Biol223 Smith 2007-2008Spring FINAL

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Biology 223 Spring 2007-2008 FINAL, 5 June 2008

No notes, no calculators, no phones, etc.

Write your <u>name</u> and <u>student ID</u> number at the top of this page and <u>most importantly</u>, on the <u>answer page</u>.

Only the answer page will be graded, you must place your answers in the space provided.

Write legibly, if I cannot read or understand your answer, you will receive no credit. If it takes too much effort, you may lose points.

Unanswered questions receive zero credit.

Within parts of multi-part questions, incorrect answers may subtract from correct parts.

Unjustifiable, frivolous, and grossly incorrect answers may be assigned negative points. Thus, it is possible to receive a negative score on the exam.

If you find any mistakes of mine in the question, note it on your exam answer page and you may receive extra credit.

100 points possible each section.

Part I: Russell, 2nd edition, chapters 1, 2, 3, 4, 11, 12, 15, 16

Part II: Russell, 2nd edition, chapters 18 (fine mapping and complementation), 19 (Lac operon only)

Note points per question and spend your effort accordingly!

SECTION I [100 pts]

Question 1 for 16 points (5 minutes)

Describe the 8 base pairs shown below in the table, writing Y (yes) or N (no) in the table to indicate whether it has Watson-Crick geometry (row WC), and the number (0, 1, or 2) of standard bases found in it (row #).

pair 1-2 3-4 5-6 7-8 9-10 11-12 13-14 15-16 WC # | | | | | |

Question 2 for 16 points (5 minute)

The single strand of DNA below was annealed to two radioactively-labeled RNA primers: 5'-UGACUUGCUGA-3' and 5'-GGUUCUAUAUACG-3'. The RNAs are radioactively labeled only at G nucleotides (shown underlined). Calculate the total lengths of the radioactive, single-strand product(s) expected from the addition of *Escherichia coli* DNA polymerase I or III in suitable buffer (Mg++, etc), without exposure to RNase, and the following dNTPs (your answers should be one or more whole numbers in each box):

5-ATCCGTCCGTCAGCAAGTCATGGTTCTATATACGCTTCGTATATAGAACCCTGACTTGCTGAG-3

dNTPs added	<u>dATP</u>	dATP+dCTP	dATP+dCTP+dGTP	all dNTPs
DNA pol I				
DNA pol III				

Question 3 for 10 points (3 minutes)

A cell line is thought to have its cell cycle comprising G1= 17 hours, G2= 13 hours, M=2 hours, S=4 hours.

a) For how many hours would you leave tritiated thymidine in the medium in order to label one quarter of the cells?

b) For how many hours would you leave tritiated thymidine in the medium in order to label one half of the cells?

a) one quarter	b) one half			

Question 4 for 16 points (10 minutes)

In a prototrophic strain of *Neurospora crassa*, intermediate A is synthesized from minimal medium by enzyme 1, etc. Consider the diagrammed hypothesis, where compounds D, E, and H are essential, but compound <u>C is toxic</u>, and all possible strains having single non-functional mutations in genes 1-8. Which mutant strains (numbered by mutant gene) would grow in minimal medium supplemented with:

supplement	strains that grow
В	
D	
F	
G	

Question 5 for 16 points (10 minutes)

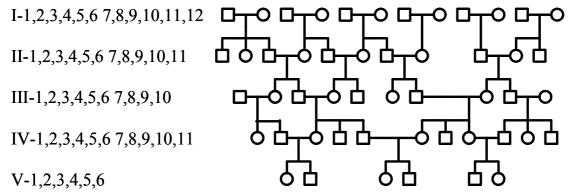
A *Drosophila* strain was test crossed, and ~1000 progeny were phenotyped. Using proper notation and the data below:

- a) determine the gene order, labeled by loci.
- b) describe the genotype of the parent being test crossed in complete, proper notation, including order and linkage.
- c) determine between which two loci is the least separation and the approximate distance in map units.

+	b	+	d	+	104
+	b	С	d	+	98
+ + a a + + a a + + a a + + a a + + a a a + + a a a + a a + a a a + a	b b + + + b b b + + + b b - + + b b - + + + b b - + + + +	+ 0 + 0 + 0 + 0 + 0 + 0 + 0 + 0 + 0 + 0	d d + d + <td< td=""><td>+ + 0 0 0 0 0 + + + + 0 0 0 0 0 + + + +</td><td>104 98 94 89 81 77 72 68 38 37 34 32 19 12 11 10 9 7 7 6 3 3 3 1</td></td<>	+ + 0 0 0 0 0 + + + + 0 0 0 0 0 + + + +	104 98 94 89 81 77 72 68 38 37 34 32 19 12 11 10 9 7 7 6 3 3 3 1
а	+	С	+	Ф	89
+	+	+	d	Φ	81
+	+	C	d	Φ	77
а	b	+	+	+	72
а	b	C	+	+	68
+	b	+	+	+	38
+	b	U	+	+	37
а	+	+	d	Φ	34
а	+	С	d	е	33
+	b	+	d	Ψ	27
+	b	C	d	Φ	24
а	+	+	+	+	22
а	+	С	+	+	19
+	+	+	+	е	12
+	+	С	+	е	12
а	b	+	d	+	11
а	b	U	d	+	10
+	+	+	d	+	9
+	+	С	d	+	7
а	b	+	+	е	7
а	b	С	+	е	6
+	b	+	+	е	3
+	b	С	+	е	3
a	+	+	d	+	2
а	+	С	d	+	1

