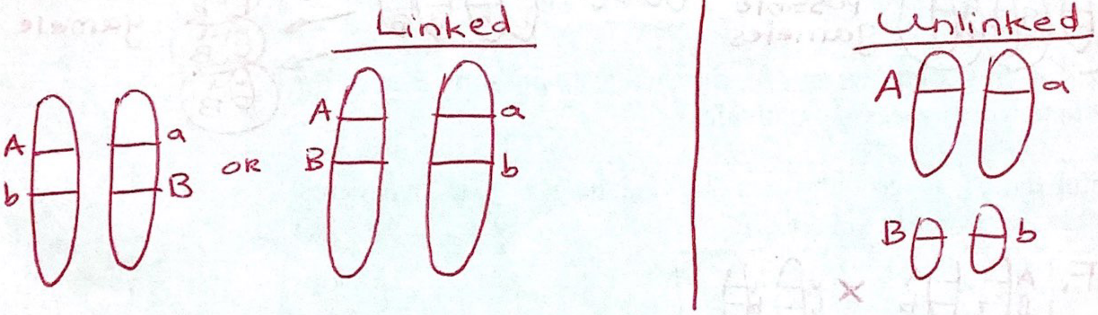
**Name** Key

**AP Bio: Linkage Analysis Worksheet**

1. A. Define linkage between two genes.

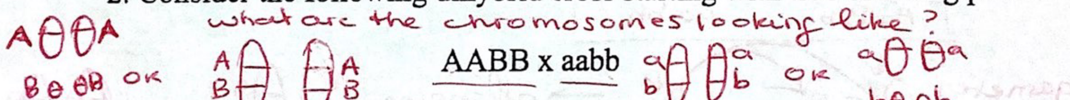
2 genes located on the same chromosome / DNA molecule

B. Illustrate the distinction between linked vs unlinked genes with a diagram showing two gene pairs ( Aa , Bb ) which are unlinked vs linked.




2. Consider the following dihybrid cross starting with true breeding parents

what are the chromosomes looking like?

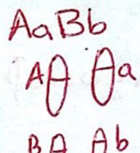



A. What is the genotype of the F1 offspring?

| | A | A |
|---|---|---|
| a | Aa | Aa |
| a | Aa | Aa |

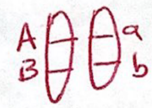
| | B | B |
|---|---|---|
| b | Bb | Bb |
| b | Bb | Bb |

if unlinked: AaBb




if linked: only 1 gamete possible (Both genes on one chromosome)

| | AB |
|---|---|
| ab | AaBb |



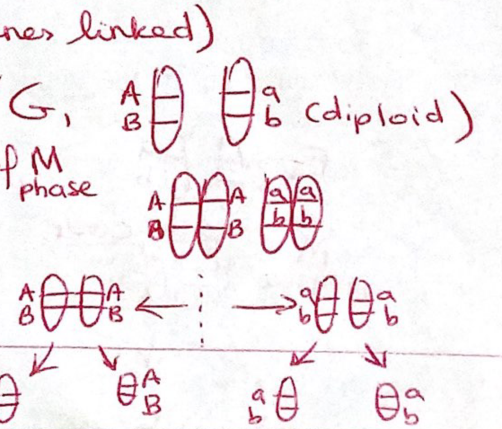

B. Assuming the a and b loci are linked, draw the possible unreplicated(single stranded)chromosomes resulting from meiosis assuming that there is no crossing over. Note that there are only two possible chromosomes here.

F1 AaBb (assume genes linked)

1) Prior to M phase / G1 (diploid)

