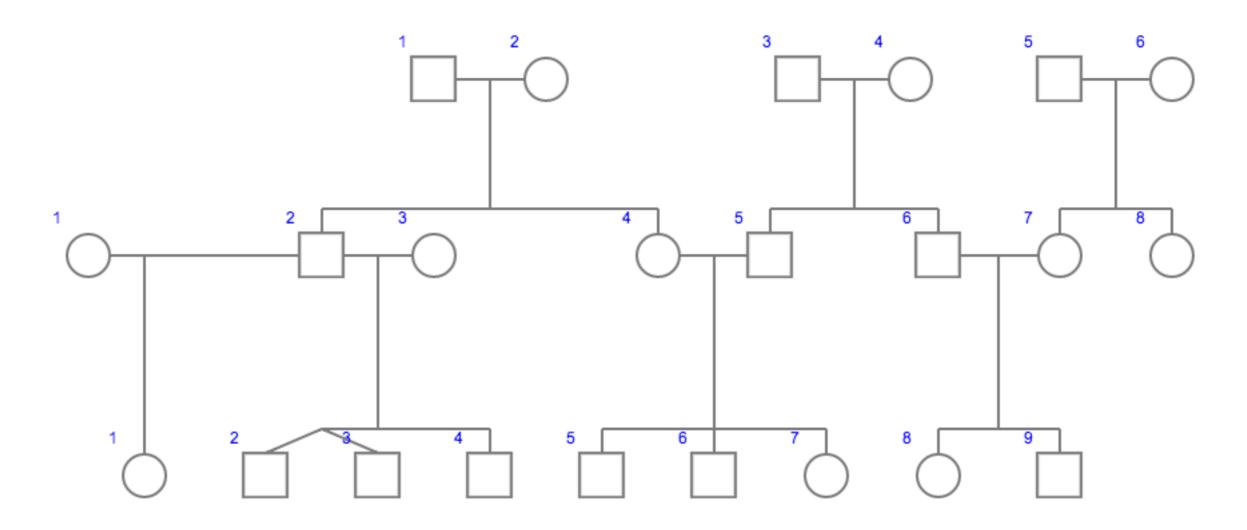
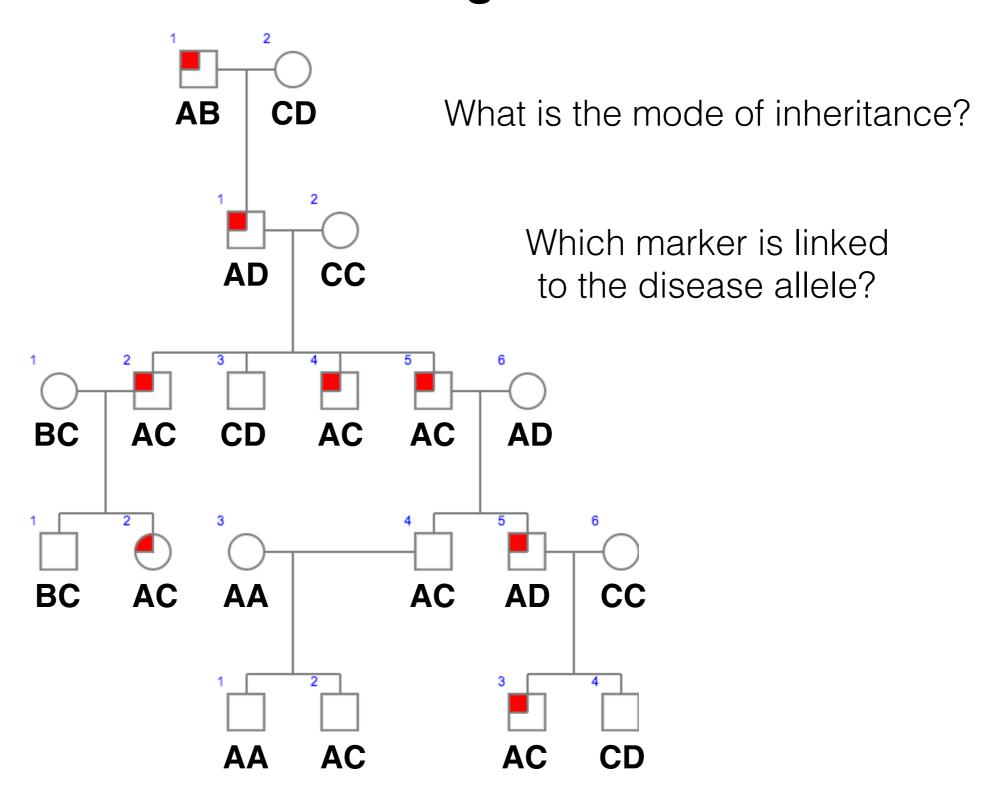
Bio393: Genetic Analysis

Linkage mapping in families



The goal of linkage analysis is to identify a marker nearby the disease-causing allele



The odds ratio is a statistical method to measure association of some attribute with the presence or absence of another attribute.

