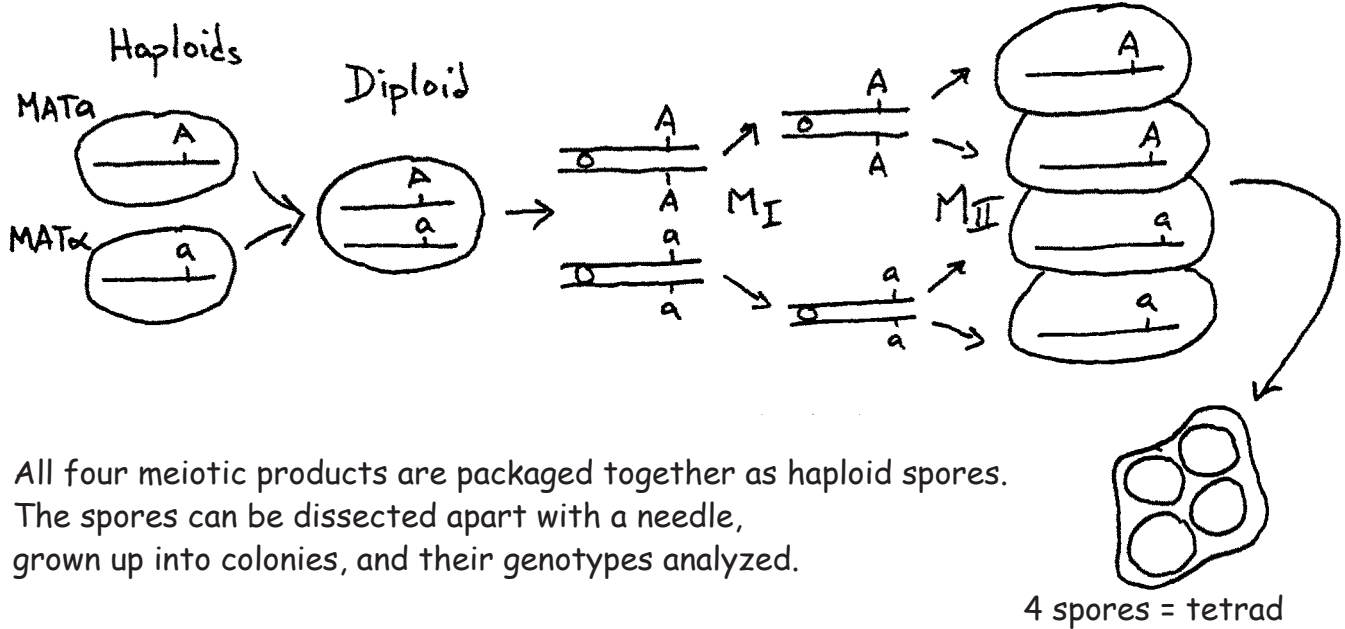


Lecture 9

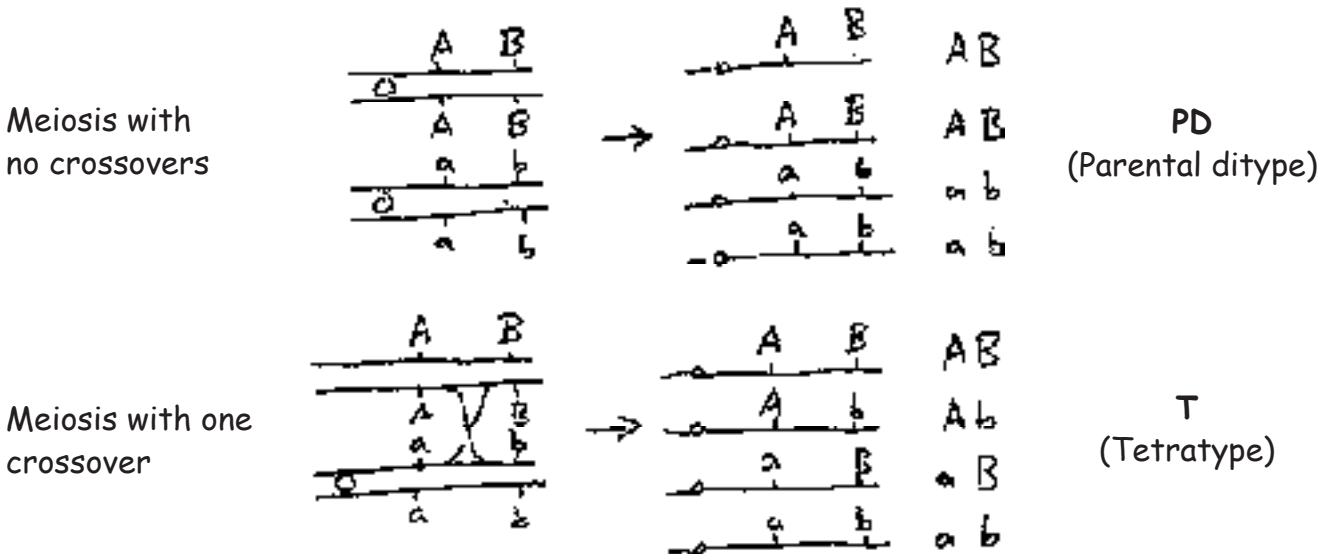
Meiosis in yeast is particularly easy to study.