Question 6 for 8 points (10 minutes)

A breeding program has been designed for a human colony on Mars. Only the first generation has been born, the later generations are planned. Your concern are two alleles. Allele A is an autosomal dominant gene conferring the ability to survive dehydration. Allele x is an X-linked recessive gene causing edema in low pressure. All males in generation I are heterozygous for allele A, wild type in x. All females are wild-type for A, but carriers of allele x. Individuals III-1 and III-10 are to be wild-type humans thawed from frozen embryo stocks. Calculate the precise probability of the 4 individuals in the table below (leave factors unmultiplied):



	a) III-4	b) IV-4	c) V-1	d) V-4
probability has				
phenotype A				
probability has single				
allele of x				

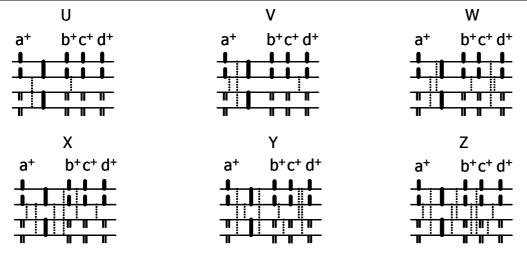
Question 7 for 18 points (5 minutes)

Locus $\underline{\mathbf{a}}$ is on the short arm of a chromosome, while $\underline{\mathbf{b}}$, $\underline{\mathbf{c}}$, and $\underline{\mathbf{d}}$ are on the long arm of a chromosome of *Neurospora crassa*. One parent is \mathbf{a}^+ , \mathbf{b}^+ , \mathbf{c}^+ , \mathbf{d}^+ (**solid bar**), the other is a, b, c, d (<u>double bar</u>). Eight chiasmata are shown, where the centromeres are represented as thick lines, and crossing over is indicated from the <u>ends</u> of the thin dotted lines. There may be unmatched chiasmata and asci.

- a) For each ascus in the table, indicate its type (PD, NPD, or T) only with respect to locus a and c.
- b) Match the asci indicated with the chiasmata, by writing the chiasma labels (U-Z) below the asci genotypes. If no chiasma would create that ascus, write 0.

REMEMBER **SOLID** IS + AND **DOUBLE** IS NULL

	1	2	3	4	5	6	7	8	9
1 pair	++++	++++	+bcd	+bc+	a++d	abcd	abcd	+++d	a+cd
2 pair	++++	a+cd	+bc+	+b+d	+b++	a+c+	++C+	+b++	ab++
3 pair	abcd	ab++	a+++	a+c+	+bcd	+b++	ab+d	abcd	+bcd
4 pair	abcd	+bcd	a++d	a++d	a+c+	+++d	++++	a+c+	++++
a) type (a, c)									
b) contributing									
chiasmata									



SECTION II [100 pts]

Question 8 for 50 points (10 minute)

Use the table below describing the results of a pairwise recombination test to form a map of 8 independently-isolated deletion mutants of the rII region of bacteriophage T4.

	A	В	С	D	Е	F	G	Н
I	0	0	0	+	0	+	0	0
Н	+	+	+	+	0	+	+	
G	0	0	0	+	+	+		•
F	+	+	+	+	0		•'	
Е	+	+	0	+		·		
D	+	0	+		•'			
С	0	0		•'				
В	+		3"					

Draw your map here, marking Xs where overlap occurs (there are more than sufficient columns).

А							
В							
С							
D							
E							
F							
G							
Н							
I							

Question 9 for 50 points (5 minutes)

HSV-1 is a complex double-stranded DNA virus that infects primate cells. It has multiple steps in the assembly of new virus particle, each depending on a separate viral gene. Nine mutants have blocked assembly at high temperature (restrictive conditions), yet assemble infectious virus at low temperature (permissive). The table below shows the results when the viruses are used to co-infect cells under permissive conditions, and the resulting supernatants used to infect cells under permissive conditions (where + indicates plaque formation):

	1	2	3	4	5	6	7	8
9	0	+	+	+	0	0	+	+
8	+	+	0	+	+	+	+	
7	+	0	+	0	+	+		-
6	0	+	+	+	0		-	
5	0	+	+	+		-		
4	+	+	+					
3	+	+		-				
2	+		<u>-</u> '					
1		<u>-</u> '						

- a) How many genes are involved, and which mutants have defects in the same gene?
- b) How would one alter the experiment to map the mutations (25 word limit; you must be clear and succinct)?