PROBLEMS

Problem 1 Mapping the distance between two genes

Starting with pure breeding lines,
Cross Parent 1(AA BB) with Parent 2(aa bb)
So Parental chromosomes in the F1 have to be AB and ab

Now cross (AB ab) F1 progeny with (ab ab) tester to look for recombination on these chromosomes.
Suppose you Get……

AB ab	583	<parental
ab ab	597	<parental
Ab ab	134	<recombinant
aB ab	134	<recombinant
total=	1448	

so…. 268 recombinants /1448 progeny x 100 =
0.185 recombinants/progeny x100 = 18.5% recombinants= 18.5 cM

Problem 2: Mapping (and ordering) three genes

Starting with pure breeding lines, Cross Parent 1(AA BB DD) with Parent 2(aa bb dd)

So you know the Parental chromosomes in the F1 have to be ABD and abc

Cross (ABD abd) F1 progeny with (abd abd) tester

Suppose you Get……

ABD abd	580	<parental
ABd abd	3	
abD abd	5	<parental
abd abd	592	
AbD abd	45	<recombinant
Abd abd	89	
aBD abd	94	
aBd abd	40	<recombinant
	total= 1448	

Ab + aB =
(45+89)+(94+40) recom
268 recom/1448 total
=0.185 **A-B** =18.5mu

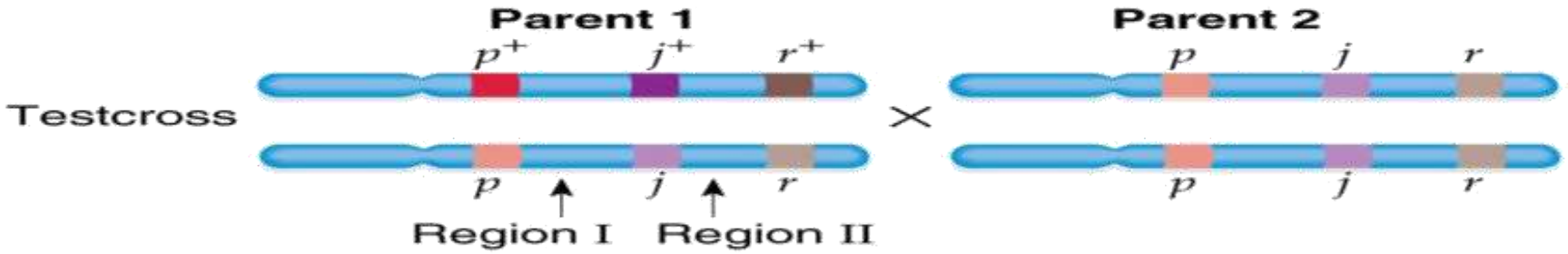
Bd + bD = (3+40)+(5+45)
93 recom/1448 total= 0.064
B-D =6.4mu

Ad + aD = (3+89)+(5+94)
191 recom/1448 total= 0.132
A-D =13.2mu

so the order must be **A-----D---B**
-13.2--6.4-
----18.5----

So How come 13.2 + 6.4 does not equal 18.5? Due to double crossing over

Problem 3: Calculate recombination frequencies and construct the linkage map.



Testcross progeny

Class	Genotype of gamete from heterozygous parent			Number	Origin
1	p^+	j^+	r^+	179	Parentals, no crossover
2	p	j	r	173	
3	p^+	j	r	52	Recombinants, single crossover region I
4	p	j^+	r^+	46	
5	p^+	j^+	r	22	Recombinants, single crossover region II
6	p	j	r^+	22	
7	p^+	j	r^+	4	Recombinants, double crossover
8	p	j^+	r	2	
				Total = 500	

