Exams

Fall 1995

7.03 Exam 1

Name: Exam Solutions

Section: _____ **TA:** _____

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

There are five pages including this cover page

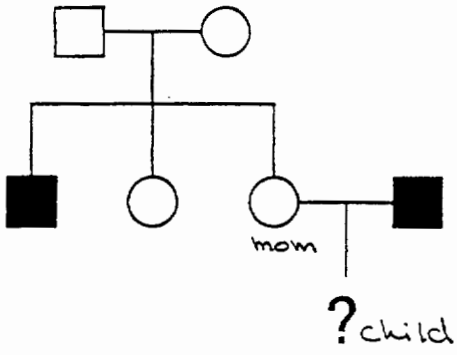
Remember to write your name on each page.

Question 1	30 points
Question 2	20 points
Question 3	20 points
Question 4	30 points

Name: Solutions

1. For the following pedigrees circles are female, squares are male and individuals with a particular trait are shown as filled-in symbols. Assume complete penetrance and that no new mutations occur in the families shown.

(a)



(5 pts.) If the trait is autosomal recessive what is the probability that the indicated child will show the trait?

p(mom is a carrier) × p(child inherits diseased allele)

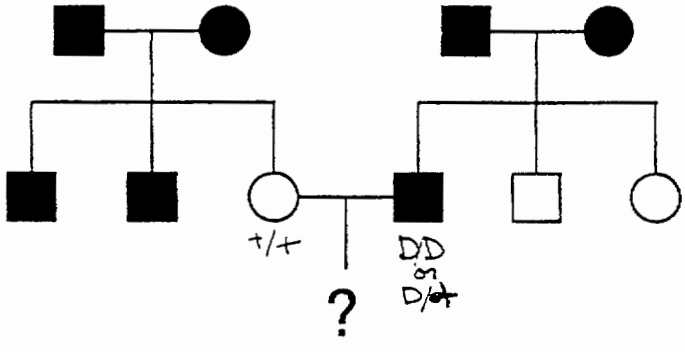
$2/3 \times 1/2 = 1/3$

(5 pts.) If the trait is X-linked recessive what is the probability that the indicated child will show the trait?

p(mom is a carrier) × p(child inherits diseased allele)

$1/2 \times 1/2 = 1/4$

(b)



D = dominant allele

+ = wt

(10 pts.) What is the probability that the indicated child will show the trait?

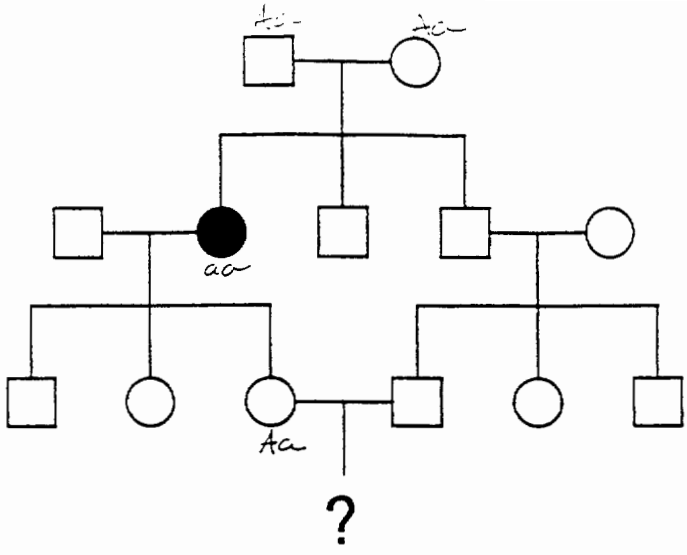
the trait has to be dominant

p(Dad is D/+)(p Dad passing on D allele) +

p (Dad being D/D)(p Dad passing on D allele) =

$(2/3)(1/2) + (1/3)(1) = 2/3$

(c)



(10 pts.) Assuming that this is a very rare trait what is the probability that the indicated child will show the trait?

p(mom is a carrier) × p(dad is a carrier) × p(child gets recessive allele from both mom + dad)

$1 \times (2/3)(1/2) \times (1/2)(1/2) = 1/12$

2. (**a** 10 pts.) Consider a gene that specifies diabetes in mice. When a true breeding diabetic mouse is crossed to wild type the progeny are always diabetic. Two different mutations in this gene designated **db-1** and **db-2** are 0.1 cM apart. A true breeding **db-1** mouse is crossed to a true breeding **db-2** mouse and the F_1 progeny are then crossed to wild type mice. On average, how many of the progeny from this backcross to wild type would you need to examine in order to find one mouse that is not diabetic?

