

Problem Set 1  
 Advanced Genetics  
 Yeast Genetics  
 March 5, 2009

1. You analyze tetrads for a variety of markers  
 The markers A-B give values of 25:23: 3200 (PD:NPD:TT)  
 The markers B-D give values of 40:0:45.  
 The markers A-D give values of 42:48:0.

Determine for the each pair of markers if they are linked or unlinked and the map distances to fill in the table below.

Markers	Linked or unlinked	Distance between markers, if applicable	Distance from marker to its centromere
A-B			
A-D			
B-D			

2. Below are tetrad data for three markers in a cross of two parents with the genes X, Y and Z segregating in the cross.

XYZ	XYZ	XYz	xYz	xYZ	xYz
XYZ	XYz	XYz	xYZ	xYZ	xYz
xyz	xyZ	xyZ	XyZ	Xyz	XyZ
xyz	xyz	xyZ	Xyz	Xyz	XyZ
20	30	19	35	18	23

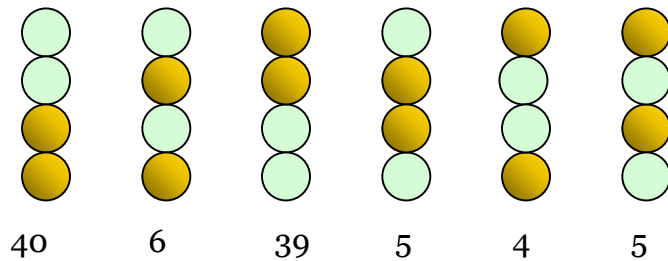
Fill the table below

Markers	Linked or unlinked	Distance between markers, if applicable	Distance from marker to its centromere
X-Y			
Y-Z			
X-Z			

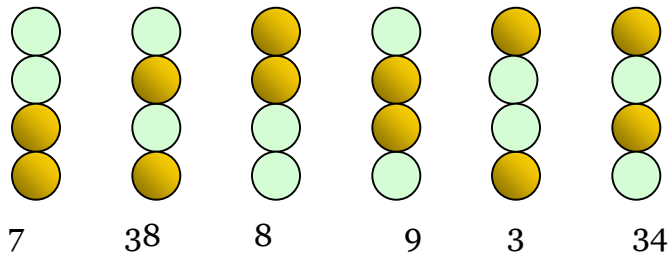
Draw the chromosomes in a meiosis I cell that could give rise to the second column of data above.

3. You obtain tetrad data for two markers in the fungus *Podospora* that give values of 10:40:40 (PD: NPD: TT). Give a model to explain what aspect of meiosis may be altered in this organism.

4. Linear tetrads are useful for centromere mapping in *Aspergillus* and *Neurospora*. The order can be used to map centromeres. The spores above the midline arise from one meiosis I daughter and the spores below the midline arise from the other meiosis I daughter. A rare *Saccharomyces cerevisiae* strain gives linear tetrads rather than tetrahedral tetrads that have no order. The two phenotypes are shaded ● and unshaded ○. Below are tetrads in the order that they were found and scored. Determine if shaded gene is linked to its centromere and what is the distance from the gene to its centromere if it can be determined.



You isolate a mutant and name the gene *AXS1*. You repeat the cross with the shaded and unshaded alleles above and the get results shown below.



Propose a model to explain these results.

5. Define:  
Homolog:

Sister chromatid:

Reductional Division:

Epistasis:

Synthetic lethality:

Monopolin

6. You streak out a yeast strain from the freezer and find that it grows like the St Louis arch instead of a round colony. You decide to devote your graduate career to understanding how arches instead of colonies form. You mutagenize yeast strains and find nine more mutants. You do a dominance and complementation test. + indicates normal flat colony phenotype and A indicates the arch phenotype.

	Mut1	Mut2	Mut3	Mut4	Mut5	Mut6	Mut7	Mut8	Mut9	Mut10
WT	+	+	+	A	+	+	+	+	+	+
1	A	+	+	A	A	A	+	A	+	+
2		A	A	A	+	+	+	+	+	+
3			A	A	+	+	+	+	A	+
4				A	A	A	A	A	A	A
5					A	A	+	A	+	+
6						A	+	A	+	+
7							A	+	+	A
8								A	+	+
9									A	+
10										A

- Are any of the mutants dominant? If so, which one(s)?
- How many complementation groups are in this collection? List the members of each group.
- Are there any entries that are confusing? Explain.
- You cross mutant 6 by wild-type and examine tetrads. You get 50 tetrads that give 2 arch and normal colonies, and you get 20 tetrads that give only three viable spores. There are two normal colonies and one arch colony. How do you explain this data? What crosses would you do next and why?

7. You obtain the heterozygous yeast deletion collection of 5700 strains. You screen for cells that are sensitive to monosodium glutamate and die. You find 9 strains. Describe a set of three experiments that would you conduct on these 9 strains to determine the basis of death.

8. Mutations in the *STE5* gene render yeast strains unable to mate. You transform a library 2micron based plasmids with wild-type DNA into the strain and select for cells that have regained the ability to mate. You find over 50 plasmids that rescue and they fall into three classes.

Plasmid one rescues all *ste5* alleles (over 20 alleles that include nonsense and missense mutations). Plasmid two rescues only the *ste5-1* allele. Plasmid three rescues both *ste5-1* and mutations in another gene, *STE4*.

Propose a hypothesis for the mode of action of each plasmid.

Propose an experiment to test your hypotheses.

9. How would you determine that loss or nondisjunction occurred with a CEN-based plasmid in yeast?