Probability of pedigree under linkage versus no linkage

LOD =
$$log_{10}$$
 $\frac{P(pedigree with linkage)}{P(pedigree with no linkage)}$

LOD > 3 is good evidence of linkage 1 in 1,000 chance of data by chance

LOD < 0 means data are more likely by chance

How linked is our marker to the disease-causing allele? Recombination frequency

Recombination frequency is written as θ

Percentage of recombinant gametes passed down

 θ = 0 is perfect linkage

 θ = 0.5 is no linkage

The odds ratio is a statistical method to measure association of some attribute with the presence or absence of another attribute.

Probability of pedigree under linkage versus no linkage

LOD =
$$log_{10}$$
 $\frac{P(pedigree with linkage)}{P(pedigree with no linkage)}$

LOD =
$$log_{10}$$

$$\frac{P(data \mid \boldsymbol{\theta})}{P(data \mid \boldsymbol{\theta} = 0.5)}$$
 P(data) = probability that a particular gamete was inherited

LOD =
$$log_{10}$$

$$\frac{P(data | \theta)}{P(data | \theta = 0.5)}$$
 P(data) = probability that a particular gamete was inherited

$$P(data | \theta) =$$

Probability that recombination did not occur for parental 1 - θ

Probability that recombination did occur for recombinant θ

Probability of phase of parent

Each individual is independent.
Use product rule to multiply probabilities.

LOD =
$$log_{10}$$

$$\frac{P(data \mid \boldsymbol{\theta})}{P(data \mid \boldsymbol{\theta} = 0.5)}$$
 P(data) = probability that a particular gamete was inherited

$$P(data | \theta = 0.5)$$

Equal probability of two loci independently assorting and one gamete being passed down

Each individual is independent.
Use product rule to multiply probabilities.

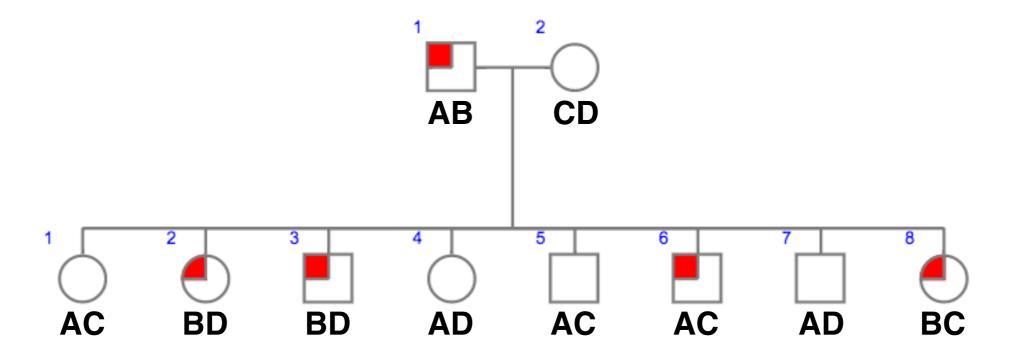
Probability of pedigree under linkage versus no linkage

LOD =
$$log_{10}$$
 $\frac{P(pedigree with linkage)}{P(pedigree with no linkage)}$

LOD =
$$log_{10}$$

$$\frac{P(data \mid \boldsymbol{\theta})}{P(data \mid \boldsymbol{\theta} = 0.5)}$$
 P(data) = probability that a particular gamete was inherited

LOD =
$$\log_{10}$$
 $\frac{(1 - \theta)^{NR} \times \theta^{R}}{0.5^{(NR + R)}}$ Use this equation when we know phase.