(F1) $\frac{db\text{-}1\ +}{+\ db\text{-}2} \times \frac{+\ +}{+\ +}$ (wt)

parental ↓ crossover

(F2)

$\frac{db\text{-}1\ +}{+\ +}$	$\frac{+\ +}{+\ +}$
$\frac{+\ db\text{-}2}{+\ +}$	$\frac{db\text{-}1\ db\text{-}2}{+\ +}$

.1cM = .1% recombinant gametes

(½ are ++, ½ are db-1 db-2)

↑ wt = non diabetic

⇒ .05% (++) gametes

⇒ 1 in 2000 mice will be non diabetic

(**b** 10 pts.) Suppose that the gene for diabetes is 1 cM from the gene for albinism. A true breeding **db-1** and albino mouse is crossed to a true breeding **db-2** mouse with normal fur. The progeny from this cross are non diabetic and have normal fur. Several of these mice are then crossed to non diabetic albino mice. Three non diabetic mice are found among the progeny from this cross and all three of these mice are albino. Draw a map showing the order and positions of the gene for albinism and the mutations **db-1** and **db-2**.

There are 2 possible orders apriori:

1. db-1 db-2 a

or

2. db-2 db-1 a

Since the 3 non diabetic mice are also albino, then only the 1st possibility is correct.

1. db-1 db-2 a

$\frac{+\ +\ a}{+\ +\ a}$ (non diabetic albino mice)

3. The *Drosophilia* traits **bar eyes**, **fused veins**, and **bobbed hairs** are all X-linked recessive traits. Two true breeding mutant lines are crossed to produce a female fly that is normal in appearance. This female is then crossed to a wild type male fly and the phenotypes of 100 of the male progeny are given below:

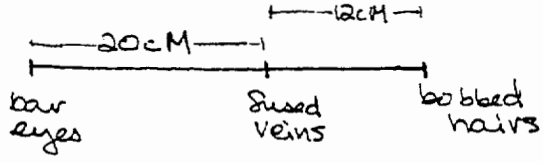
38	bar, bobbed } parental
32	fused } parental
10	bar, fused
8	bobbed
6	bar
4	fused, bobbed
2	normal
0	fused, bobbed, bar } DCO

(a 5 pts.) What did the two true breeding lines crossed to produce the female look like?

line 1 – bar eyes, bobbed hairs

line 2 – fused veins

(b 15 pts.) Draw a map of the X chromosome showing the order and distances between **bar**, **bobbed** and **fused** with as much precision as you can.



4. (a 10 pts.) You are studying two yeast mutations that have the interesting property that neither mutation by itself affects yeast growth but the two mutations are lethal when they are combined in the same cell. You cross a MAT**a** strain carrying one of the mutations with a MATα strain carrying the other mutation. The resulting diploid is sporulated and tetrads are dissected. Out of 50 tetrads you find: 24 tetrads with four viable spores, 22 tetrads with three viable spores, and 4 tetrads with two viable spores.

Are the two mutations on the same chromosome? If so, how far apart are they in cM?

viable : dead	#	class
4 : 0	24	PD
3 : 1	22	T
2 : 2	4	NPD

PD >> NPD ∴ genes are linked

$$\text{distance} = \frac{1}{2} \times \frac{T + 6\,NPD}{T + NPD + PD} \times 100$$

$$= \frac{1}{2} \times \frac{22 + 6(4)}{50} \times 100$$

$$= 46\ cM$$

Name: solutions

(c 10 pts.) A MAT**a** **His2**$^-$ strain is crossed to a MATα **His4**$^-$ strain and tetrads are dissected. One of the tetrads is chosen for further analysis. The phenotypes of the four spores are as follows:

Spore 1: MAT**a** His$^+$
Spore 2: MATα His$^-$
Spore 3: MAT**a** His$^-$
Spore 4: MATα His$^-$

The four possible matings among these four spores are performed (remember only MAT**a** and MATα can mate) and the phenotypes of the resulting diploids are given below.

Cross	Phenotype of Diploid
Spore 1 x Spore 2	His$^+$
Spore 1 x Spore 4	His$^+$
Spore 3 x Spore 2	His$^-$
Spore 3 x Spore 4	His$^-$

Which if any of these four spores is a double mutant? Spore 3

Spore 3 (His$^-$) does not yield a His$^+$ diploid when mated to Spore 2 (His$^-$) or Spore 4 (His$^-$).

(b 10 pts.) You are studying the expression of the enzyme invertase in yeast and have found two interesting mutations. The first mutation (**mut1**) causes an abnormally high level of invertase expression whereas the other mutation (**mut2**) causes an abnormally low level of invertase expression. You cross a MAT**a** **mut1** strain with a MATα **mut2** strain. The resulting diploid is sporulated and out of 50 tetrads there are three types:

NPD 20 tetrads have two normal spores and two spores with a high level of invertase.

PD 22 tetrads have two spores with a high level of invertase and two spores with a low level of invertase.

T 8 tetrads have two spores with a high level of invertase, one spore with a normal level of invertase, and one spore with a low level of invertase.

