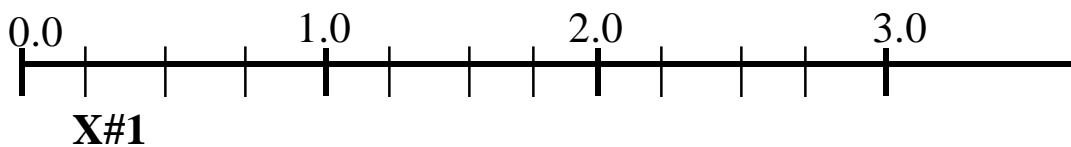


Name:

Problem Set 3 Genetics 320 Due Sept 19

- Recombination and complementation in phage
- Describe how you would do a recombination and complementation test, given you have permissive and restrictive host cells for phage yabadabdo. Be succinct.
- Below are the data you generated in analysis of the mutants. Mutant #1 is given with an "X". On the map below, place where the other 5 mutations lie. If one of the mutations is a deletion, draw a bar to indicate the region deleted (note bar for mutation #7 as an example). AND, >50% recombination means the mutations are not linked.
- B. Which mutations are recessive and which recessive.
- Indicate the location of the genes consistent with the data (label genes A, B etc)

Cross	Complementation			Recombination (%)
	10	20	30	
1x1				0
1x2		-		0.25
1x3		+		2.25
1x4		+		1.5
1x5		+		1.75
1x6		+		52
2x3		+		2.0
2x4		+		1.25
2x5		+		1.5
2x6		+		51
3x4		+		0.25
3x5		+		0.5
3x6		+		53
4x5		-		0
4x6		+		51
5x6		+		51



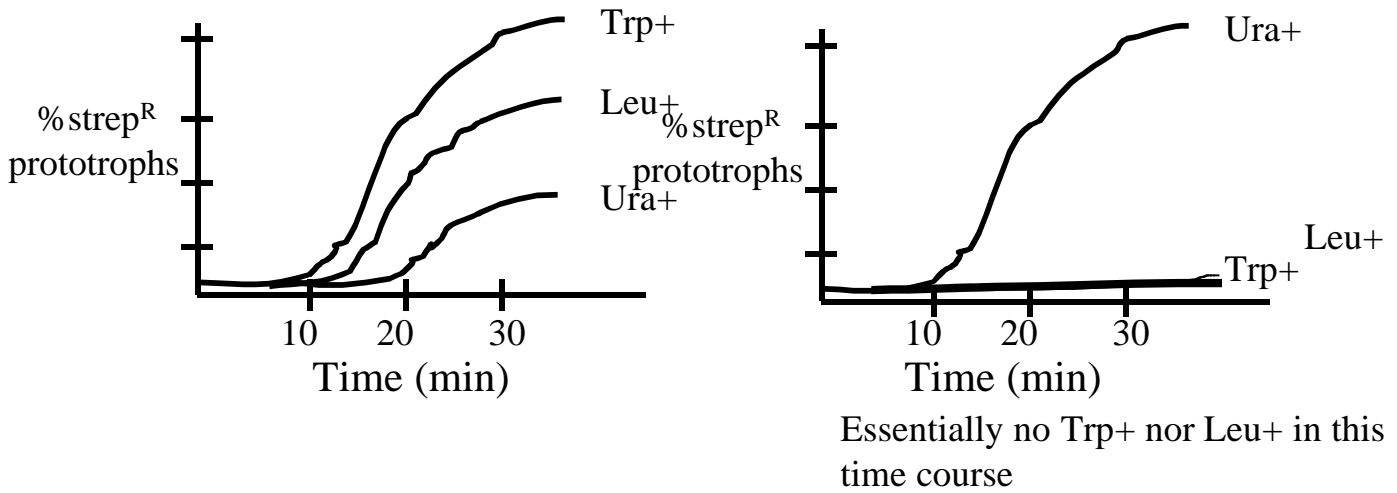
#7 is a deletion 1.25 away from #1)


Name:

2. An Hfr cross is performed with the following two Hfr strains (Hfr1 and Hfr2)

A. Hfr1 Leu1+ Trp2+ Ura3+ Strp^S by F- Leu1- Trp2- Ura3- Strp^R

B. Hfr2 Leu1+ Trp2+ Ura3+ Strp^S by F- Leu1- Trp2- Ura3- Strp^R



From these data, place on the line below where each of the two Hfr are located and their direction of transfer.  Use this to indicate direction- arrow points to first gene transferred!

3. Here is another Hfr cross and data.

Hfr3 Bio1+ Ade2+ Arg2+strep^R x F-bio1- Ade2- Arg2- Strep^S

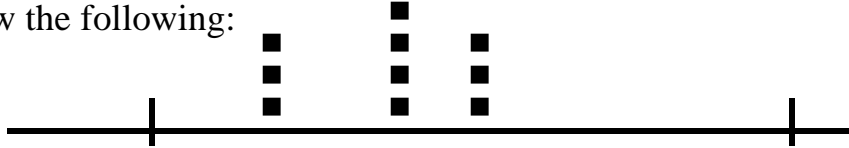
F- recipient	Frequencies of transfer
Bio1+ Ade2+ Arg2+	620
Bio1+ Ade2+ Arg2-	20
Bio1+ Ade2- Arg2+	300
Bio1+ Ade2- Arg2-	270

Indicate the likely gene order.

Name:

4. Crick-Brenner test of the genetic code

A new scientist tried to repeat the phage experiments. He used a mutagen, like EMS, that alkylates bases, and therefore changes base-pairing. When plated on B, he got mostly fuzzy roundish plaques that did not form plaques on K. He mapped the mutations and saw the following:



- i. Provide 1 reason why there are “hotspots” of mutation.
- ii. There were some round plaques. These mutations were never suppressed by proflavin-induced mutations. Explain.
- iii. These fuzzy mutations were also not suppressed by proflavin-induced mutations. Explain.

5. The original rII-1 proflavin-induced mutation was used to isolate suppressors, which were then separated by recombination from rII-1. The suppressors were used to isolate suppressor, etc. Each suppressor was then given a “sign”.

rII-1 +
rII-2 -
rII-73 -
rII-46 -
rII-19 +
rII-23 +

- A new mutation, rII-X, was isolated as a suppressor of rII-73. How would you determine if this is a new mutation, or whether it is a mutation identical to another mutation already on this list?
- List 2 sets of 3 mutations (I.e. 2 triple mutants) that should show suppression, and 2 sets of 3 mutations (I.e. 2 triple mutants) that will not.