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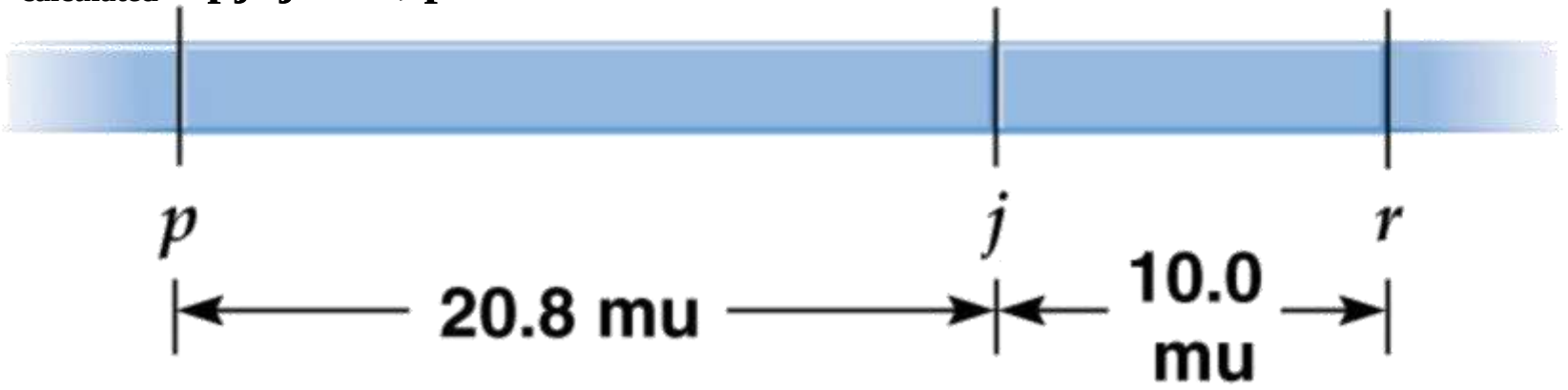
Calculate (%):

p x j (%) =
(52+46+4+2)x100/500 = 20.8%
i.e. distance= 20.8 cM

j x r (%) =
(22+22+4+2)x 100/500 = 10.0%
i.e. distance=10 cM

p x r (%) =
(52+46+22+22)x100/500 = 28.4%
i.e. distance= 28.4 cM
pr $_{calculated}$ < pj+jr so, presence of double crossover.



Problem 4: In rabbits, black (B) is dominant to brown (b), while full color (F) is dominant to chinchilla (f). The genes controlling these traits are *linked*.

- The following cross was made: rabbits heterozygous for both traits that express black, full color, with rabbits that are brown, chinchilla. The following results were obtained:
  - 31 brown, chinchilla
  - 35 black, full
  - 16 brown, full
  - 19 black, chinchilla

- Determine the genotype of the heterozygous parents, and the map distance between the 2 genes.

Solution

The genotypes of the parents (this cross was a testcross)

BbFf x bbff

We're given the numbers for each of the expected phenotypic classes amongst the offspring:

31 bbff

34 BbFf

16 bbFf

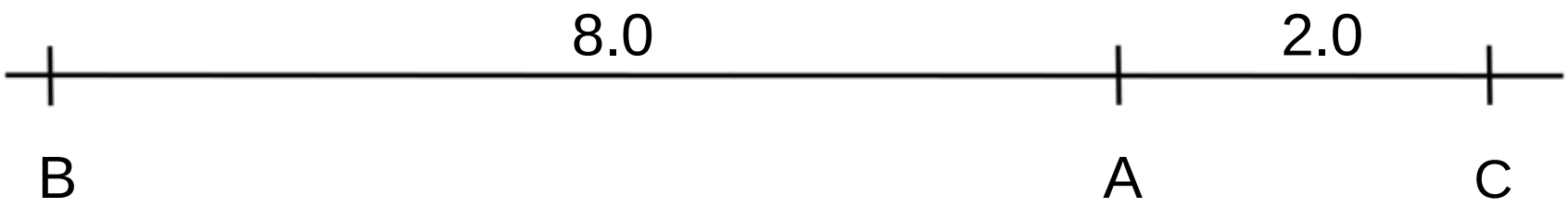
19 Bbff

The latter two classes, which have considerably fewer members, must be the non-parental.

The recombination frequency = (16 + 19) / (31 + 34 + 16 + 19) x 100 = 35%.

Problem 5: Draw a linkage map based on the following cross over percentages:

- A – B = 8%
- B – C = 10%
- A – C = 2%



$$8.0 + 2.0 = 10.0$$

Problem 6:

The following testcross produces the progeny shown:

AaBb × aabb → 40 AaBb, 10 aaBb, 10 aaBb, and 40 aabb.

What is the percentage of recombination between the A and B loci?

% recombination=
(10+10)/100 X100= 20%.

