2**.

21. Wild-type yeast make white colonies. You have isolated two mutants that make red colonies, which you call **red-1** and **red-2**. A **red1** haploid mutant is crossed to a **red2** haploid mutant. The resulting diploid is induced to sporulate, and twelve resulting tetrads are analyzed as shown below, where a dark circle indicates a red colony, and a white circle indicates a white colony:



(a) How many tetrads of each type are there?

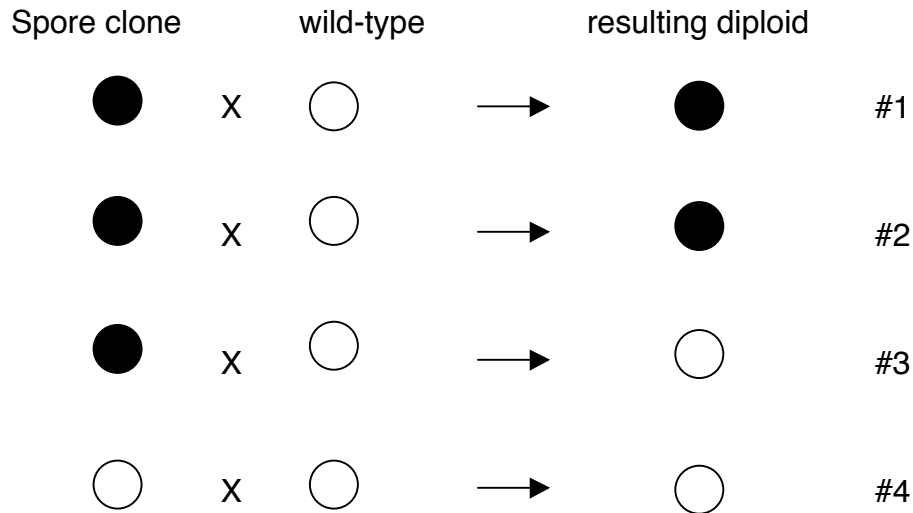
PD

NPD

TT

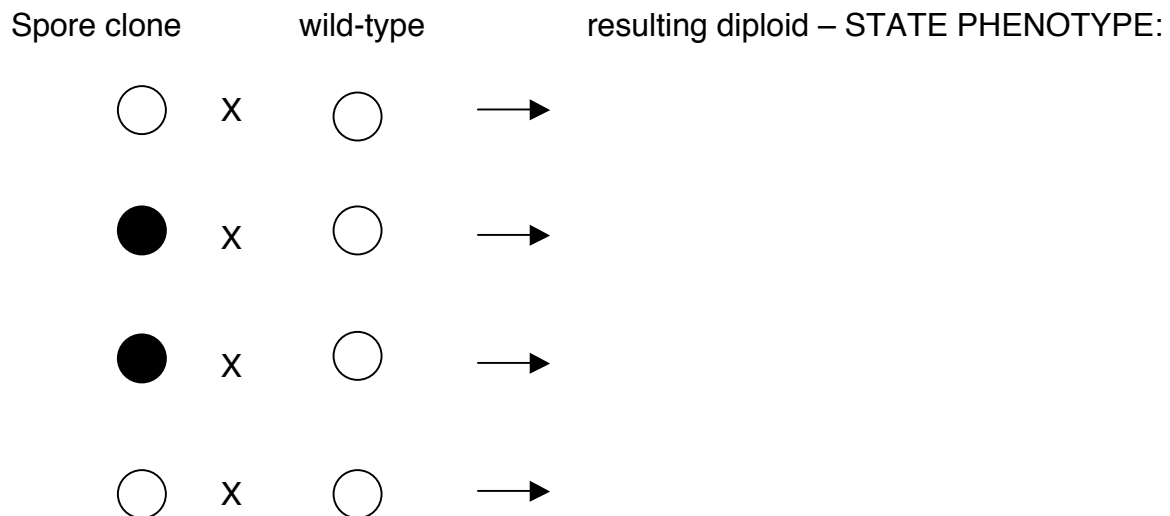
(b) Are the **red1** and **red2** loci linked? If so, how far apart are they in cM?

One of the tetrads from above is selected for further testing. Each of the four spore clones is mated to a wild-type haploid yeast. The phenotypes of the resulting diploids are shown below:



(c) When diploid #3 is induced to sporulate, what will the tetrads look like with respect to red and white phenotypes?

(d) A second tetrad from part (a) is chosen, and each of the four spore clones is again mated to a wild-type haploid yeast. In the diagram below, fill in the expected phenotypes of the resulting diploids. State any ambiguities that may exist.



22. Wild-type *Drosophila* have red eyes, and white eyes is an X-linked recessive phenotype caused by a single mutation. A new single mutation that gives the recessive phenotype of apricot colored eyes is isolated. A female from a true-breeding apricot-eyed strain is crossed to a male from a true-breeding white-eyed strain. All of the resulting F1 flies have apricot eyes.

(a) Are the white-eye and apricot-eye mutations in the same gene or in different genes? Explain your answer.

