Tetrad Analysis Problems

1. The yeast cross ***a trp1*** x ***α trp +*** produces the following tetrads. Determine the genetic map.

I	II
a trp1	a trp+
a trp1	a trp+
α trp+	α trp1
α trp+	α trp1
157	*153*

2. The yeast cross ***a leu2*** x ***α leu+*** produces the following tetrads. Determine the genetic map.

I	II
a leu2	a leu2
a leu2	a leu+
α leu+	α leu2
α leu+	α leu+
127	*15*

3. From the tetrads below, determine the map for the cross ***a trp1*** x ***α his5***:

I	II	III	IV
a trp1 his+	*a trp1 his+*	*a trp1 his+*	*a trp1 his+*
a trp1 his+	*a trp+ his+*	*α trp1 his+*	*a trp1 his5*
α trp+ his5	*α trp1 his5*	*a trp+ his5*	*α trp+ his+*
α trp+ his5	*α trp+ his5*	*α trp+ his5*	*α trp+ his5*
86	41	7	46

4. From the tetrads below, determine the map for the cross ***a trp1*** x ***α his5***:

I	II	III	IV
a trp1 his+	*a trp1 his+*	*a trp1 his+*	*a trp1 his+*
a trp1 his+	*a trp+ his+*	*α trp1 his+*	*a trp1 his5*
α trp+ his5	*α trp1 his5*	*a trp+ his5*	*α trp+ his+*
α trp+ his5	*α trp+ his5*	*α trp+ his5*	*α trp+ his5*
112	27	33	3

5. From the tetrads below, determine the map for the cross ***a ura1*** x ***α leu5***:

I	II	III	IV
a ura1 leu+	*a ura1 leu+*	*a ura1 leu+*	*a ura1 leu+*
a ura1 leu+	*a ura+ leu+*	*α ura1 leu+*	*a ura1 leu5*
α ura+ leu5	*α ura1 leu5*	*a ura+ leu5*	*α ura+ leu+*
α ura+ leu5	*α ura+ leu5*	*α ura+ leu5*	*α ura+ leu5*
511	6	106	71

6. In the cross ***a met2*** x ***α arg7***, two genes are linked and one is unlinked. Determine the map for the linked genes.

I	II	III	IV
a met2 arg+	*a met+ arg+*	*a met2 arg+*	*a met+ arg+*
a met2 arg+	*a met+ arg+*	*a met2 arg7*	*a met+ arg7*
α met+ arg7	*α met2 arg7*	*α met+ arg+*	*α met2 arg+*
α met+ arg7	*α met2 arg7*	*α met+ arg7*	*α met2 arg7*
119	125	33	27

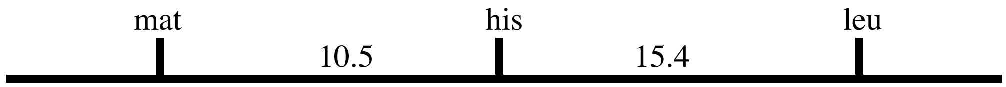
7. In the cross ***a trp3*** x ***α his2***, two genes are linked and one is unlinked. Determine the map for the linked genes.

I	II	III	IV
a trp3 his+	*α trp3 his+*	*α trp3 his+*	*a trp3 his+*
a trp3 his+	*α trp3 his+*	*α trp+ his+*	*a trp+ his+*
α trp+ his2	*a trp+ his2*	*a trp3 his2*	*α trp3 his2*
α trp+ his2	*a trp+ his2*	*a trp+ his2*	*α trp+his2*
91	85	10	16

8. In the cross ***a met2*** x ***α arg7***, two genes are linked and one is unlinked. Determine the map for the linked genes.

I	II	III	IV
a met2 arg+	*a met2 arg7*	*a met2 arg7*	*a met2 arg+*
a met2 arg+	*a met2 arg7*	*a met+ arg7*	*a met+ arg+*
α met+ arg7	*α met+ arg+*	*α met2 arg+*	*α met+ arg7*
α met+ arg7	*α met+ arg+*	*α met+ arg+*	*α met2 arg7*
87	93	15	12

9. From the map below, predict the type and number of tetrads from the cross ***a leu1*** x ***α his4.*** Assume you recover 900 tetrads.



10. From the map below, predict the type and number of tetrads from the cross ***a met1*** x ***α thr6***. Assume your recover 1200 tetrads.

11. From the map below, predict the type and number of tetrads from the cross ***a glu6*** x ***α ala4***. Assume you recover 750 tetrads.