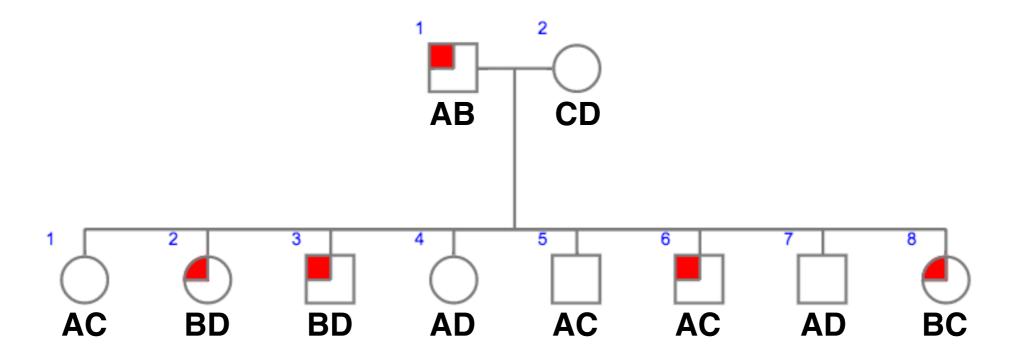
Do we know the phase of I-1?

NO

Every child has an equal chance of being a recombinant or parental

Difference between being informative and knowing phase

Informative = Parent heterozygous at each of two loci



With unknown phase of parent, the LOD equation is...

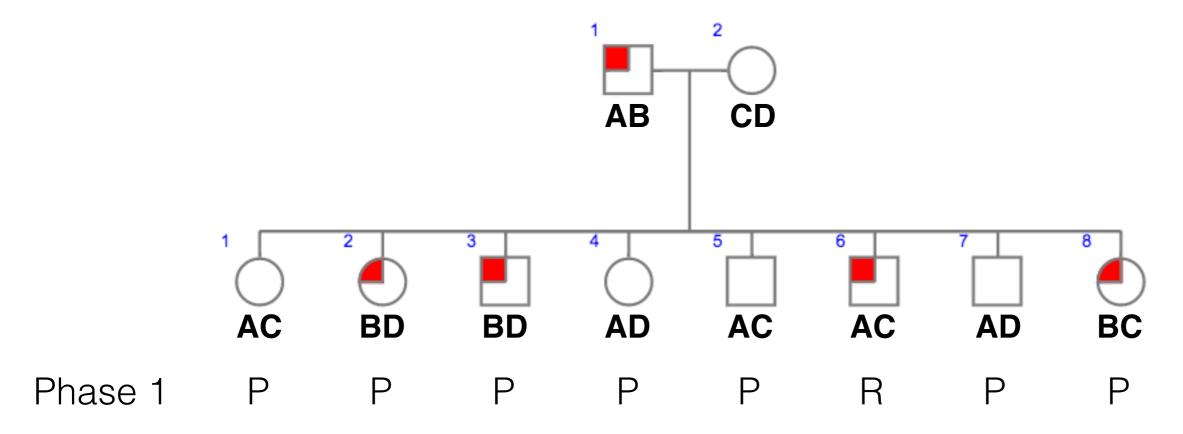
LOD =
$$log_{10}$$
 $\frac{1/2((1 - \theta)^{NR} \times \theta^{R}) + 1/2((1 - \theta)^{NR} \times \theta^{R})}{(0.5^{(NR + R)})}$

½ chance for each phase

Phase 1

$$\frac{D}{d}$$
 A

$$\frac{D}{d}$$
 B



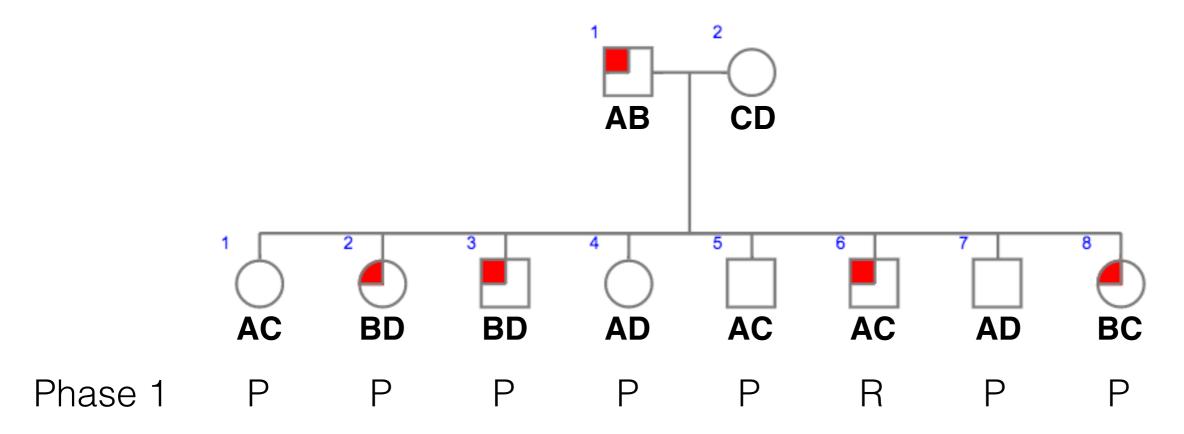
LOD =
$$log_{10}$$
 $\frac{1/2((1 - \theta)^{NR} \times \theta^{R}) + 1/2((1 - \theta)^{NR} \times \theta^{R})}{(0.5^{(NR + R)})}$