Problem 7:

Write the genotypes of all recombinant and non recombinant progeny expected from the following three-point cross:

$$\frac{M \quad P \quad S}{m \quad p \quad s} \times \frac{m \quad p \quad s}{m \quad p \quad s}$$

Problem 7:

Write the genotypes of all recombinant and non recombinant progeny expected from the following three-point cross:

$$\frac{M \quad P \quad S}{m \quad p \quad s} \times \frac{m \quad p \quad s}{m \quad p \quad s}$$

Answer:

$$\frac{MPS}{mps} \quad \frac{Mps}{mps} \quad \frac{mPS}{mps} \quad \frac{MPs}{mps} \quad \frac{mps}{mps} \quad \frac{MpS}{mps} \quad \frac{mPs}{mps} \quad \frac{mps}{mps}$$

Problem 8:

A three-point test cross is carried out between three linked genes. The resulting non recombinant progeny are $s^{+}\ r^{+}\ c^{+}$ and s r c, and the double-crossover progeny are s r c^{+} and $s^{+}\ r^{+}$ c. Which is the middle locus?

the C locus

Problem 9

How many gametes are in the original parental configuration (PL or pl) and how many are in the recombinant configuration (Pl or pL).

- **Original parents: PP LL x pp ll**
- **F1 test cross: Pp Ll x pp ll**

Phenotype	obs
purple long	392
purple round	116
red long	127
red round	365
total	1000

Answer

- The parental types have the same combination of alleles that were in the original parents, and the recombinant types have a combination of the mother's and father's alleles.
- Parental: 392 PL + 365 pl = 757.

  757/1000 total offspring = 75.7% parental
- Recombinant: 116 Pl + 127 pL = 243.

  243 /1000 = 24.3% recombinant.
- If the genes were unlinked, 50% would be recombinant.
- These genes are linked, with 24.3% recombination between the P gene and the L gene.
- The percentage of recombinants is always between 0% and 50%, and the percentage of parental is always between 50% and 100%.

Problem 10

- In corn, c gives a green plant body, while its wildtype allele c^+ gives a purple plant body.
- bz (bronze) gives brown seeds, while the wildtype allele bz^+ gives purple seeds.
- wx (waxy) gives waxy endosperm in the seeds; wx^+ gives starchy endosperm.
- The genes are arranged on the chromosome in the order c-bz-wx.
- The cross:

c bz wx / + + + x c bz wx.

- Note the +'s are the dominant wildtype alleles of the corresponding gene.
- **Construct linkage map.**

phenotype	count
c bz wx	318
+ + +	324
c bz +	105
+ + wx	108
c + +	18
+ bz wx	20
c + wx	4
+ bz +	3
total	900

Notes on the Data

- Genes are arranged in reciprocal pairs: each pair has 1 copy of the mutant allele and the wildtype allele for each gene. The counts are roughly equal for reciprocal pairs, because they are both products of the same crossing over events.
- Parentals are the largest groups: c bz wx and + + +.
- Double crossovers, one between c and bz and another between bz and wx, are the smallest groups.

Calculating Map Distances

- Basic process: determine the percentage of offspring that had a crossover between each pair of genes.

1. Examine c and bz first.

Parental configuration was c bz and + +. Therefore, the recombinant configurations are c + and + bz.

- Count recombinants, ignoring the other gene (wx): 18 (c + +) , 20 (+ bz wx), 4 (c + wx), 3 (+ bz +).
- Total is 45 recombinants out of 900 total offspring. 45 / 900 = 0.05.
- Need to multiply by 100 to get percentage: 0.05 x 100 = 5.0 map units between c and bz.

More Calculating Map Distances

- **2. Next examine bz and wx.**
  - Parentals are bz wx and + +, so recombinants are bz + and + wx.
  - Ignoring c, the count of recombinants is:
  - 105 (c bz +), 108 (+ + wx), 4 (c + wx), 3 (+ bz +).
  - Total = 220 recombinants. 220 / 900 = 0.244.
  - 0.244 x 100 = 24.4 map units between bz and wx.

- **3. Now do c and wx.** Parentals are c wx and + +, so recombinant offspring are c + and + wx.
  - Ignoring bz, the recombinants are 105 (c bz +), 108 (+ + wx), 18 (c + +) , 20 (+ bz wx).
  - Total = 251. 251/ 900 x 100 = 27.9 map units.

Map of c, bz, and wx

- All 3 genes are in the proper order, and all 3 distances between pairs of genes are shown.
- Note that distances don't add up.
- This is due to double crossover.