Answers To Tetrad Analysis Problems

1. Tetrad I is a parental ditype
   Tetrad II is a non parental ditype

   PD = NPD therefore ***trp*** and ***mat*** are unlinked

2. Tetrad I is a parental ditype
   Tetrad II is a non parental ditype

   PD > T > NPD Therefore, ***leu*** and ***mat*** are linked

   cM = .5 T/(PD +T) x 100 = [.5 (15)/(127 + 15)] x 100 = 5.28 cM

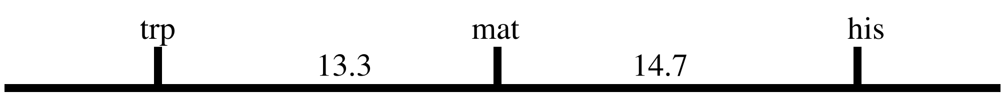
3. Tetrad I is a parental ditype
   Tetrad III is the rarest tetratype and represents the double recombinants
   Tetrads II and IV are intermediate tetratypes and represent single recombinants

   For each pair of genes, PD > T > NPD
   Therefore all three genes are linked

   In the double recombinants, ***mat*** switches linkage
   Therefore the sequence is: ***trp---mat---his***

   II = ***mat*** - ***trp*** **=** [0.5(41 +7)/(86 + 41 + 7 +46)] x 100 = 13.3 cM

   IV = ***mat - trp*** = [0.5(46 +7)/(86 + 41 + 7 +46)] x 100 = 14.7 cM



4. Tetrad I is a parental ditype
Tetrad IV is the rarest tetratype and represents the double recombinants
Tetrads II and III are intermediate tetratypes and represent single recombinants

For each pair of genes, PD > T > NPD
Therefore all three genes are linked

In the double recombinants, ***his*** switches linkage
Therefore the sequence is: ***met---his---trp***

II = ***his*** - ***trp*** **=** [0.5(27 + 3)/(112 + 27 + 33 + 3)] x 100 = 8.57 cM

III = ***mat - trp*** = [0.5(33 + 3)/(112 + 27 + 33 + 3)] x 100 = 10.29 cM

5. Tetrad I is a parental ditype
Tetrad II is the rarest tetratype and represents the double recombinants
Tetrads III and IV are intermediate tetratypes and represent single recombinants

For each pair of genes, PD > T > NPD
Therefore all three genes are linked

In the double recombinants, ***ura*** switches linkage
Therefore the sequence is: ***mat---ura---leu***

III = ***mat-urp*** **=** [0.5(106 + 6)/(511 + 6 + 106 +71)] x 100 = 8.07 cM

IV = ***mat - trp*** = [0.5(71 + 6)/(511 + 6 + 106 +71)] x 100 = 5.55 cM

6. No obvious highest and lowest classes: Look at genes in pairs

Tetrad	mat/met	mat/arg	met/arg
I = 119	PD	PD	PD
II = 125	NPD	PD	NPD
III =33	PD	T	T
IV = 27	NPD	T	T
	PD = NPD	PD>T>NPD	PD=NPD
conclusion:	unlinked	linked	unlinked

mat - arg $= [0.5(III + IV)/ (I + II + III + IV)] \times 100$

$= [0.5(33 + 27)/(119 + 125 + 33 +27)] \times 100$

$= 9.87$ cM

7. No obvious highest and lowest classes: Look at genes in pairs

Tetrad	mat/trp	mat/his	trp/his
I = 91	PD	PD	PD
II = 85	NPD	NPD	PD
III =10	T	NPD	T
IV = 16	T	PD	T
	PD = NPD	PD = NPD	PD>T>NPD
conclusion:	unlinked	unlinked	linked

mat - arg $= [0.5(III + IV)/ (I + II + III + IV)] \times 100$

$= [0.5(10 + 16)/(91 + 85 + 10 + 16)] \times 100$

$= 6.44$ cM

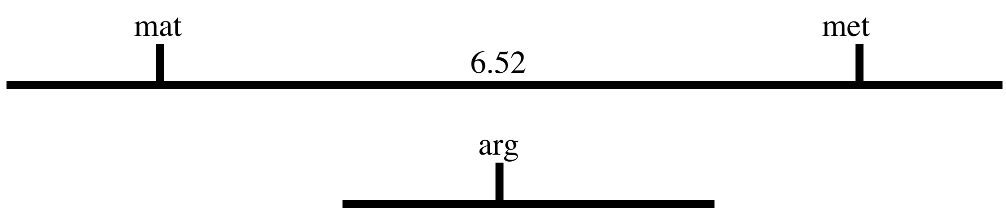
8. No obvious highest and lowest classes: Look at genes in pairs

	Tetrad	mat/met	mat/arg	met/arg
	I = 87	PD	PD	PD
	II = 93	PD	NPD	NPD
	III =15	T	NPD	T
	IV = 12	T	PD	T
		PD>T>NPD	PD = NPD	PD = NPD
conclusion:		linked	unlinked	unlinked

