

# **INBREEDING AND RELATEDNESS**

# Questions of Interest

If genotypic data are available, individual inbreeding and kinship values can be estimated:

- What is the Genetic Relatedness Matrix? (association mapping)
- How do social behaviors evolve?
- How should captive breeding programs be managed? (conservation genetics)
- Are these remains from a person in this family? (disaster victim identification)

## Kinship vs Inbreeding

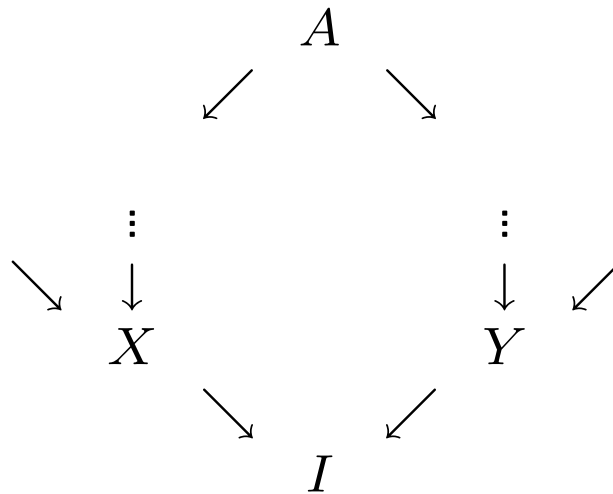
The *kinship* of individuals  $j, j'$  in population  $i$  is the probability an allele from  $j$  is ibd to an allele from  $j'$ . This is  $\theta_{jj'}^i$ .

The inbreeding of individual  $j$  in population  $i$  is the probability the two alleles in that individual are ibd. Write this as  $F_j^i$ .

Two alleles drawn from individual  $j$  are equally likely to be the same allele or different alleles:

$$\theta_{jj}^i = \frac{1}{2} (1 + F_j^i)$$

## Predicted Values: Path Counting



If there are  $n$  individuals (including  $X, Y, A$ ) in the path linking the parents through  $A$ , then the inbreeding  $F_I$  of  $I$ , or the kinship  $\theta_{XY}$  of  $X$  and  $Y$ , is

$$F_I = \theta_{XY} = \left(\frac{1}{2}\right)^n (1 + F_A)$$

If there are several ancestors, this expression is summed over all the ancestors.

## Average Kinships

The average over all pairs of distinct individuals,  $j \neq j'$ , of the kinships  $\theta_{jj'}^i$  is written as  $\theta_S^i$ . The average of this over populations is  $\theta_S$ . *These are probabilities for individuals.*

When there is random mating and Hardy-Weinberg equilibrium in a population, any pair of distinct alleles in a population (within or between individuals) is equivalent and then the average ibd probability for all these pairs is written as  $\theta_W^i$ , where  $W$  means within populations. The average over populations is  $\theta_W$ . *These are probabilities for distinct alleles.*

The ibd probability for any allele from population  $i$  and any allele from population  $i'$  is  $\theta_B^{ii'}$ , where  $B$  means between populations. Averaging over all pairs of distinct populations gives  $\theta_B$ .

## Within-population Inbreeding: $F_{IS}$

For population  $i$ , the inbreeding coefficient for individual  $j$ , *relative to* the identity of pairs of alleles between individuals in that population, is

$$\beta_j^i = \frac{F_j^i - \theta_S^i}{1 - \theta_S^i}$$

The average over individuals within this population is the population-specific  $F_{IS}^i$ , and it compares within-individual ibd to between-individual ibd in the same population. It is the quantity  $f$  being addressed by Hardy-Weinberg testing in population  $i$ .

If the reference set of alleles is for pairs of individuals within populations, averaged over populations, then the average relative inbreeding coefficient is  $\beta_{IS} = (F_I - \theta_S)/(1 - \theta_S)$  where  $F_I$  is the average of  $F_j^i$  over individuals  $j$  and populations  $i$ . It is generally called  $F_{IS}$ .

## Total Inbreeding: $F_{IT}$

For population  $i$ , the inbreeding coefficient for individual  $j$ , *relative to* the identity of pairs of alleles from different populations averaged over all pairs of populations, is

$$\beta_j^i = \frac{F_j^i - \theta_B}{1 - \theta_B}$$

The average over individuals within this population is the population-specific  $F_{IT}^i$ . The average of these over all populations is the total inbreeding coefficient  $F_{IT} = (F_I - \theta_B)/(1 - \theta_B)$ .

## Within-population Kinship

For population  $i$ , the kinship of individuals  $j, j'$  relative to the kinship for all pairs of individuals in that population is

$$\beta_{jj'}^i = \frac{\theta_{jj'}^i - \theta_S^i}{1 - \theta_S^i}$$

and these average zero over all pairs of individuals in the population.

If the reference set is all pairs of alleles, one from each of two populations,

$$\beta_{jj'}^i = \frac{\theta_{jj'}^i - \theta_B}{1 - \theta_B}$$

The average  $\beta_{ST}^i$  over all pairs of individuals in population  $i$  is the population-specific  $F_{ST}^i$ , and averaging this over populations gives the global  $F_{ST} = (\theta_S - \theta_B)/(1 - \theta_B)$ . It is the ibd probability between individuals within populations relative to the ibd probability between populations.



# Genotypic Measures

When individuals are distinguished:

$$(1 - F_{IT}) = (1 - F_{IS})(1 - F_{ST})$$

$$F_{IS} = \frac{F_{IT} - F_{ST}}{1 - F_{ST}}$$

This classic result also holds for population-specific values

$$(1 - F_{IT}^i) = (1 - F_{IS}^i)(1 - F_{ST}^i)$$

$$F_{IS}^i = \frac{F_{IT}^i - F_{ST}^i}{1 - F_{ST}^i}$$