Resemblance Between Relatives

Lynch & Walsh, Chapter 7 (pp. 131–145)

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Lab Meeting

Why is resemblance among relatives important?

Resemblance between relatives is the foundation for understanding how quantitative traits are transmitted across generations.

It allows us to:

- quantify how much genetic information is shared between individuals,
- derive expected covariances among relatives,
- estimate additive genetic variance and heritability,
- connect pedigree theory with modern genomic relationship matrices used in breeding.

1. Measure of relatedness

The resemblance between two relatives depends on the probability that they share alleles inherited from a common ancestor.

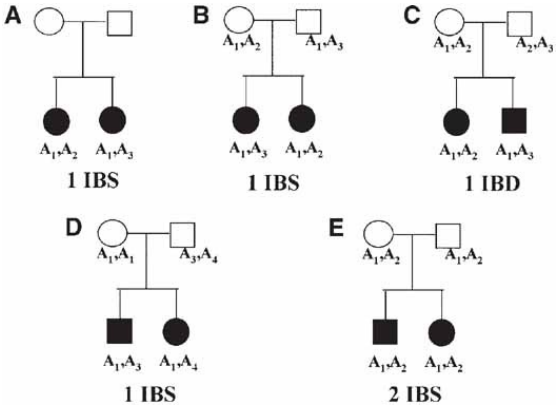
Two key ideas:

- **Identity by descent (IBD):** two alleles are copies of the same ancestral allele.
- **Relatedness:** a probabilistic measure of how much genetic material two individuals share through pedigree.

Thus, before discussing covariance, we first need to define the **probabilities of gene sharing** among relatives.

1. Measure of relatedness

- **Identity by descent (IBD)**
- **Identity by state (IBS)**
- See Example 7.1 from Chapter 7



2. Coefficients of identity

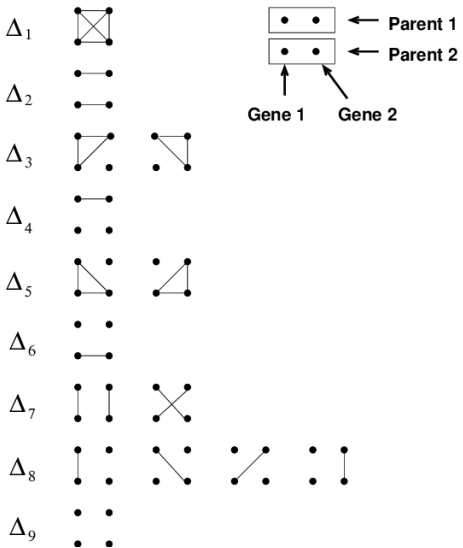
For a pair of diploid individuals, the **coefficients of identity** describe the probabilities of all possible IBD configurations among the four alleles present at a locus.

These coefficients provide the most general description of genetic resemblance because they track:

- whether one allele is shared IBD,
- whether both alleles are shared IBD,
- and which allelic configurations generate additive or dominance covariance.

They are the probabilistic building blocks underlying coancestry, inbreeding, and genetic covariance between relatives.

2. Coefficients of identity



- See Example 7.2 from Chapter 7
- Genes that are identical by descent are connected by lines

Example adapted from Lynch & Walsh, Chapter 7.

3. Coefficient of coancestry and coefficient of relationship

The **coefficient of coancestry** between individuals X and Y, denoted Θ_{XY}, is the probability that a randomly chosen allele from X and a randomly chosen allele from Y are identical by descent.

The **coefficient of relationship** is:

$$r_{XY} = 2\Theta_{XY}$$

Common examples:

Relationship	Θ_{XY}	r_{XY}
Parent–offspring	$\frac{1}{4}$	$\frac{1}{2}$
Full sibs	$\frac{1}{4}$	$\frac{1}{2}$
Half sibs	$\frac{1}{8}$	$\frac{1}{4}$
Grandparent–grandchild	$\frac{1}{8}$	$\frac{1}{4}$

4. Coefficient of inbreeding

The **inbreeding coefficient** of individual X, denoted F_X, is the probability that the two alleles at a locus in X are identical by descent.

If the parents of X are A and B, then:

$$F_X = \Theta_{AB}$$

Interpretation:

- if the parents are related, the offspring has an elevated probability of homozygosity by descent;
- inbreeding changes genotype frequencies and can alter the expected resemblance structure within a pedigree.

5. Genetic covariance between relatives

Once gene-sharing probabilities are defined, we can express the expected covariance between relatives.

The classical expression is:

$$\sigma_{G(X,Y)} = 2\Theta_{XY}\sigma_A^2 + \Delta_{XY}\sigma_D^2$$

where:

- Θ_{XY} = coefficient of coancestry,
- $2\Theta_{XY}$ = coefficient of relationship,
- Δ_{XY} = probability that both alleles are identical by descent in the pair,
- σ_A^2 and σ_D^2 are additive and dominance variances, respectively.

Thus, additive covariance depends on coancestry, while dominance covariance depends on deeper identity structure.