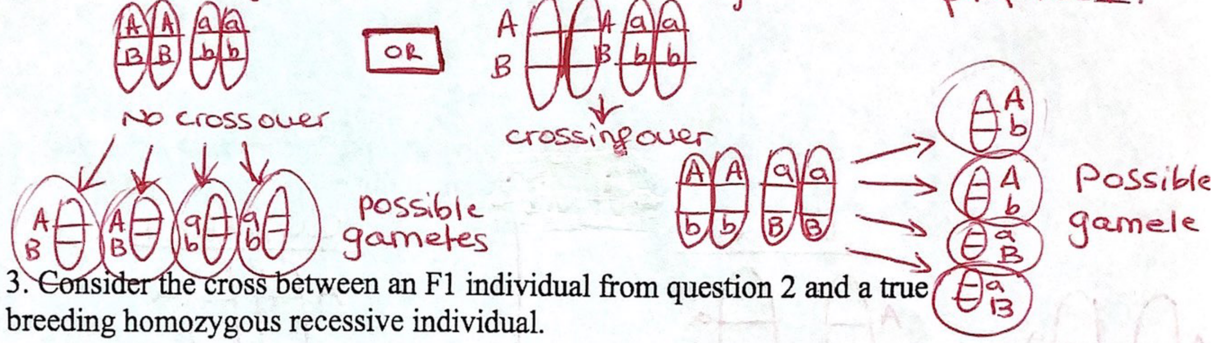
2) After S phase / start of M phase

3) Meiosis separates homologs + later separates sister chromatids



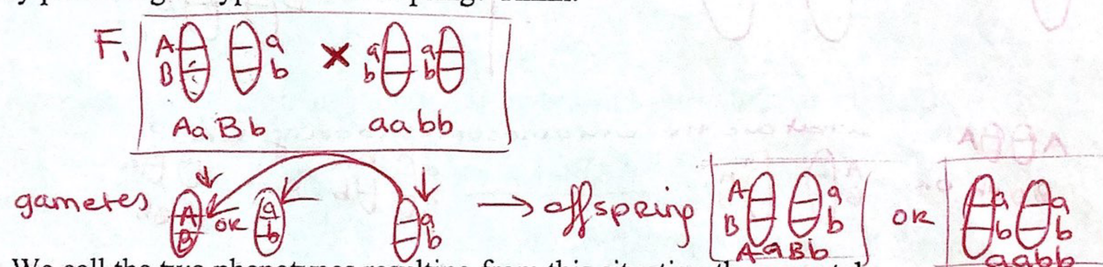
D. Draw the two other possible unreplicated chromosomes from meiosis after a cross over event happens.

Crossing over would happen during tetrad formation in prophase I.




3. Consider the cross between an F1 individual from question 2 and a true breeding homozygous recessive individual.

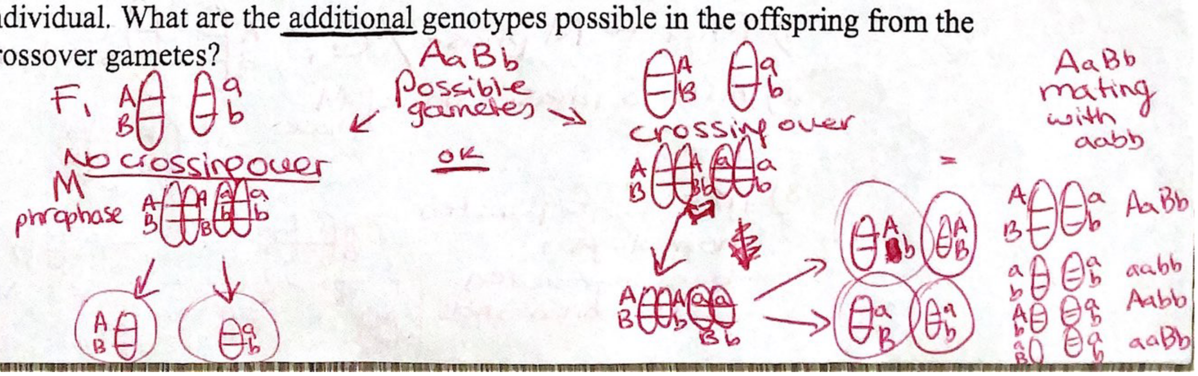
A. Assuming there is no crossing over between the gene pairs, what are the only possible genotypes in the offspring? Think!




B. We call the two phenotypes resulting from this situation the parental phenotypes. Why?

Match phenotype of 1 of the 2 parents.

C. Suppose there is a cross over event involving the gene pair for the F1 individual. What are the additional genotypes possible in the offspring from the crossover gametes?

