

Incorporating Relatives

Relatives

Because DNA profiles are inherited, relatives are more likely to share a DNA profile than unrelated individuals.

H_p : The DNA in the sample came from the suspect.

H_d : The DNA in the sample came from an unrelated individual.

H_p : The DNA in the sample came from the suspect.

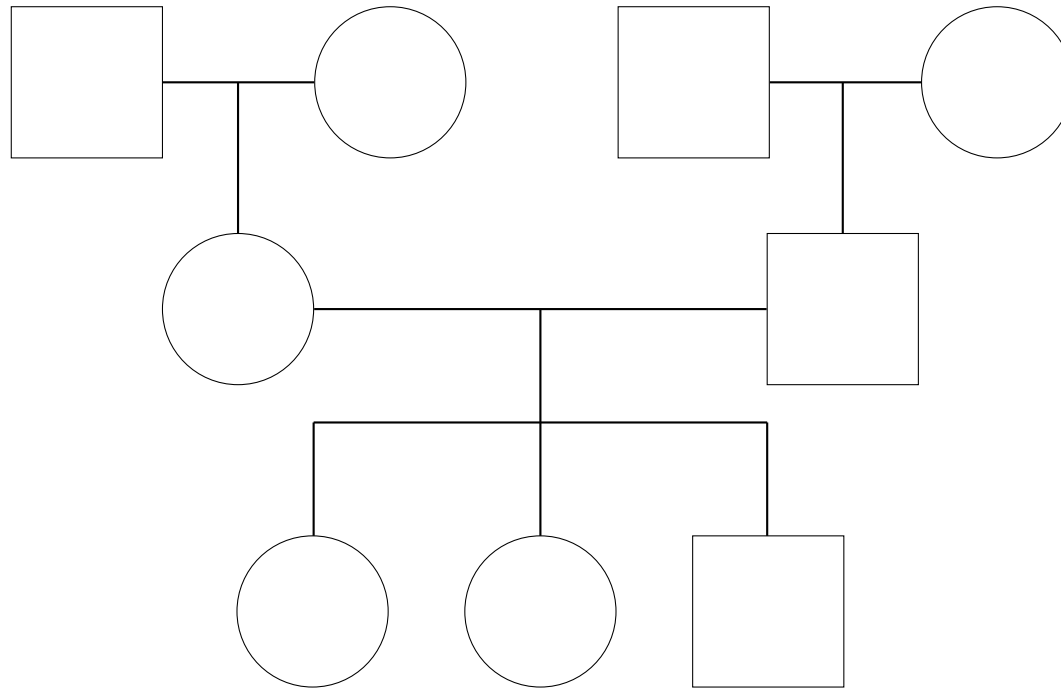
H_d : The DNA in the sample came from a brother of the suspect.

The relationship type can be anything: parent, child, sibling, uncle, cousin, etc.

The more distant the relationship, the closer the value will become to the LR considering unrelated individuals.

Pedigrees

Pedigrees provide a graphical representation of relationships.



Individuals are said to be related if they share a common ancestor. Relationships can be unilateral (one-sided) or bilateral (two-sided).

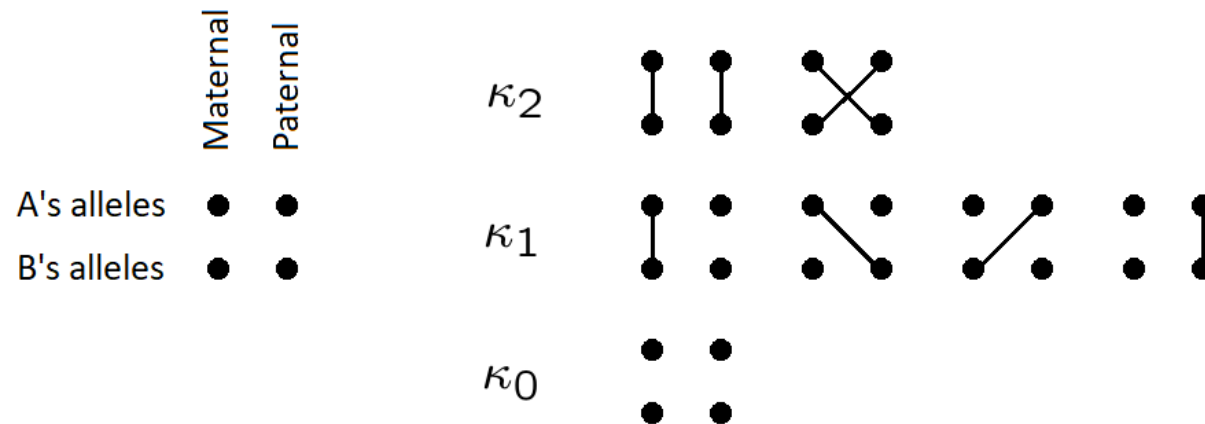
Identity By Descent

- Relatives are similar because they share alleles that are *identical by descent* (IBD).
- IBD alleles are copies of the same allelic type inherited through a common ancestor (and ignores mutation).
- A pedigree or relationship determines IBD probabilities, which determine probabilities of joint genotypes.

IBD Coefficients

For *non-inbred* relatives, there are three IBD classes. We write κ_i to denote the IBD probabilities:

$$\kappa_i = \Pr(i \text{ alleles IBD})$$



IBD Coefficients

The following table shows IBD probabilities for common relationships:

Relationship	κ_0	κ_1	κ_2
Unrelated	1	0	0
Parent/child	0	1	0
Identical twins	0	0	1
Siblings	1/4	1/2	1/4
Half-sibs	1/2	1/2	0
First cousins	3/4	1/4	0

These IBD probabilities give the expected relatedness between individuals (the realized relatedness is variable).

Match Probabilities for Relatives

If $\kappa_0 = 1$, we are in the original situation and write M_2 for the appropriate match probability:

$$M_2 = \begin{cases} p_A^2, & \text{for homozygous loci } AA, \\ 2p_A p_B, & \text{for heterozygous loci } AB. \end{cases}$$

If $\kappa_1 = 1$, the match probability M_1 changes to:

$$M_1 = \begin{cases} p_A, & \text{for homozygous loci } AA, \\ \frac{1}{2}(p_A + p_B), & \text{for heterozygous loci } AB. \end{cases}$$

If $\kappa_2 = 1$, both alleles are IBD and the match probability is 1.

Match Probabilities for Relatives

Combining the terms leads to the overall single-locus match probability for relatives:

$$\kappa_2 + \kappa_1 M_1 + \kappa_0 M_2,$$

which yields a standard match probability of M_2 for unrelated individuals.

LRs for Relatives

With this approach we can incorporate specific relatives. But what if no specific alternative is available?

H_d : The DNA in the sample came from an unrelated individual.

H_d : The DNA in the sample came from a brother of the suspect.

H_d : The DNA in the sample came from an unknown individual from the population.

LRs Including Relatives

- We can model a situation where relatives of the suspect make up a small proportion of the total population.
- Background information may be used to assess plausible values for the number of relatives in each category.
- An overall LR can be calculated as a weighted average over the sets.