Are the **mut1** and **mut2** mutations on the same chromosome? NO
PD = NPD ∴ genes are unlinked
PD > 1/4 T ∴ both genes are centromere linked
⇒ must be on different chromosomes

What is the phenotype of a strain that contains both **mut1** and **mut2**?

PD
+ +
+ +] hi

+ 2
+ 2] low

NPD
+ +
+ +] normal

1 2
1 2] high

∴ phenotype of double mutant is a high level of invertase

7.03 Exam 2

Name: Corrected Solution Set

Section: 1995 TA: _____

The exam starts at 11:05 and ends at 11:55

Remember...

Stay calm, show your work, check your answers, and if you get stuck move on to an easier problem.

Best of luck.

There are five pages including this cover page

Please write your name on each page.

Question 1	30 points
Question 2	17 points
Question 3	17 points
Question 4	36 points

Name: _____

1. You have been given three new mutants of phage λ. Two make plaques that are smaller than normal (**Sm1** and **Sm2**) and one makes clear plaques (**C1**). The **C1** mutation is known to lie between **Sm1** and **Sm2**.

(**a** 10pts.) λ **Sm1** and λ **C1** mutants are coinfected into *E. coli* at a high multiplicity of infection. The resulting lysate is plated and 100 plaques are examined. (Wild type λ makes large turbid plaques.)

Plaque phenotype		Number of plaques	# of crossover events
large turbid	wt	9	odd (1)
small turbid	Sm1	37	even (0 or 2)
large clear	c1	43	even (0 or 2)
small clear	Sm1 c1	11	odd (1)

note: small turbid plaques and large clear plaques are mostly the result of 0 rather than 2 crossover events

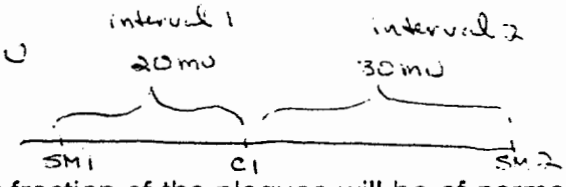
Sm2 and **C1** mutants are similarly crossed and the following results are obtained:

Plaque phenotype	genotype	Number of plaques	# of crossover events
large turbid	wt	17	odd (1)
small turbid	Sm2	36	even (0 or 2)
large clear	c1	34	even (0 or 2)
small clear	Sm2 c1	13	odd (1)

Draw a map of the λ chromosome showing the distances between the **Sm1**, **Sm2**, and **C1** mutations. m.u. = $\frac{\text{recombinants}}{\text{total}} \times 100$

Sm1/c1 distance = $\frac{9+11}{100} \times 100 = 20$ mu

Sm2/c1 distance = $\frac{17+13}{100} \times 100 = 30$ mu



(**b** 10 pts.) When **Sm1** and **Sm2** are crossed what fraction of the plaques will be of normal size? (To get full credit for your answer you must take the effect of double crossovers into account.)

p1 = probability of having a crossover in region 1
p2 = " " " " " " " " 2
1 − p1 = probability of not having a crossover in region 1
1 − p2 = " " " " " " " " 2

p1 = .2
p2 = .3

$\therefore p1(1-p2) + p2(1-p1) = p1 - p1p2 + p2 - p1p2 = p1 + p2 - 2p1p2$
$= .2 + .3 - 2(.2)(.3)$
$= .38$

$.38/2 = .19 = \boxed{19\%}$ with a normal size

* NOTE: NO double CROSSOVER, the Distance between Sm1 and Sm2 is .2 + .3 = .5

You have to consider the effect of a double crossover in interval 1 and interval 2. You do not have to substract out a double crossover just in region 1 and a double crossover just in region 2 since they are already not included in .2 and .3.

Name: Solutions

(**c** 10 pts.) A second clear plaque mutant (**C 2**) is isolated. When **C 1** and **C 2** are crossed all of the 200 plaques examined are clear, meaning that the two mutations are very close together. Fortunately you find an *E. coli* strain that is restrictive for **C 1** or **C 2** mutants. That is, wild type λ will form plaques on the restrictive strain but **C** mutants will not. **C 1** and **C 2** mutants are crossed and then plated on the permissive and restrictive hosts. The lysate from the cross gives 10^8 plaques per ml on the permissive host and gives 3×10^5 plaques per ml on the restrictive host. What is the distance between **C 1** and **C 2** in map units?

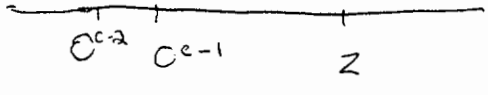
wt give rise to plaques
C1 C2 double mutant does not

$$\therefore \quad m.u. = \frac{2 \times 3 \times 10^5}{10^8} \times 100 = .6 \text{ mu}$$

2. (**a** 7 pts.) You have isolated two new operator mutations in the **Lac** operon, **O^c-1** and **O^c-2**. The cis-trans test for **O^c-1** is shown in the table below. Indicate with (+) or (–) where β-galactosidase should be produced.