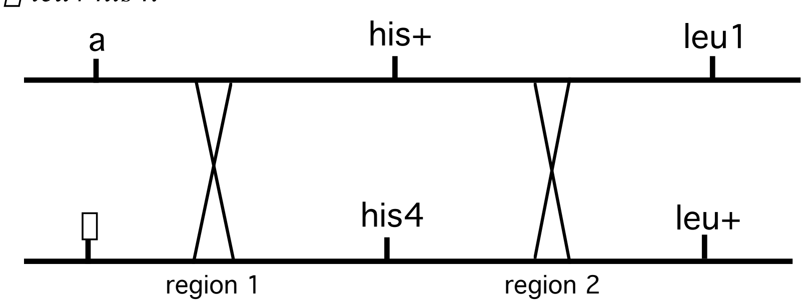
mat - arg $= [0.5(III + IV)/ (I + II + III + IV)] \times 100$

$= [0.5(15 + 12)/(87 + 93+ 15 +12)] \times 100$

$= 6.52$ cM



9. The cross is *a leu1 his+* x *□ leu+ his4:*



Four events can occur:
1 no recombination
2 a single recombination event in region 1
3 a single recombination event in region 2
4 two recombination events, one in region 1 and the other in region 2

#1 will produce a parental ditype = Tetrad I
#2 will produce a tetratype in which **mat** changes linkage = Tetrad II
#3 will produce a tetratype in which **leu** changes linkage = Tetrad III
#4 will produce a tetratype in which **his** changes linkage = Tetrad IV

I	II	III	IV
no recomb	recomb region 1	recomb region 2	recomb regs 1 & 2
a leu-1 his +	**a** leu-1 his +	a **leu-1** his +	a leu-1 **his +**
a leu-1 his +	□ leu-1 his +	a **leu-+** his +	□ leu-1 **his-4**
□ leu + his-4	**a** leu + his-4	□ **leu-1** his-4	□ leu + **his +**
□ leu + his-4	□ leu + his-4	□ **leu** + his-4	□ **l**eu + **his-4**

The distance between two genes is

cM = 0.5 [(single XO's + double XO's) / total] x 100

Equation #1 tells us the total number of recombination events occurring between two loci whose distance is known. It is derived by simple algebra from the mapping formula:

Total XO's = single XO's + double XO's = 2 [(cM x total) / 100]

This tells us the total number of recombinants, but to get the number of singles, we must subtract the doubles. The doubles must be calculated independently. cM expresses the probability of a recombination event. If two recombinations are independent of one another, then the number of double recombinants can be calculated by determining the product of their independent probabilities and multiplying by the total. In **Equation #2**:

double XO's = 2 [(cM reg 1) / 100] x [(cM reg 2) / 100] x total

This will give the number of tetrads showing the IV pattern. (The factor of 2 in the equation is derived from the **1/2** that we use when dealing with tetrads.) Now, the total number of single recombinations between two loci can be calculated, giving the numbers of II and III tetrads. All that is left is to calculate the number of non recombinants:

Total Tetrads = I + II + III + IV

or **Non Recombinants = I = Total Tetrads - II - III - IV**

double XO's = tetrad IV = 2 [(10.5 / 100) x (15.4 / 100) x 900 = **29.1**

single XO's in region 1 = tetrad II = **mat - his** = 2 [(10.5 x 900) / 100] - 29 = **160**

single XO's in region 2 = tetrad III = **his -leu** = 2 [(15.4 x 900) / 100] - 29 = **248**

non recombinants = tetrad I = 900 - 160 - 248 - 29 = **463**

10. # 10 is set up exactly like #9:

double XO's = tetrad IV = 2 [(2.7 / 100) x (15.9 / 100) x 1200 = **<u>10</u>**

single XO's in region 1 = tetrad II = **thr - mat** = 2 [(2.7 x 1200) / 100] - 10 = **<u>55</u>**

single XO's in region 2 = tetrad III = **mat - met** = 2 [(15.9 x 1200) / 100] - 10 = **<u>372</u>**

non recombinants = tetrad I = 1200 - 55 - 372 - 10 = **<u>763</u>**

11. #11 is set up exactly like #9

double XO's = tetrad IV = 2 [(18.2 / 100) x (9.1 / 100) x 750 = **<u>25</u>**

single XO's in region 1 = tetrad II = **glu - ala** = 2 [(18.2 x 750 / 100] - 10 = **<u>248</u>**

single XO's in region 2 = tetrad III = **ala - mat** = 2 [(9.1 x 750) / 100] - 10 = **<u>112</u>**

non recombinants = tetrad I = 750 - 112 - 248 - 25= **<u>365</u>**