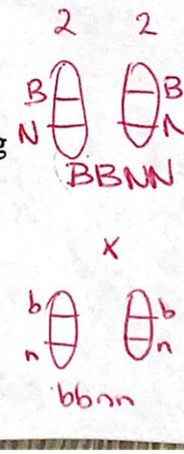


D. We call the resulting phenotypes the non-parental phenotypes. Why?

2 out of the 4 phenotypes look like a hybrid of parental phenotypes. They half one phenotype that matches that of parent #1 and the other phenotype that matches a phenotype of parent #2.

N = normal B - brown
n = vestigal b. - cinnebar

4. Some real data(Ok,semi-real). In fruit flies, a mutation, cinnabar eyes,is linked to a mutation for vestigial wing on the second chromosome. Pure breeding wild type flies (Brown eye, normal wing) are bred with pure breeding cinnabar, vestigial wing flies(double homozygous recessive).



These result in a series of F1 individuals. Female F1's are bred with pure breeding cinnabar vestigial wing males and the offspring were scored with respect to phenotype and the following results were obtained:

$F_1$ B/N, b/n × b/n, b/n

Bb Nn     bb nn

↓

? $F_2$

Phenotype of offspring:

Wild type eyes, wild type wings 465

Wild type eyes, vestigial wings 45

Cinnabar, wild type wings 35

Cinnabar, vestigial wings 455

A. What fraction of offspring would you expect to find if the genes **had been** unlinked?

$F_1$ B, b × b, b

N, n     n, n

Bb Nn     bbnn ↳ gametes

gametes ← parent #1: (bn), (BN), (Bn), (bN)

parent #2 gamete: (bn) =

possible mating results

bbnn 1/4

BbNn 1/4

Bbnn 1/4

bbNn 1/4

Expected genotypes 1:1:1:1

Expected phenotypes 1:1:1:1

B. Calculate the expected number of offspring of each phenotype using your answer from A (Hint! you will need first to calculate the total number of offspring resulting from this cross)

Total # of offspring produced was 465 + 45 + 35 + 455 = 1000

If I expect $\frac{1}{4}$ of each of 4 phenotypes =

$\frac{1}{4}$ × 1000 = 250 bbnn

$\frac{1}{4}$ × 1000 = 250 Bb Nn

$\frac{1}{4}$ 1000 = 250 Bbnn

$\frac{1}{4}$ 1000 = 250 bb Nn

C. Calculation of map distance. Distance between linked genes is often expressed in terms of map units. A map unit is defined as 1% recombination

In real life 45 + 35 = Recombinant phenotype = 80

Total # offspring produced = 1000

Recombination frequency = $\frac{80}{1000}$ = .08 × 100% = 8%

8 mu

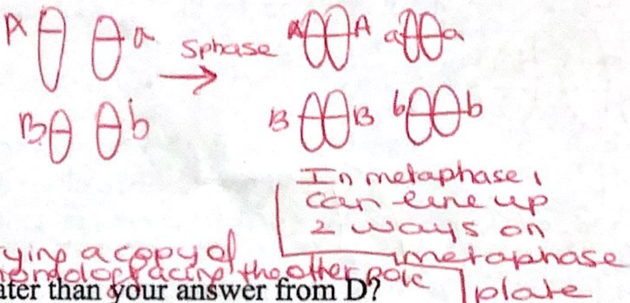
between the two gene pairs. How many map units are the genes for eye color and wing length from each other?

8 map units

D. Suppose the genes were on separate chromosomes. What would be the expected map distance between the two genes? Explain in terms of independent assortment.