Work sheet problems

In Pea

- A heterozygous trihybrid Pea (*Pisum sativa*) with tall stem, purple-flowered and round seeds was test crossed. Where, tall stem (T) is dominant over dwarf one (t), purple flower (P) is dominant over white one (p) and rounded seed (R) is dominant over wrinkled one (r).

The F1 results of these cross were:

230 Tall stem, purple-flowered with rounded seeds

230 Dwarf stem, purple-flowered with rounded seeds

230 Tall stem, white-flowered with wrinkled seeds

230 Dwarf stem, white-flowered with wrinkled seeds

20 Tall stem, white-flowered with rounded seeds

20 Dwarf stem, white-flowered with rounded seeds

20 Tall stem, purple-flowered with wrinkled seeds

20 Dwarf stem, purple-flowered with wrinkled seeds

- What are the genotype of the parental cross and each the F1 generation?
- Which of the genes are linked? If so, construct a chromosome map showing the relative position for these genes on chromosome.

Solve

- **What are the genotype of the parental cross and each the F1 generation?**
- **Parents** TtPpRr X ttpprr

The F_1 results of these cross were:

230 Tall stem, purple-flowered with rounded seeds (TtPpRr)

230 Dwarf stem, purple-flowered with rounded seeds (ttPpRr)

230 Tall stem, white-flowered with wrinkled seeds (Ttpprr)

230 Dwarf stem, white-flowered with wrinkled seeds (ttpprr)

20 Tall stem, white-flowered with rounded seeds (TtppRr)

20 Dwarf stem, white-flowered with rounded seeds (ttppRr)

20 Tall stem, purple-flowered with wrinkled seeds (TtPprr)

20 Dwarf stem, purple-flowered with wrinkled seeds (ttPprr)

Which of the genes are linked?

- **For T and P**

If not linked the results must be:

Parents TtPp X ttpp

Gametes TP Tp tP tp tp tp tp tp

F_1 TtPp : Ttpp : ttPp : ttpp

1 : 1 : 1 : 1

From the provided data, the ratios among offspring for these 2 genes are:

TtPp : Ttpp : ttPp : ttpp

230+20 : 230+20 : 230+20 : 230+20

250 : 250 : 250 : 250

i.e. 1 : 1 : 1 : 1

so, T and P are not Linked

For T and R

If not linked the results must be:

Parents TtRr X ttrr

Gametes TR Tr tR tr tr tr tr tr

F_1 TtRr : Ttrr : ttRr : ttrr

1 : 1 : 1 : 1

From the provided data, the ratios among offspring for these 2 genes are:

TtRr : Ttrr : ttRr : ttrr

230+20 : 230+20 : 230+20 : 230+20

250 : 250 : 250 : 250

i.e. 1 : 1 : 1 : 1

so, T and R are not Linked

For P and R

If not linked the results must be:

Parents PpRr X pprr

Gametes PR Pr pR pr pr pr pr pr

F_1 PpRr : Pprr : ppRr : pprr

1 : 1 : 1 : 1

From the provided data, the ratios among offspring for these 2 genes are: PpRr : Pprr : ppRr : pprr

230+230 : 20+20 : 20+20 : 230+230

i.e. 460 : 40 : 40 : 460

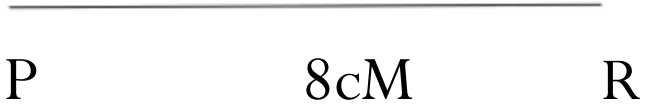
so, P and R are Linked

Total number of offspring= (230 x 4) + (20 x 4) = 920 + 80 = 1000

Recombination frequency between P and R= (20+20+20+20/ 1000) x 100= 8%

Distance between P and R = 8 cM

Construct a chromosome map showing the relative position for these genes on chromosome.



Another way of solving the Problem

- **What are the genotype of the parental cross and each the F1 generation?**
- **Parents** TtPpRr X ttpprr

The F_1 results of these cross were:

230 Tall stem, purple-flowered with rounded seeds (TtPpRr)

230 Dwarf stem, purple-flowered with rounded seeds (ttPpRr)

230 Tall stem, white-flowered with wrinkled seeds (Ttpprr)

230 Dwarf stem, white-flowered with wrinkled seeds (ttpprr)

20 Tall stem, white-flowered with rounded seeds (TtppRr)

20 Dwarf stem, white-flowered with rounded seeds (ttppRr)

20 Tall stem, purple-flowered with wrinkled seeds (TtPprr)

20 Dwarf stem, purple-flowered with wrinkled seeds (ttPprr)

Which of the genes are linked?