	–IPTG	+IPTG
O^c-1 Z$^+$ / F' O$^+$ Z$^-$	+	+
O^c-1 Z$^-$ / F' O$^+$ Z$^+$	–	+

(**b** 10 pts.) To find the relative positions of the **O^c-1** and **O^c-2** mutations you perform the following **P 1** transduction experiments. **P 1** is grown on a host that is **O^c-1 Z$^+$**. The lysate is used to transduce an **O^c-2 Z$^-$** strain by selecting for **Z$^+$**. You note that all of the **Z$^+$** transductants show constitutive expression of β-galactosidase (1000 transductants are examined). In a second experiment, **P 1** is grown on a host that is **O^c-2 Z$^+$**. This lysate is used to transduce an **O^c-1 Z$^-$** strain by selecting for **Z$^+$**. For this cross, 90% of the **Z$^+$** transductants show constitutive expression of β-galactosidase and 10% show regulated experssion. Draw a map showing the order of **O^c-1** and **O^c-2** relative to the **Z$^-$** mutation.



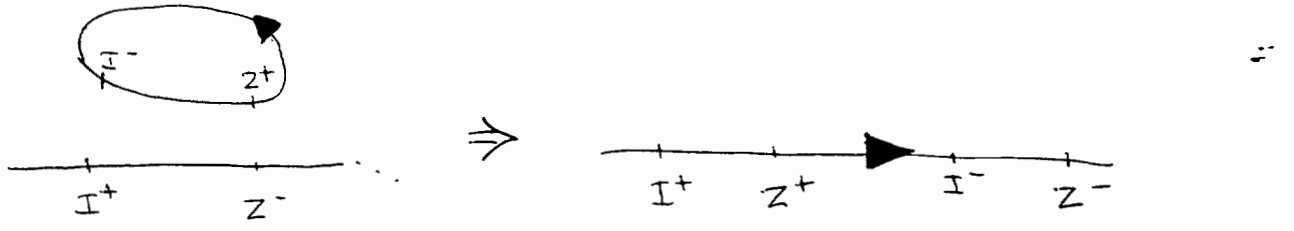
Name: Solutions

3. An *E. coli* strain has a **LacZ⁻** mutation on the chromosome and carries an **F'** with the **Lac** operon that has a **LacI⁻** mutation (**I⁺ Z⁻ / F' I⁻ Z⁺**).

(a 3 pts.) What is the **Lac** phenotype of this strain (constitutive, uninducible, or regulated)?

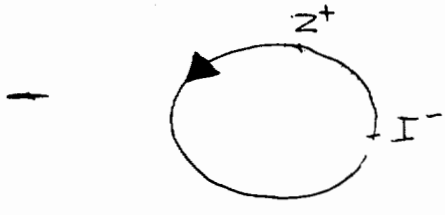
regulated

(b 4 pts.) Homologous recombination between the **Lac** regions on the **F'** and on the chromosome convert the strain into an **Hfr**. This **Hfr** now carries two different versions of the **Lac** operon. By mating to an **F⁻** strain that is deleted for the **Lac** operon it is found that the version of the **Lac** operon transferred early by the **Hfr** is regulated. Give the genotype of the version of the **Lac** operon that would be transferred late by this strain.



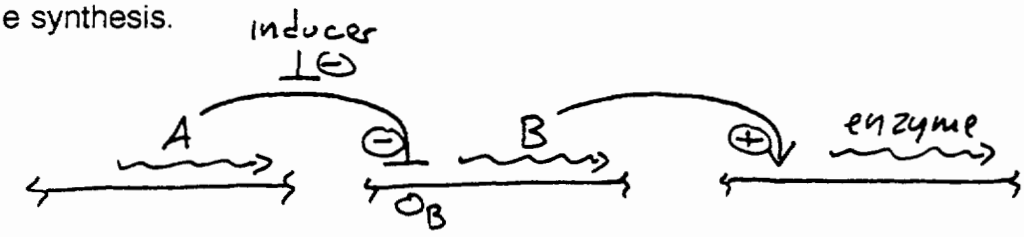
∴ I⁻ z⁻ genotype transferred late

(c 10 pts.) Draw a map of the **F'** showing the orientation of the origin of transfer relative to the **I** and **Z** genes.



Name: Solutions

4. An enzyme in *E. coli* is regulated as follows. **A** is a repressor of the **B** gene and **B** is an activator of transcription of the enzyme. The inducer molecule binds to **A** and prevents **A** from binding to the operator. Thus, when inducer is present **B** is expressed, and activates enzyme synthesis.