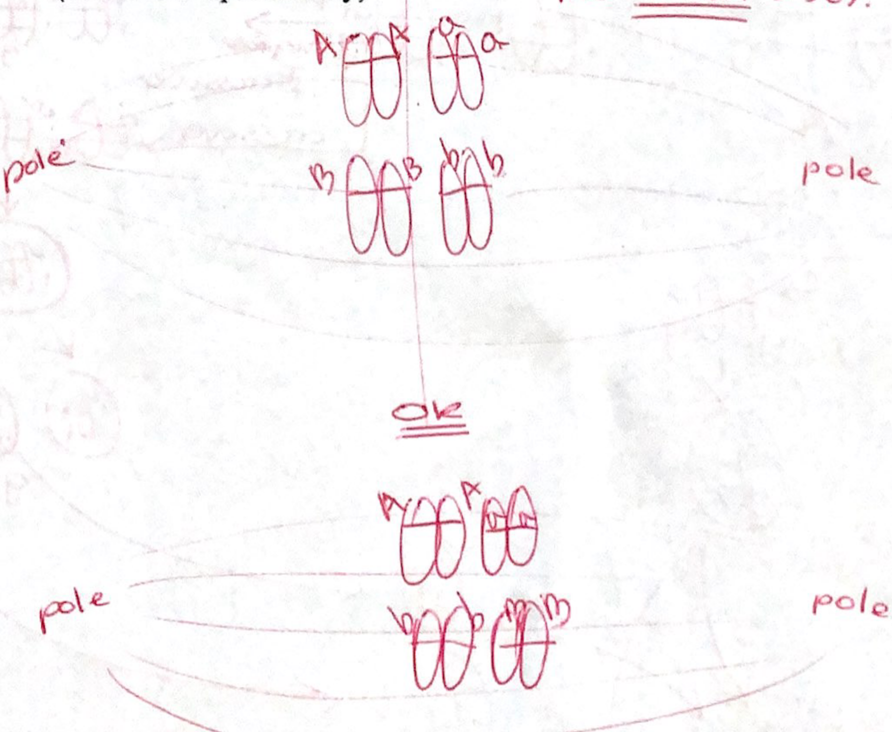
50%.

Tetrads line up at metaphase I plate independent of each other, one homolog carrying a copy of the gene facing one pole. The other homolog facing the other pole



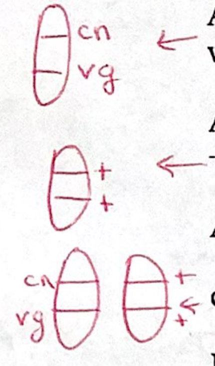

E. Can you ever observe a map distance greater than your answer from D? (Think about probability)

No - Never > 50%.




5. Some notation: Switch to a more convenient notation for each gene pair. Let + = the wild type allele. Let cn be the cinnabar allele. For the wing length genes

let vg = vestigial, and + = the wild type. Note that non mutant allele is always called +.



A chromatid containing the alleles for cinnabar and vestigial wing would be written as: cn vg.

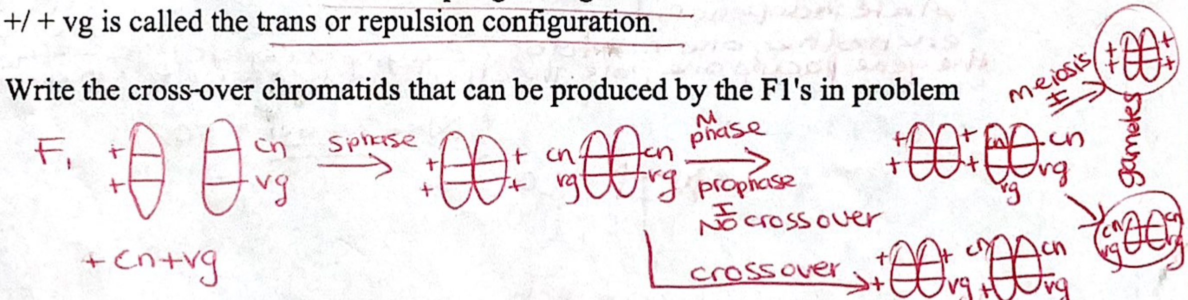
A chromatid containing only wild type alleles at each locus would be written as + + .

A heterozygote for the F1 from the geneticist's cross would be.

cn vg / + +

Note this kind of configuration where both mutant alleles are together on the same chromsome is called a cis or coupling configuration. On the other hand, cn +/ + vg is called the trans or repulsion configuration.

A. Write the cross-over chromatids that can be produced by the F1's in problem 4.



B. Write the two non-parental genotypes resulting from a crossover event in the F1's mated to a cn vg male.