½ chance for each phase

Phase 1

$$\frac{D}{d}$$
 A

$$\frac{D}{d}$$
 B



LOD =
$$log_{10}$$

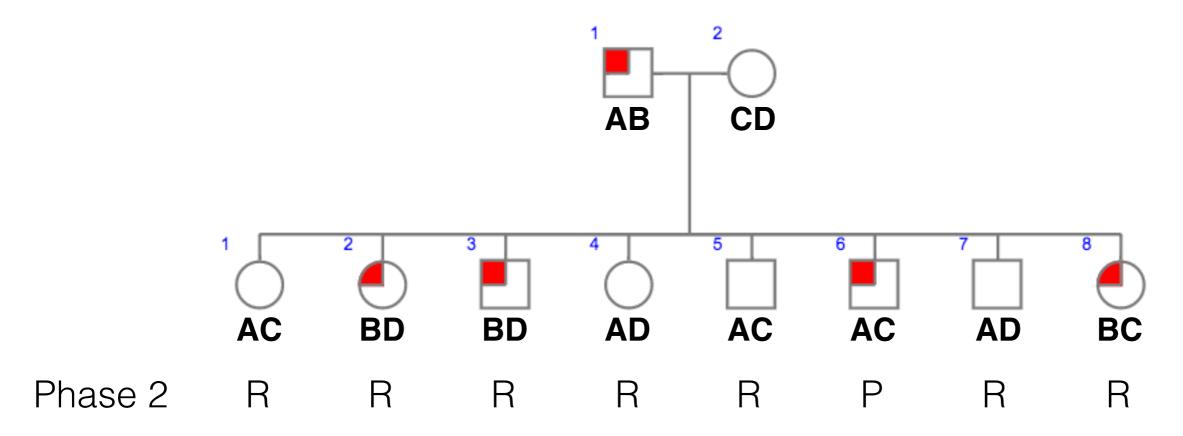
$$\frac{\frac{1}{2}((1 - \theta)^7 \times \theta^1) + \frac{1}{2}((1 - \theta)^{NR} \times \theta^R)}{(0.5^{(8)})}$$

½ chance for each phase

Phase 1

$$\frac{D}{d}$$
 A

$$\frac{D}{d}$$
 B



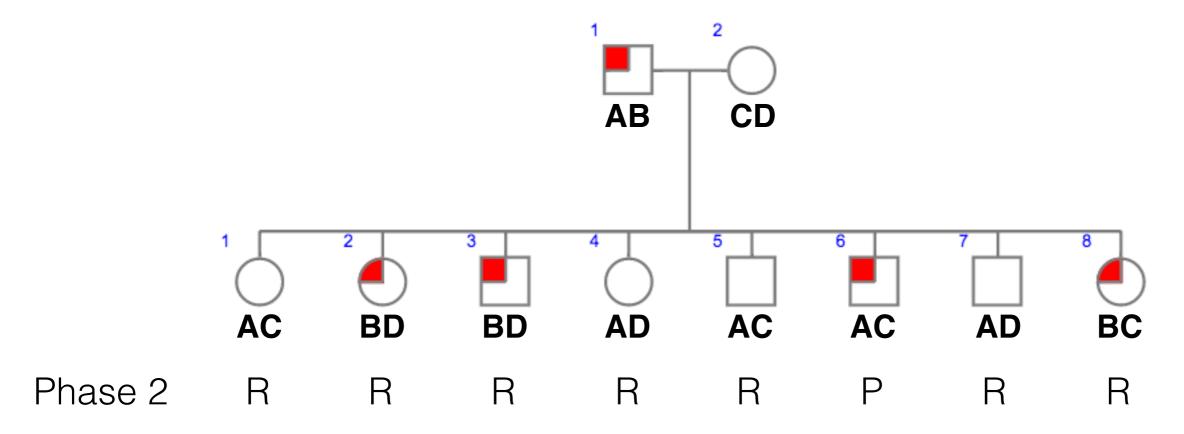
LOD =
$$\log_{10} \frac{\frac{1}{2}((1-\theta)^{7} \times \theta^{1}) + \frac{1}{2}((1-\theta)^{1} \times \theta^{7})}{(0.5^{(8)})}$$