(a 12 pts.) Fill in the table below indicating whether the enzyme will be synthesized (use **+** or **–**).

	– inducer	+ inducer
A^-	+	+
B^-	–	–
$A^- B^-$	–	–

(b 12 pts.) An allele of the **A** gene (**A^s**) is isolated that binds to the operator and represses regardless of whether inducer is present or not. An allele of the operator site of the **B** gene (**O^c_B**) is isolated that will not bind the **A** repressor. As above, indicate in the table below where the enzyme will be synthesized.

	– inducer	+ inducer
A^s	–	–
O^c_B	+	+
$A^s O^c_B$	+	+

(c 12 pts.) An allele of the **B** gene (**B^{-d}**) is isolated that will not activate transcription and will also interfere with the ability of wild type **B** protein to activate transcription. Indicate in the table below where the enzyme will be synthesized.

	– inducer	+ inducer
B^{-d}	–	–
B^{-d} / F' B^+	–	–
O^+_B B^{-d} / F' O^c_B B^+	+	–

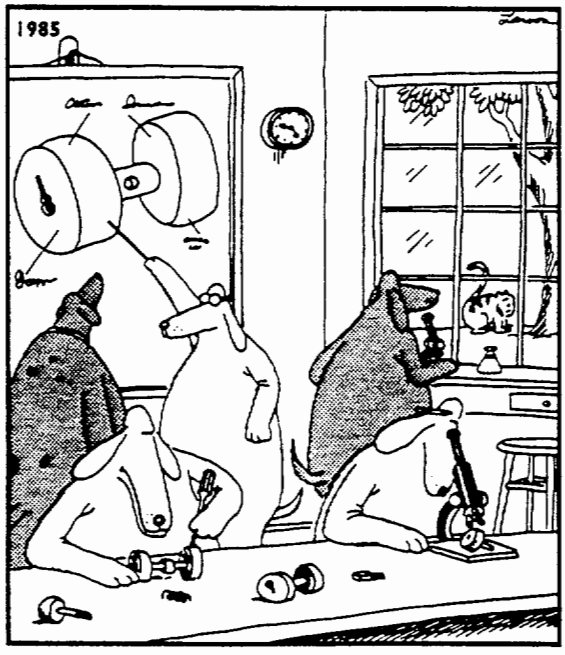
Name: Solutions

Recitation day _____, Time _____, TA _____

7.03 Exam 3
November 22, 1995

Write your name on all 8 pages.
Indicate your recitation section on this page.
Write all answers on this handout only.
Exam begins at 11:05 and ends at 11:55.
Time will be announced when 5 and 1 minutes remain.

Problem 1	25
Problem 2	35
Problem 3	40
Total	100 points



Knowing how it could change the lives of canines everywhere, the dog scientists struggled diligently to understand the Doorknob Principle.

Name:_____

Question 1 omitted

2. (35 points) You are studying flower color in the diploid tulip. There are many different flower colors in the tulip controlled by unlinked genes.

(a. 10 points) You obtain two true breeding strains that are independent isolates. Both produce purple flowers.

purple 1	X	purple 2
	↓	
F1	all purple flowers	
	↓	
F2	149 plants with purple flowers	
	9 plants with white flowers	

What are the genotypes of the following plants: purple 1, purple 2, F2 purple, and F2 white? Explain how the F2 genotypes produce the observed phenotypes.

purple 1 = AAbb
purple 2 = aaBB

F1 = AaBb

F2 = 9 A_B_ } purple
3 A_bb } purple
3 aaB_ } purple
1 aabb white

15 : 1
purple white

This is an example of redundancy. You only need one copy of either A or B to get the purple phenotype. If you're homozygous recessive for both genes (aabb), you get the white phenotype

(b. 15 points) You also obtain a true breeding strain that makes blue flowers and cross it to a true breeding strain with orange flowers.

blue	X	orange
	↓	
F1	all blue flowers	
	↓	
F2	259 plants with blue flowers	
	61 plants with orange flowers	

What are the genotypes of the following plants: parental blue strain, parental orange strain, F2 blue, and F2 orange? Explain how the F2 genotypes produce the observed phenotypes.

P blue = AAdd orange = aaDD

F1 AaDd

F2 9 A_D_ blue
3 A_dd blue
3 aaD_ orange
1 aadd blue

13:3 ratio
blue orange

Possible Explanations:

① d is a recessive suppressor of a (a is also, recessive aadd is blue → suppressed aaD_ is orange → not suppressed

② d is epistatic to a

③ the flowers are normally blue. D is a dominant mutation that makes orange pigment. A is a dominant suppressor of D.