- **For T and P**

TtPp X ttpp

Total number of offspring= (230 x 4)+ (20 x 4) = 920 + 80 = 1000

Number of Parental combination (230x2) + (20x2) = 500

% Parental combination = 500\1000 x100 = 50%

Number of New Combination (230x2) + (20x2) = 500

% New combination between T and P = 500\1000 x100 = 50% so, T and P are not Linked

- **For T and R**

TtRr X ttrr

Total number of offspring= (230 x 4)+ (20 x 4) = 920 + 80 = 1000

Number of Parental combination (230x2) + (20x2) = 500

% Parental combination = 500\1000 x100 = 50%

Number of New Combination (230x2) + (20x2) = 500

% New combination between T and R = 500\1000 x100 = 50%

so, T and R are not Linked

- **For P and R**

PpRr X pprr

Total number of offspring= (230 x 4)+ (20 x 4) = 920 + 80 = 1000

Number of Parental combination 230x4 = 920

% Parental combination = 920\1000 x100 =

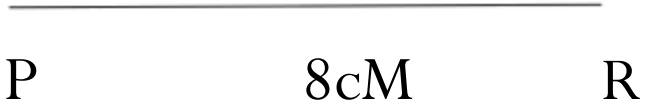
92% Number of New Combination 20x4 = 80

% New combination between P and R = 80\1000 x100 =

8% so, P and R are Linked

Distance between P and R = 8 cM

Construct a chromosome map showing the relative position for these genes on chromosome.



1. In Corn:

Long stem (A) is dominant While short stem (a) is recessive
Rounded seed (B) is dominant While wrinkled seed (b) is recessive
Smooth stem (C) is dominant While rough stem (c) is recessive

A heterozygous trihybrid plant with Long stem, Rounded seed and Smooth stem was test crossed.

The Results of F1 was:

410 Long stem, Rounded seed and Smooth stem
410 short stem, wrinkled seed and rough stem
50 Long stem, wrinkled seed and rough stem
50 short stem, Rounded seed and Smooth stem
40 Long stem, wrinkled seed and Smooth stem
40 short stem, Rounded seed and rough stem

Construct a chromosome map showing the relative position for these genes.

410 AaBbCc	410 aabbcc
50 Aabbcc	50 aaBbCc
40 AabbCc	40 aaBbcc

Recombination Frequency for A and C: [(50+50)/1000]X100 = 10%

Distance between A and C is 10 centimorgan

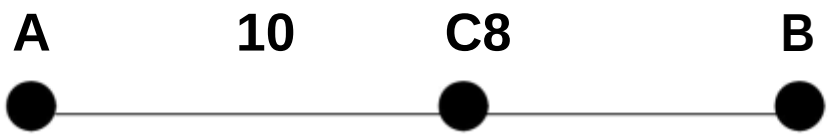
Recombination Frequency for B and C: [(40+40)/1000]X100 = 8%

Distance between B and C is 8 centimorgan

Recombination Frequency for A and B: [(50+50+40+40)/1000]X100 = 18%

Distance between A and B is 18 centimorgan

Thus AB = AC + BC



2. A heterozygous trihybrid plant with Long stem, Rounded seed and **Smooth stem was test crossed.**
The Results of F1 was:

415 Long stem, Rounded seed and **Smooth stem**
415 short stem, wrinkled seed and **rough stem**
35 Long stem, wrinkled seed and **Smooth stem**
35 short stem, Rounded seed and **rough stem**
45 Long stem, wrinkled seed and **rough stem**
45 short stem, Rounded seed and **Smooth stem**
5 Long stem, Rounded seed and **rough stem**
5 short stem, wrinkled seed and **Smooth stem**

Construct a chromosome map showing the relative position for these genes.

415 AaBbCc	415 aabbcc
35 AabbCc	35 aaBbcc
45 Aabbcc	45 aaBbCc
5 AaBbcc	5 aabbCc

Recombination Frequency for A and C: [(45+45+5+5)/1000]X100 = 10%

Distance between A and C is 10 centimorgan

Recombination Frequency for B and C: [(35+35+5+5)/1000]X100 = 8%

Distance between B and C is 8 centimorgan

Recombination Frequency for A and B: [(45+45+35+35)/1000]X100 = 16%

Distance between A and B is 16 centimorgan

Thus AB ≠ AC + BC