½ chance for each phase

Phase 1

$$\frac{D}{d}$$
 A

$$\frac{D}{d}$$
 B



$$LOD = log_{10} \frac{1}{2}((1 - 0.125)^7 \times 0.125^1) + \frac{1}{2}((1 - 0.125)^1 \times 0.125^7)$$

$$(0.5^{(8)})$$

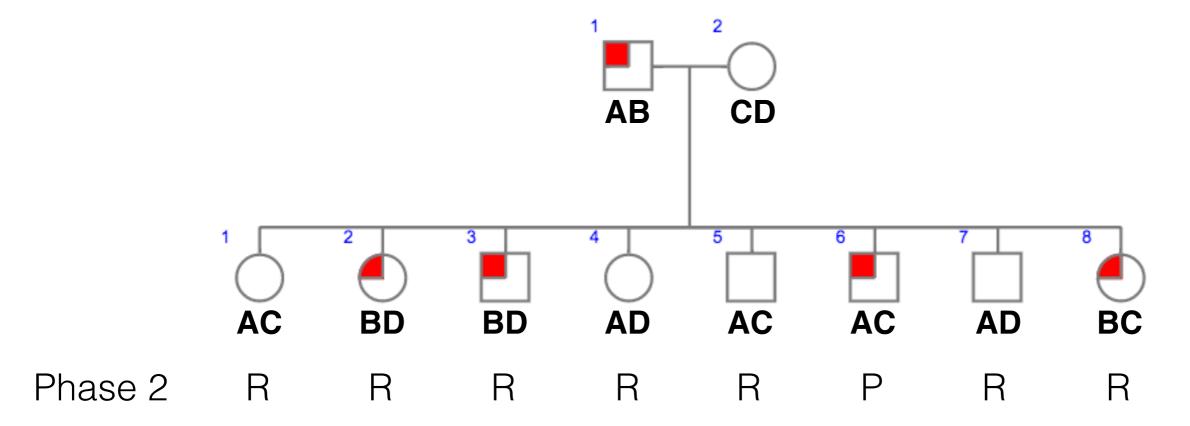
½ chance for each phase

Phase 1

$$\theta = 0.125$$

$$\frac{D}{d}$$
 A

$$\frac{D}{d}$$



$$LOD = 0.79$$

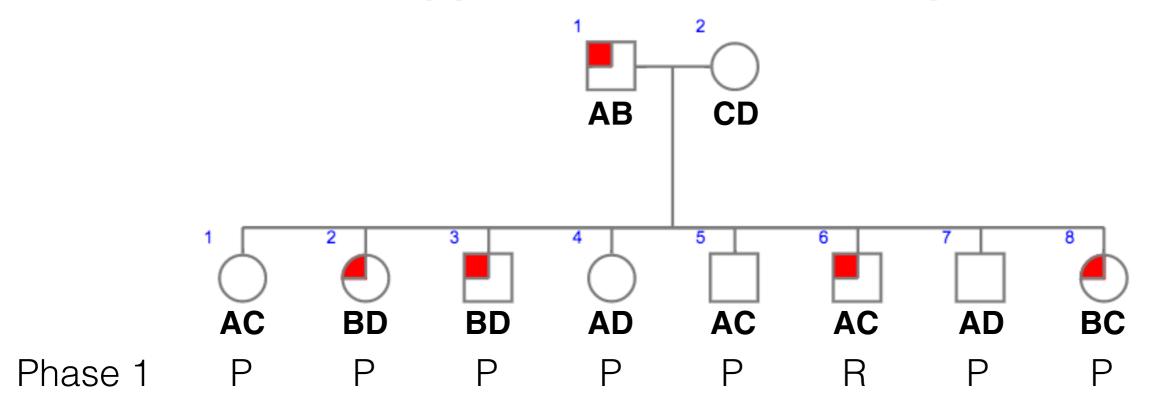
$$\theta = 0.125$$

Some properties of LOD scores

LOD scores from independent families can be added (product rule with logarithms)

Determining phase increases the LOD score

What happens when we know phase?