A collection of apricot-eyed F1 females from the cross described above are mated to males from a true-breeding white-eyed strain, and 1000 male progeny are examined. Among these progeny, only 6 flies have normal red eyes.

(b) What is the measured distance between the white-eye and apricot-eye loci in cM?

A new mutation is isolated that causes the recessive eye color “peach.” A female from a true-breeding peach-eyed strain is crossed to a male from a true-breeding white-eyed strain. All of the resulting F1 females have normal red eyes and all of the resulting F1 males have peach eyes.

(c) Is the peach-eye mutation on an autosome or on the X-chromosome? Explain your answer.

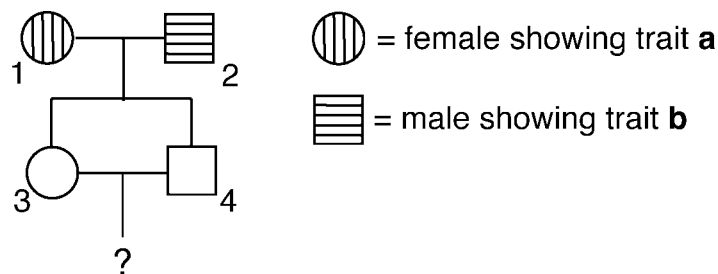
(d) Are the white-eye and peach-eye mutations in the same gene or in different genes? Explain your answer.

A mutation that causes the recessive phenotype of crossveinless wings lies on the X-chromosome. A female from a true-breeding strain with apricot eyes and crossveinless wings is crossed to a male from a single mutant true-breeding strain with white eyes and normal wings. As expected, all of the F1 females from this cross have apricot eyes and normal wings. A large collection of these F1 females are crossed to wild-type males and 10,000 **male** progeny are examined. The observed phenotypes are as follows:

<u>Phenotype</u>		<u>Number</u>
normal wings	white eyes	4,418
crossveinless wings	apricot eyes	4,330
normal wings	apricot eyes	610
crossveinless wings	white eyes	590
normal wings	red eyes	2
crossveinless wings	red eyes	50

(e) Draw a genetic map showing the relative order of the crossveinless, apricot and white loci.

23. The following mouse pedigree shows the segregation of two different autosomal recessive traits. (In this problem, assume that all phenotypes are completely penetrant and no new mutations arise.)

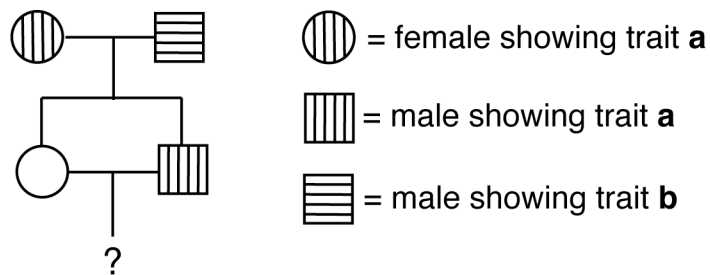


(a) What is the genotype of the mouse designated **3**? (Instructions: Use **A** and **a** to designate the alleles of the gene for trait **a** that give the dominant and recessive phenotypes respectively; and use **B** and **b** to designate the alleles of the gene for trait **b** that give the dominant and recessive phenotypes respectively.)

(b) If the genes for trait **a** and trait **b** are unlinked, what is the probability that a progeny mouse indicated by the “?” will show NEITHER recessive trait?

(c) If the genes for trait **a** and trait **b** are 20 cM apart on the same autosomal chromosome, what is the probability that a progeny mouse indicated by the “?” will show NEITHER recessive trait?

(d) The pedigree below shows the segregation of two recessive X-linked traits.



If the genes for the two traits are 20 cM apart on the X chromosome, what is the probability that that a **female** progeny mouse indicated by the “?” will show NEITHER recessive trait?

24. You have isolated a new mutation of phage λ that makes plaques with rough edges. You call the mutation $r1^-$. Phage mutants in the repressor gene (cl^-) make clear plaques rather than the normal turbid plaques. You cross a $r1^-$ phage with a cl^- phage by coinfecting *E. coli* with phage of both types. One hundred plaques resulting from the cross are examined and the following phenotypes and numbers are seen:

<u>Plaque Phenotype</u>	<u>Number of Plaques</u>
rough, turbid	44
rough, clear	4
smooth, turbid	6
smooth, clear	46

(a) What is the distance between the $r1$ and the cl loci in map units?

Next you isolate a second mutation that makes rough plaques that you call $r2^-$. Note that an $r1^- r2^-$ double mutant would be phenotypically rough. When a $r1^-$, cl^- double mutant phage is crossed to a $r2^-$ mutant phage, the following plaque types and numbers are seen:

<u>Plaque Phenotype</u>	<u>Number of Plaques</u>
rough, turbid	491
rough, clear	499
smooth, turbid	9
smooth, clear	1

(b) What is the distance between the $r1$ and $r2$ loci in map units?

(c) Draw a genetic map showing the relative order of the cl , $r1$, and $r2$ loci, as well as the distances that you have determined in parts (a) and (b).