Part C omitted

Question 3 omitted

Name:_____

Recitation day_____, time_____,
TA_____

7.03 Final Exam
Dec. 19, 1995

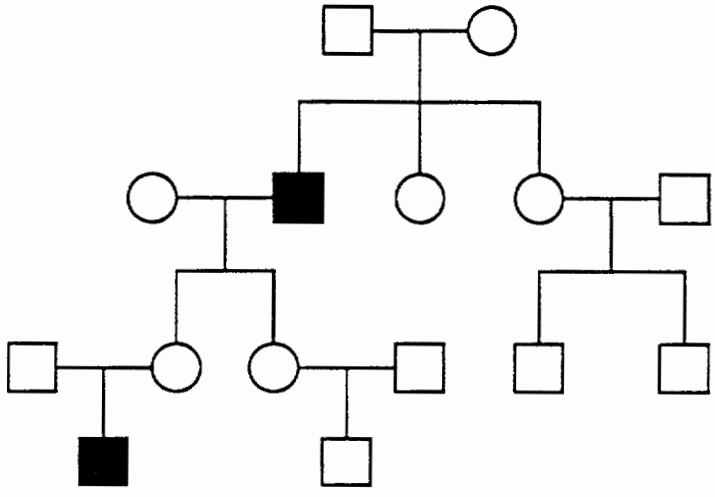
Write your name on all 18 pages.
Indicate your recitation section on this page.
Write all answers on this handout only.
Exam begins at 1:30 and ends at 4:30.
Time will be announced when 15, 5, and 1 minutes remain.

Problem 1	20 points
Problem 2	20 points
Problem 3	30 points
Problem 4	25 points
Problem 5	25 points
Problem 6	25 points
Problem 7	30 points
Problem 8	25 points
Total	**200 points**

Name:_____

1. The following are pedigrees for rare genetic diseases that show complete penetrance. The affected individuals are shown by solid symbols. **For each pedigree give the most likely mode of inheritance and briefly explain your reasoning.**

a. (5 points)

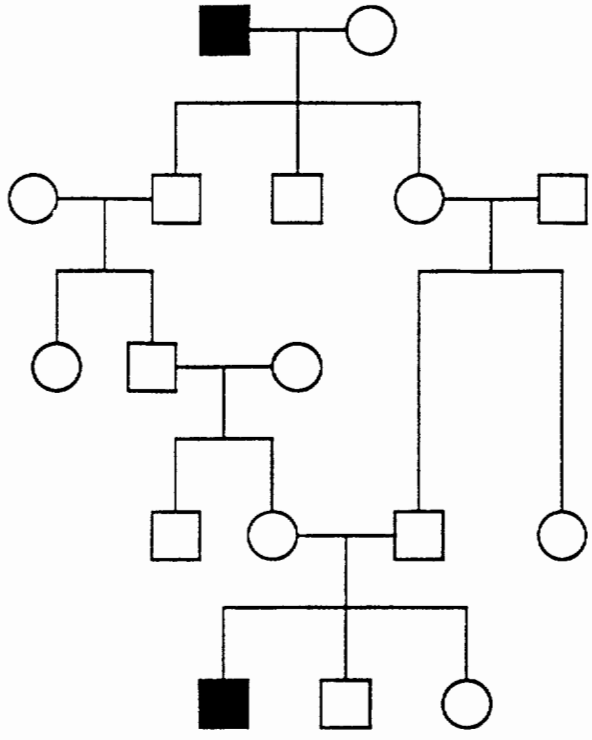


X-linked

Skips generations
Only ♂'s affected

Name:_____

b. (5 points)



Rec. Aut

Skips generations

Inbreeding

Parts c+d omitted

Name:_____

2. The *malT* gene of *E. coli* is a transcriptional activator for expression of the genes needed for maltose utilization. Wild-type *E. coli* can grow on maltose but *malT*$^-$ strains can't. You have isolated three *malT*$^-$ mutants: *malT–1*, *malT–2*, and *malT–3*.

a. (5 points) Phage P1 is grown on a *lysA*$^+$, *malT–1* strain. The phage lysate is used to infect a *lysA*$^-$, *mal*$^+$ strain and *lys*$^+$ transductants are selected. Of 100 *lys*$^+$ transductants, 35 can grow on maltose. **What is the distance between the *lysA* and *malT* genes?**

65%

b. (5 points) P1 is grown on a *lysA*$^+$, *malT–1* strain and the phage lysate is used to infect a *lysA*$^-$, *malT–2* strain. Of 1000 *lys*$^+$ transductants, 5 can grow on maltose. Next, P1 is grown on a *lysA*$^+$, *malT–2* strain and the phage lysate is used to infect a *lysA*$^-$, *malT–1* strain. Of 1000 *lys*$^+$ transductants, 50 can grow on maltose. **What is the order of the *malT–1* and *malT–2* mutations with respect to the *lysA* gene?**