Decomposition of total genetic covariance

The total genetic covariance between relatives x and y can be decomposed as:

$$\begin{aligned}\sigma_{G,xy} = \sigma_{A,xy} &+ \sigma_{D,xy} \\ &+ \sigma_{AA,xy} + \sigma_{AD,xy} + \sigma_{DD,xy} \\ &+ \sigma_{AAA,xy} + \sigma_{AAD,xy} + \sigma_{ADD,xy} + \sigma_{DDD,xy} \\ &+ \cdots\end{aligned}$$

where $\sigma_{A,xy}$ is the additive covariance, $\sigma_{D,xy}$ is the dominance covariance, and the remaining terms represent epistatic covariance components between relatives x and y.

6. Genetic covariance: common examples

Parent–offspring: $\Theta_{PO} = \frac{1}{4},\ \Delta_{PO} = 0 \quad \Rightarrow \quad \sigma_{G,PO} = \frac{1}{2}\sigma_A^2$

Half sibs: $\Theta_{HS} = \frac{1}{8},\ \Delta_{HS} = 0 \quad \Rightarrow \quad \sigma_{G,HS} = \frac{1}{4}\sigma_A^2$

Full sibs: $\Theta_{FS} = \frac{1}{4},\ \Delta_{FS} = \frac{1}{4} \quad \Rightarrow \quad \sigma_{G,FS} = \frac{1}{2}\sigma_A^2 + \frac{1}{4}\sigma_D^2$

Interpretation:

- parent–offspring and half-sib resemblance mainly reflect additive variance,
- full-sib resemblance includes both additive and dominance components.

7. Phenotypic value and variance decomposition

For a quantitative trait,

$$P = G + E$$

where P is the phenotypic value, G is the genetic value, and E is the environmental deviation.

The genetic value can be decomposed as:

$$G = A + D + I$$

where A is additive, D is dominance, and I is epistatic deviation.

Therefore,

$$P = A + D + I + E$$

$$\sigma_P^2 = \sigma_G^2 + \sigma_E^2 \qquad \text{with} \qquad \sigma_G^2 = \sigma_A^2 + \sigma_D^2 + \sigma_I^2$$

8. Decomposition of total genetic variance

When epistasis is expanded by interaction order, the total genetic variance can be written as:

$$\begin{aligned}\sigma_G^2 = \sigma_A^2 + \sigma_D^2 \\ &+ \sigma_{AA}^2 + \sigma_{AD}^2 + \sigma_{DD}^2 \\ &+ \sigma_{AAA}^2 + \sigma_{AAD}^2 + \sigma_{ADD}^2 + \sigma_{DDD}^2 \\ &+ \cdots\end{aligned}$$

where:

- σ_A^2 = additive variance,
- σ_D^2 = dominance variance,
- $\sigma_{AA}^2, \sigma_{AD}^2, \sigma_{DD}^2$ = pairwise epistatic variance components,
- higher-order terms represent interactions among three or more loci.

For breeding, the most critical component is usually **additive variance**, because it is transmitted most predictably across generations.

9. Resemblance and heritability

Narrow-sense heritability is defined as:

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2}$$

For offspring–parent regression,

$$b_{OP} = \frac{\sigma_{G,(O,P)}}{\sigma_P^2} = \frac{\frac{1}{2}\sigma_A^2}{\sigma_P^2} = \frac{1}{2}h^2$$

so that:

$$h^2 = 2b_{OP}$$

This shows why resemblance between relatives is so important: it provides a direct route to estimating additive genetic variance and expected response to selection.

10. Why this matters for breeding

These concepts are central in breeding because the breeder wants to predict which individuals will transmit favorable alleles to the next generation.

Implications:

- **Half-sib and parent–offspring designs** are especially informative for additive variance.
- **Full-sib resemblance** may be inflated by dominance and shared environment.
- **Inbreeding** changes relatedness structure and can affect expected covariance.
- Modern mixed models replace pedigree expectations with marker-based realized relationships.

11. From pedigree relatedness to genomic relatedness

The same biological idea extends naturally to genomics: resemblance can be estimated directly from markers rather than only from pedigree expectation.

A standard mixed-model representation is:

$$\boldsymbol{y} = \boldsymbol{X}\beta + \boldsymbol{Z}\boldsymbol{u} + \boldsymbol{e}, \qquad \boldsymbol{u} \sim N(0, \boldsymbol{K}\sigma_A^2)$$

where $\boldsymbol{K}$ is the genomic relationship matrix.

This provides the bridge from classical resemblance between relatives to modern genomic prediction and breeding applications.

12. Questions for discussion: implementation in breeding

1. Which relative pairs are most informative for estimating additive variance in breeding populations?
2. When can full-sib resemblance be misleading because of dominance or shared environment?
3. How does inbreeding change resemblance patterns in selfing crops?
4. When is pedigree-based relatedness sufficient, and when should marker-based relatedness be preferred?
5. How can these covariance ideas be incorporated into genomic prediction and selection pipelines?

Take-home message

The logic of the chapter is:

relatedness $\rightarrow$ identity coefficients $\rightarrow$ coancestry/inbreeding $\rightarrow$ genetic covariance $\rightarrow$ breeding applications

Resemblance between relatives is therefore the conceptual foundation linking classical quantitative genetics, heritability estimation, and modern genomic prediction.