Kinship Coefficients and Covariance Between Relatives

Biostatistics 666

Kinship Coefficients

- Measure:
 - Relatedness between two individuals
 - Inbreeding in a single individual
- Useful predictors of covariance and correlation between relatives

Definition

- Given two individuals
 - One with genes (g_i, g_j)
 - The other with genes (g_k, g_l)
- The kinship coefficient is:
 - $\frac{1}{4}P(g_i \equiv g_k) + \frac{1}{4}P(g_i \equiv g_l) + \frac{1}{4}P(g_j \equiv g_k) + \frac{1}{4}P(g_j \equiv g_l)$
- Probability that two genes sampled at random from each individual are identical

Inbreeding Coefficient

For any given individual...

The inbreeding coefficient is the kinship coefficient between the individual's parents

Should be zero if individual is not inbred



- φ_{ij} Kinship between individuals i and j as
- f_i
 - Inbreeding for individual i
- Note
 - $\phi_{ii} = \frac{1}{2} (1 + f_i)$ $f_i = \phi_{mother(i)father(i)}$



Computing Kinship Coefficients

- φ_{ij} kinship coefficient between *i* and *j* Order individuals so ancestors always precede their descendants
 - If *i>j*, then *i* is not ancestor of *j*

$$\varphi_{ij} = \begin{cases} 0 & i \text{ and } j \text{ are founders} \\ \frac{1}{2} & i = j, i \text{ is a founder} \\ \frac{1}{2}(\varphi_{mother(i)j} + \varphi_{father(i)j}) & i \neq j \\ \frac{1}{2}(1 + \varphi_{mother(i)father(i)}) & i = j \end{cases}$$

More Kinship Coefficients...



Relationship to IBD probabilities

 In non-inbred pedigrees, kinship coefficients can be derived from IBD probabilities:

$$\varphi_{ij} = \frac{1}{4} P(IBD_{ij} = 1) + \frac{1}{2} P(IBD_{ij} = 2)$$

Model Setup

Consider a gene with two alleles

- Define g_i as an indicator variable
 - I if allele A is present
 - 0 if another allele is present
- For a single gene, calculate
 E(g_i)
 V(g_i)

Now consider a pair of genes

- If g_i and g_i are sampled independently...
 - $E(g_i + g_j)$
 - $V(g_i + g_j)$
 - Cov(g_i, g_j)
- What if g_i and g_j are sampled from related individuals?
 - Results depend on kinship...

A Model for Quantitative Traits

Observed trait is sum of multiple effects:

- Population mean
 - **μ** = 0
- Environmental effects
 - N(0, σ_e²)
- Genetic effects
 - N(0, σ_g²)
 - Each allele has effect ~ N(0, σ_q^2 / 2)

Covariance between Relatives

- Consider:
 - Genes for individual i are (g_{i1}, g_{i2})
 - Genes for individual j are (g_{j1}, g_{j2})
- Contributions to phenotype:
 For individual i are (g_{i1} + g_{i2})
 For individual j are (g_{i1} + g_{i2})



$$E((g_{i1} + g_{i2})(g_{j1} + g_{j2})) =$$

$$= E(g_{i1}g_{j1} + g_{i1}g_{j2} + g_{i1}g_{j2} + g_{i2}g_{j2})$$

$$= P(g_{i1} \equiv g_{j1})V(g) + P(g_{i1} \equiv g_{j2})V(g) +$$

$$P(g_{i2} \equiv g_{j1})V(g) + P(g_{i2} \equiv g_{j2})V(g)$$

$$= 4\varphi_{ij}V(g)$$

$$= 2\varphi_{ij}\sigma_{g}^{2}$$

Implications...

- In a simple model:
 - Genes are additive the covariance
 - No shared environment
- Covariance between relatives is a simple function of kinship
- Total variance due to genes could be estimated by relating the two