Lys A^+, MalT-1, MalT-2

c. (10 points) P1 is grown on a *lysA*$^+$, *malT–3* strain and the phage lysate is used to infect a *lysA*$^-$, *malT –1* strain. Of 1000 *lys*$^+$ transductants, none can grow on maltose. When the same P1 lysate is used to infect a *lysA*$^-$, *malT–2* strain, again none of 1000 *lys*$^+$ transductants can grow on maltose. **Explain the behavior of the *malT–3* mutation.**

A deletion that includes both MalT-1 and MalT-2 sites

Name:_____

3. The yeast gene *GAL4* encodes a activator for transcription of the genes needed to metabolize galactose. *Gal4*$^-$ mutants do not transcribe the genes for galactose metabolizing enzymes and therefore can not grow when galactose is the only carbon and energy source. Starting with a *gal4*$^-$ mutant, you isolate three different derivatives of this strain that now **can** grow on galactose. These strains are designated *rev1*, *rev2* and *rev3*. You perform a number of crosses to diagnose the type of second mutation that occurred in each case. To aid this analysis you use a wild-type strain (*GAL4*$^+$), the original mutant strain (*gal4*$^-$), and a strain with a deletion of *gal4* (*gal4Δ*). You analyze 50 tetrads from each cross by testing the ability of each spore clone to grow on galactose.

a. *rev1* x *GAL4*$^+$

	Number of Tetrads
4 Gal$^+$: 0 Gal$^-$	50
3 Gal$^+$: 1 Gal$^-$	0
2 Gal$^+$: 2 Gal$^-$	0
1 Gal$^+$: 3 Gal$^-$	0
0 Gal$^+$: 4 Gal$^-$	0

rev1 x *gal4*$^-$

	Number of Tetrads
4 Gal$^+$: 0 Gal$^-$	0
3 Gal$^+$: 1 Gal$^-$	0
2 Gal$^+$: 2 Gal$^-$	50
1 Gal$^+$: 3 Gal$^-$	0
0 Gal$^+$: 4 Gal$^-$	0

rev1 x *gal4Δ*

	Number of Tetrads
4 Gal$^+$: 0 Gal$^-$	0
3 Gal$^+$: 1 Gal$^-$	0
2 Gal$^+$: 2 Gal$^-$	50
1 Gal$^+$: 3 Gal$^-$	0
0 Gal$^+$: 4 Gal$^-$	0

(5 points) What do these crosses tell you about *rev1*?

True revertant : All PD

Same gene (1 gene)

Name:_____

(5 points) What type of reversion or suppression would best explain the behavior of *rev1*?

Complete revertant

Parts b+c omitted

Name:_____

4. The pedigree on the next page shows the inheritance pattern in a family afflicted with neurofibromatosis I disease. This genetic disease results from an autosomal dominant mutation. There is a marker that is 5cM from the *NFI* gene with four alleles, A, B, C, D, that can be distinguished on Southern blots. The disease is completely penetrant.

a. (5 points) Which allele of the marker is linked to the NFI disease in this family?

C

b. (3 points) Identify the individuals who are definitely recombinants, using their generation number and individual number.

III-8

c. (2 points) Identify the individuals in which the recombination event(s) occurred, using their generation number and individual number.

II-4

d. (5 points) Identify the individuals in which the phase of the marker and disease alleles is ambiguous.

II-2, II-3, II-4

(I-2)

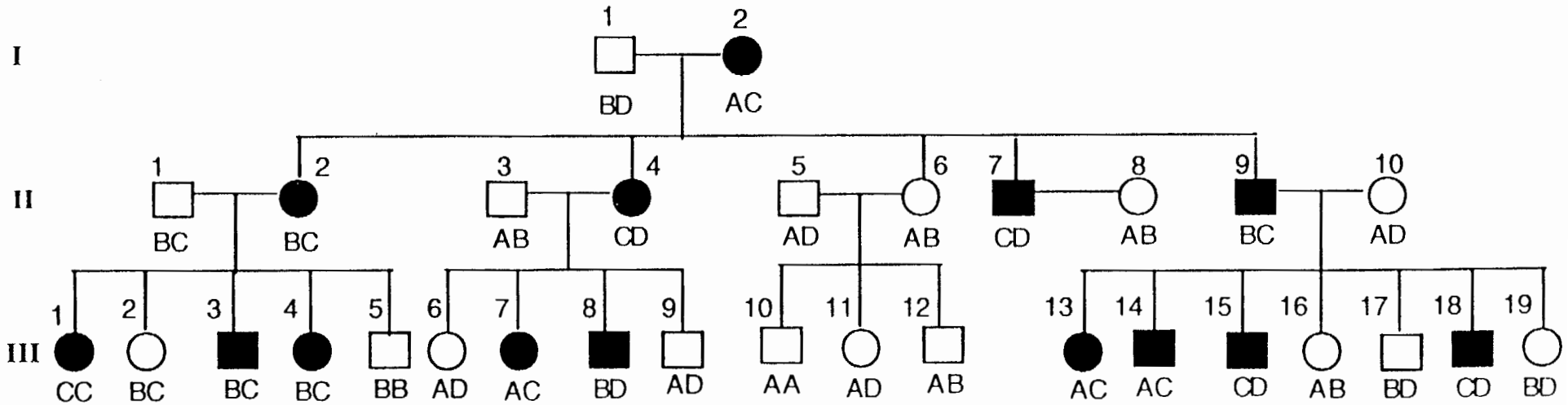
e. (5 points) Why is individual II,1 not afflicted with the disease?

