Mapping Handout

- Mapping requires genetic variation (i.e. two alleles per gene) and crossing over (recombination).
- Crossing over can be observed in heterozygotes only.

Consider mapping two genes, A and B. We must have two alleles for both genes. We must have a double heterozygote, AaBb, for crossing over to occur in. There are two ways to make this double heterozygote:

AABB x aabb: or AAbb x aaBB:

$$\frac{A \quad B}{A \quad B} \times \frac{a \quad b}{a \quad b} \qquad\qquad \frac{A \quad b}{A \quad b} \times \frac{a \quad B}{a \quad B}$$

$$\frac{A \quad B}{a \quad b} \qquad\qquad \frac{A \quad b}{a \quad B}$$

We measure the distances between the two genes by looking at the relative ratios of the four classes of gametes made by each of these double heterozygotes. But we can't take a microscope and examine gametes directly, so we "see" the gametes by looking at the progeny of the double het. We cross it to a homozygous recessive (same as a testcross).

$$\frac{A \quad B}{a \quad b} \times \frac{a \quad b}{a \quad b} \qquad\qquad \frac{A \quad b}{a \quad B} \times \frac{a \quad b}{a \quad b}$$

If the genes are not linked, then the parental (P) and recombinant (R) classes will be the same frequency (are equally likely). Thus it's just like the old Punnett square:

	AB	ab	Ab	aB
ab	AABb	aabb	Aabb	aaBb
	1 :	1 :	1 :	1

	Ab	aB	AB	ab
ab	Aabb	aaBb	AaBb	aabb
	1 :	1 :	1 :	1

We can write these cross progeny with our mapping notation instead:

$$\frac{A\ B}{a\ b} \quad \frac{a\ b}{a\ b} \quad \frac{A\ b}{a\ b} \quad \frac{a\ B}{a\ b} \qquad\qquad \frac{A\ b}{a\ b} \quad \frac{a\ B}{a\ b} \quad \frac{A\ B}{a\ b} \quad \frac{a\ b}{a\ b}$$

If there were complete linkage, i.e. A and B genes very close together, we would not see any of the recombinants. So each heterozygote would only make parental gametes, that is, only two types of gametes for each heterozygote:

	AB	ab
ab	AaBb	aabb

	Ab	aB
ab	Aabb	aaBb

Or, using the mapping notation:

$$\frac{A\ B}{a\ b} \quad \frac{a\ b}{a\ b} \qquad\qquad \frac{A\ b}{a\ b} \quad \frac{a\ B}{a\ b}$$

Now consider three traits, furry feet recessive to not furry feet (a and A), short recessive to tall (b and B), and big appetite recessive to small appetite (c and C). You would like to make a genetic map of these traits. In order to do this, you have to have an individual who is heterozygous for all traits (triple het), and who produces lots of progeny so you can detect recombinants.

You can see that there are several ways that the alleles could be arranged on the chromosomes to produce the triple heterozygote AaBbCc, without considering variations in gene order:

A B C	A B c	A b c
a b c	a b C	a B C
a B c	a B C	a b C
A b C	A b c	A B c

Unfortunately, we usually have only the cross progeny, not the heterozygous parent or the grandparents, when we do mapping.

When you get cross progeny for three genes, do these steps in order:

- What are the two most common classes? These are the parentals.
- What are the two least common classes? These are the double crossovers.
- Which marker is exchanged between the doubles and the parentals? This is the middle gene.

Now, assign the single crossovers to their correct places on the map you have made, so you can figure out the distances correctly.

Distance = [(both singles + both doubles)/total progeny] x 100