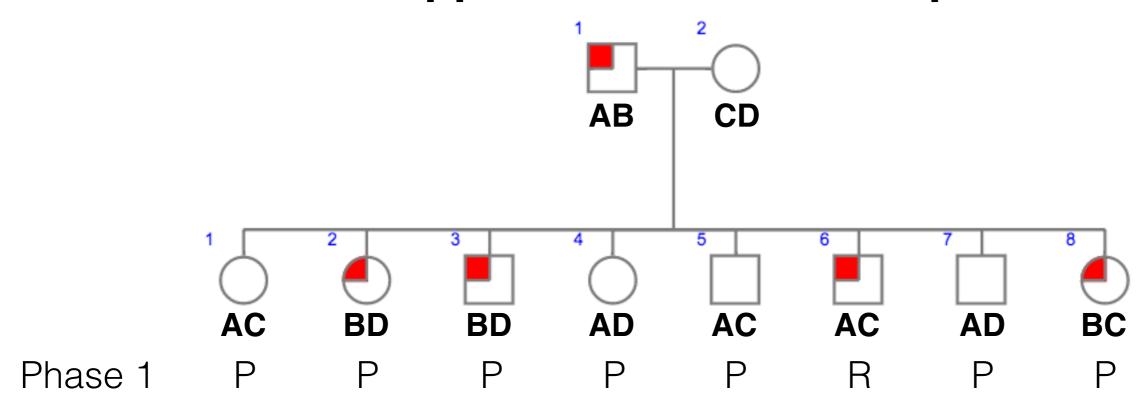
The paternal grandmother had the disease and her genotype was BD. Her husband's genotype was AA and he was not affected

LOD =
$$log_{10}$$

$$\frac{(1 - \theta)^{NR} \times \theta^{R}}{0.5^{(NR + R)}}$$

½ chance for each phase and second phase probability go away!

What happens when we know phase?

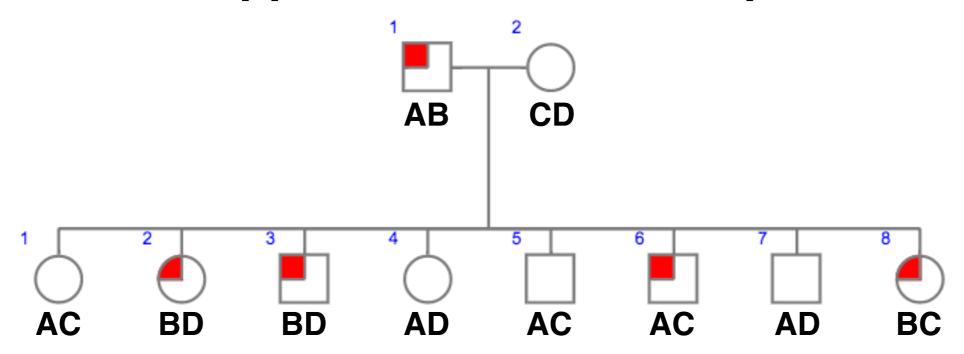


LOD =
$$log_{10}$$

$$\frac{(1 - 0.125)^7 \times 0.125}{0.5^{(7+1)}}$$

½ chance for each phase and second phase probability go away!

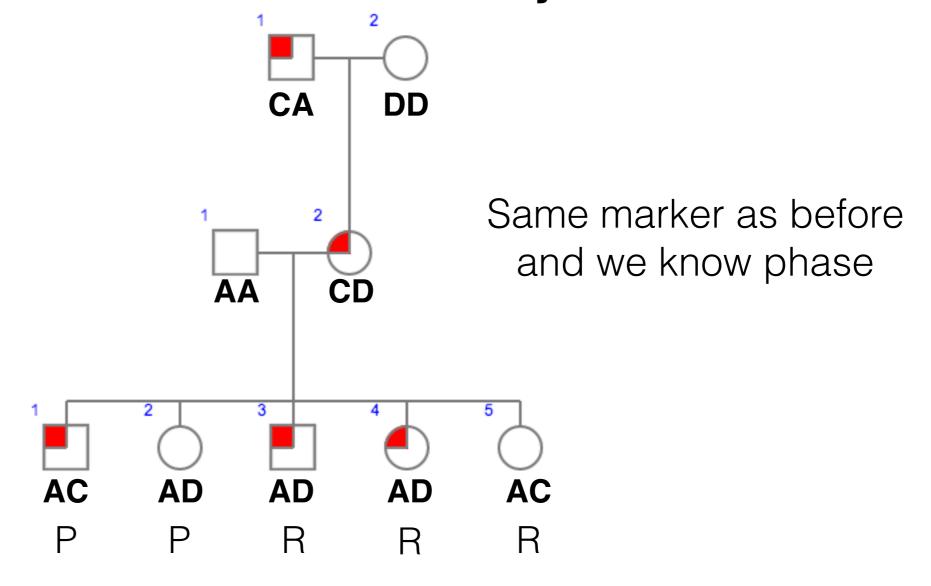
What happens when we know phase?



$$LOD = 1.1$$
 $\theta = 0.125$

½ chance for each phase and second phase probability go away!