Can have the marker w/out the disease

f. (5 points) Woman III,1 marries an unaffected man and becomes pregnant. Could you use the marker for prenatal diagnosis to determine whether her child will have the disease? Why?

no, not heterozygous for the marker

♀ III-1


I
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BD
CD
BD

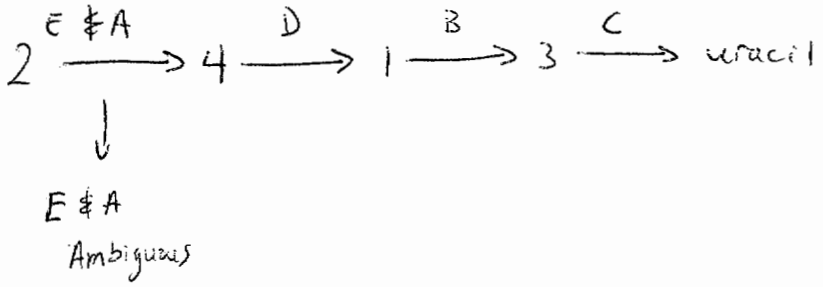
Question 5 omitted

Name:_____

6. You are studying uracil biosynthesis in E. coli. You isolate mutations in five different genes that are ura$^-$. These mutant strains, *uraA*, *uraB*, *uraC*, *uraD*, and *uraE*, are unable to grow in the absence of uracil in the media. Four biochemical intermediates for uracil synthesis are known. For simplicity we will designate these intermediate compounds as 1, 2, 3, and 4. You do a feeding experiment to test growth of each mutant on media supplemented with each of the intermediates.

	Growth on media supplemented with:				
	uracil	1	2	3	4
Mutant Strain					
uraA	+	+	–	+	+
uraB	+	–	–	+	–
uraC	+	–	–	–	–
uraD	+	+	–	+	–
uraE	+	+	–	+	+

a. (10 points) Order the genes in a pathway and indicate the positions of the intermediates. Are there any ambiguities in the pathway?



Ambiguous

Part b omitted

Name:_____

7. For a UROP project you decide to study wing formation in the butterfly by doing a genetic analysis. Your advisor gives you a true breeding wild type strain with striped wings and a true breeding mutant strain that has plain wings without stripes (*plw*).
You do the following crosses:

plw females X wild-type male	*plw* males X wild-type females
↓	↓
F 1 all striped wings	all striped wings
cross brothers and sisters	
↓	↓
F2 25% plain wings	25% plain wings

a. (5 points) Explain the inheritance pattern of the *plw* phenotype. Is *plw* recessive or dominant?

Aut rec

Parts b, c, d omitted

Name:_____

8. A newly discovered inherited disorder occurs at a frequency of 10^{-4} in a population that is in Hardy-Weinberg equilibrium. You do not know whether the allele that causes the disorder is dominant or recessive.

a. (5 points) If the allele for the disorder were DOMINANT, what would be the frequency of heterozygotes in the population?

$\approx 10^{-4}$

b. (5 points) If the allele for the disorder were RECESSIVE, what would be the frequency of heterozygotes in the population?

10^{-2}

Two neighboring islands have 10^4 inhabitants each. The populations on each island choose mates at random but because boats never travel between the islands the two populations are isolated from each other.

c. (5 points) The allele frequency for a recessive trait on one island is 0.2 and on the other island is 0.02. **On average, how many people will show the trait among the $2x10^4$ inhabitants of both islands?**

$(.2)^2 \times 10^4 + (.02)^2 \times 10^4 = 404$

d. (5 points) A new ferry line is established between the islands and after several years mating beween the two island populations is random. **After the random mixing is established, how many people will show the trait in the combined population of both islands?**

$q_{new} = \frac{.2 + .02}{2} = .11$ $\quad (.11)^2 \times 2 \times 10^4 = 242$

Name:_____

e. (5 points) A recessive disease occurs in a randomly mating population at a frequency of 10^{-6}. **If second cousins from this population have a child, what is the probability that the child will have the disease?** (Second cousins have a set of great grandparents in common.)

$q^2 = 10^{-6}$ $\quad q = 10^{-3}$

$\frac{1}{64}\ q = 1.56 \times 10^{-5}$