All four meiotic products are packaged together as haploid spores. The spores can be dissected apart with a needle, grown up into colonies, and their genotypes analyzed.

The ability to look at the genotypes of all four gametes gives us extra information about the meiosis that is not obtainable in diploid organisms (eg. mice, flies and peas) where only one of the meiotic products is selected at random.

Consider two linked genes in a cross: $A B \times a b \xrightarrow{\text{mate}} \frac{A B}{a b}$ (diploid) $\xrightarrow{\text{sporulate}}$ Tetrad



If the genes are close together multiple crossovers in this region will be very rare and only PD and T type tetrads will be seen.

The overall aim of tetrad analysis is to express distance as a function of tetrad types.

First, we apply the formula for genetic distance:

$$\text{Distance in cM} = 100 \times \frac{\text{crossover gametes}}{\text{total gametes}}$$

There are two crossover gametes in each T tetrad.

\square = number of tetrads

$$\text{Distance in cM} = 100 \times \frac{2T}{4\square} = 100 \times \frac{T}{2\square} \quad \begin{array}{l} \text{(this holds true} \\ \text{only for tightly linked genes} \\ \text{ie no double crossovers)} \end{array}$$

For genes that are far apart association of A with B is random.

There are six equally likely arrangements of B alleles with A alleles.

A	B	b	B	b	b	B
A	B	b	b	B	B	b
a	b	B	B	b	B	b
a	b	B	b	B	b	B

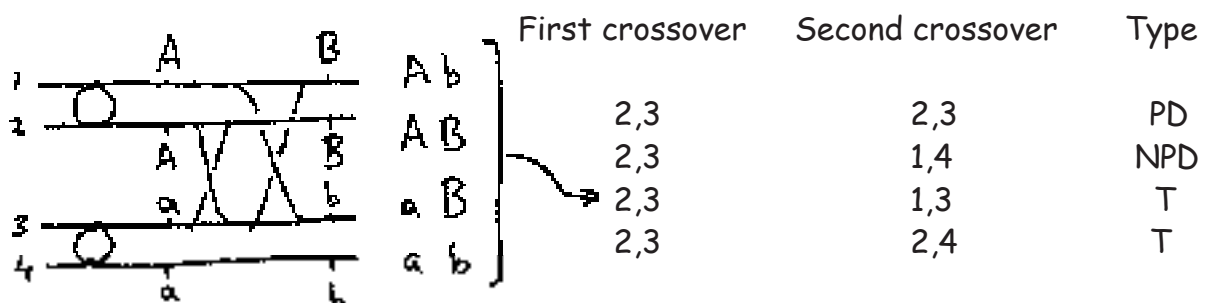
PD T T T T

NPD

(Nonparental ditype)

Thus for unlinked loci: PD T NPD
 1 : 4 : 1

Now we will see how to use tetrad analysis to make a more accurate mapping function that will take the hidden double crossovers into account.



NPD is unique designator of double crossovers that we can use to keep track of other double crossovers that look like single crossovers or no crossovers.

All four classes are equally likely, therefore:

Total double crossovers = 4 NPD, T tetrads that are doubles not singles = 2 NPD

To make a better mapping function we will take into account both single and double crossovers.

	number of tetrads	"crossover gametes"
double crossovers	4 NPD	4 (By counting all of the spores in these tetrads as crossover gametes we have a more accurate mapping function)
single crossovers	T- 2 NPD	2

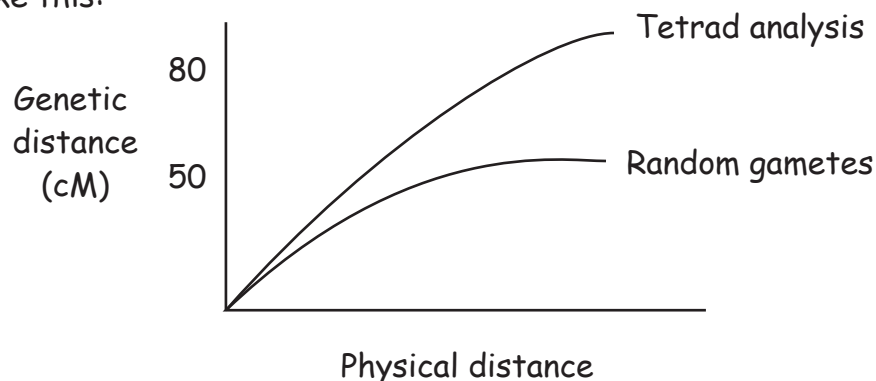
$$\begin{aligned} \text{Distance in cM} &= 100 \times \frac{2(T - 2\text{NPD}) + 4(4\text{NPD})}{4 \square} && \square = \text{number of tetrads} \\ &= 100 \times \frac{T - 2\text{NPD} + 8 \text{NPD}}{2 \square} \\ &= 100 \times \frac{T + 6 \text{NPD}}{2 \square} \end{aligned}$$

Example: 100 tetrads give: 75 PD, 20 T, 5 NPD

Applying the formula for linkage in tetrads we get: $100 \times \frac{20 + 6 \cdot 5}{200} = 25 \text{ cM}$

If we were just to count crossover gametes: $100 \times \frac{40 + 4 \cdot 5}{400} = 15 \text{ cM}$

A comparison of the mapping functions for tetrad analysis and random gametes looks something like this:



The mapping function for tetrad analysis is pretty accurate for distances $\square 40 \text{ cM}$