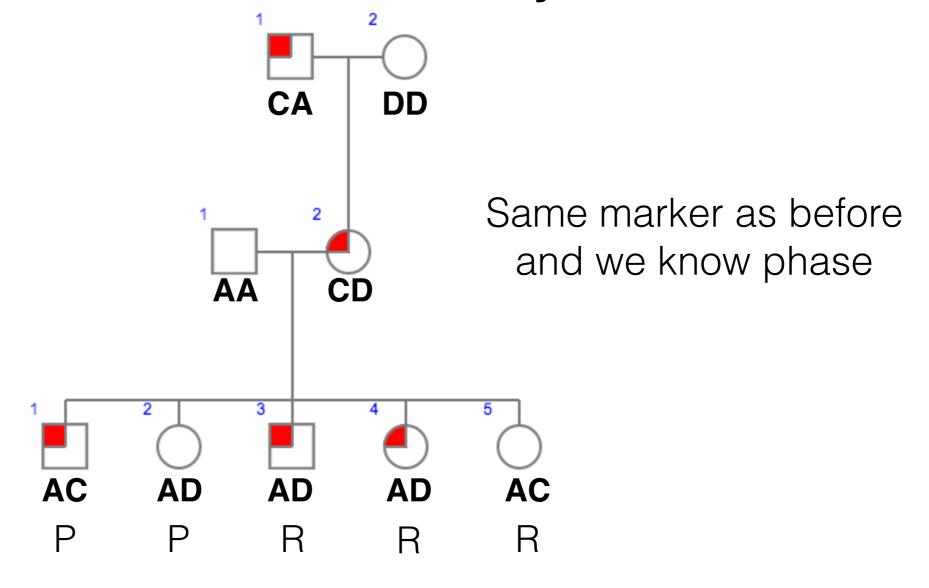
Let's add another family



LOD =
$$log_{10}$$

$$\frac{(1 - \theta)^{NR} \times \theta^{R}}{0.5^{(NR + R)}}$$

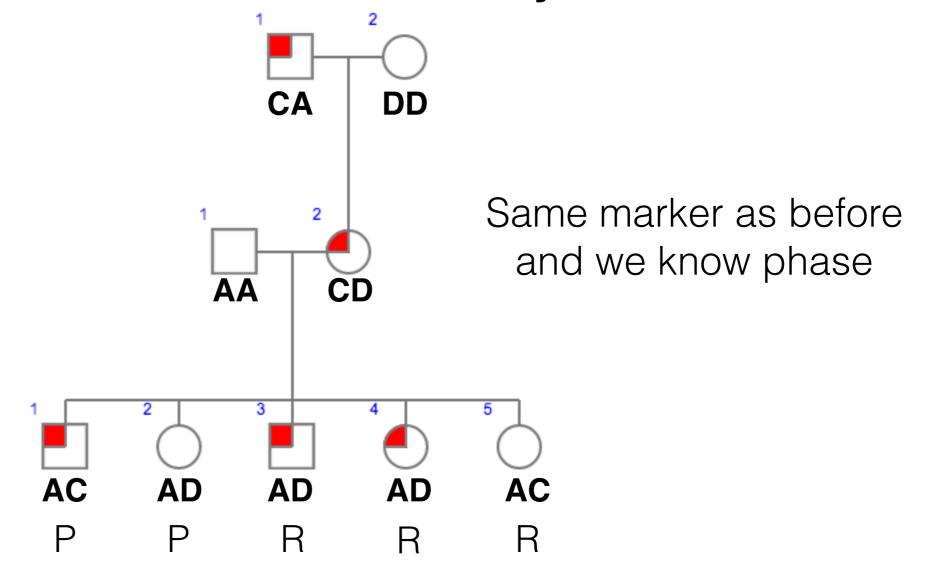
Let's add another family



LOD =
$$log_{10}$$

$$\frac{(1 - 0.125)^2 \times 0.125^3}{0.5^{(2+3)}}$$

Let's add another family

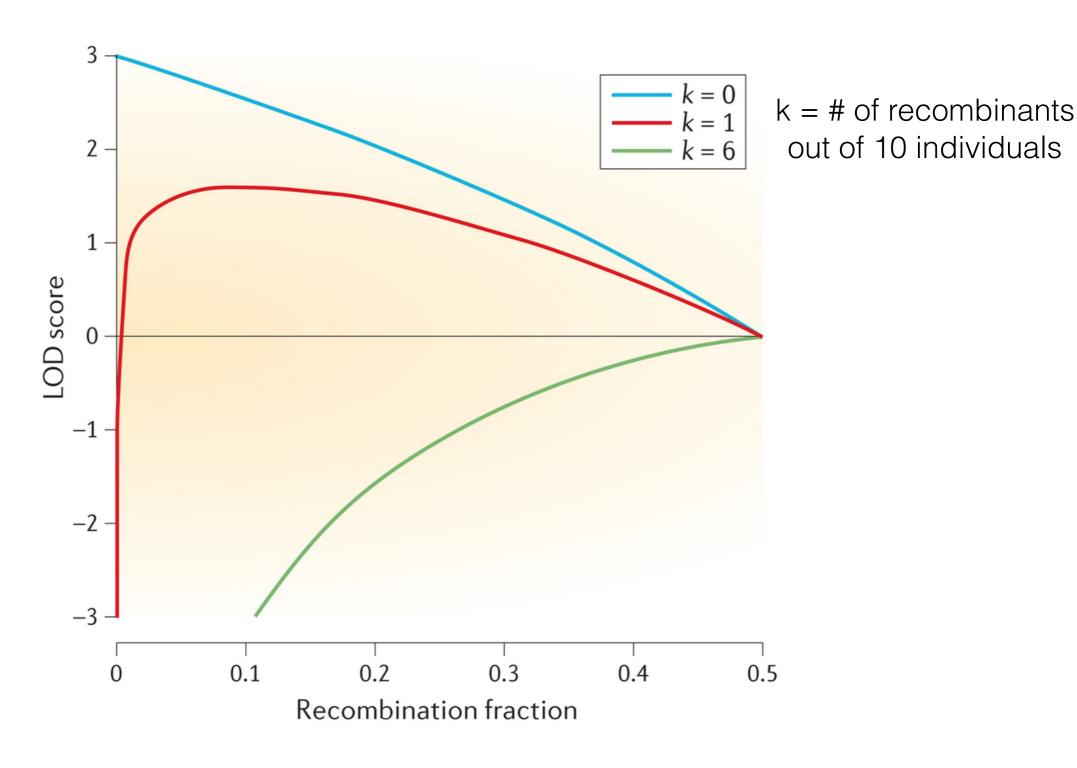


$$LOD = -0.1159$$

$$\theta = 0.125$$

Change theta to 0.6? No, 0.5 is unlinked

What if we try all possible thetas between 0 and 0.5?



Nature Reviews | Genetics

The good and the bad of family-based linkage analysis

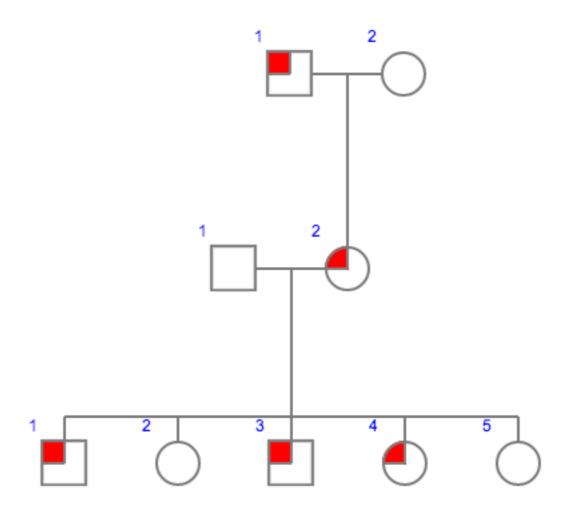
Positives:

- Less allelic heterogeneity in families
- Clearly tell recombination events
- Powerful method to find rare variant effects

Negatives:

- Large families are rare
- Different families with the "same" disease could have different genetic causes
- Mapping resolution is 5 cM or 5 megabase pairs
- Difficult for late-onset diseases

With whole-exome and whole-genome sequencing, family linkage analysis gets even more powerful



- Look at "all" markers in the genome simultaneously
- Dominant disorders mean look for heterozygous mutations linked to shared blocks of variants (haplotypes)
- X-linked lets you focus on the X chromosome
- Variants should be private to the family and deleterious

Linked markers on chromosomes allow for haplotype mapping

