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Resemblance Between Relatives

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Objectives

- Utilize population genetic concepts as a foundation to understand coefficients of inbreeding, parentage and relationship.
- Calculate coefficients of parentage and inbreeding.

Introduction

Explanation

Plant breeding populations, by definition, employ methods that force populations into states of disequilibrium. Plant breeders do not mate infinite (or even large) numbers of parents, thus drift has a major impact on population disequilibrium. They select the parents that will be used in matings, thus selection linkage and pleiotropy affect the population structure. New lines from external breeding projects are often introduced to the breeding nurseries, thus migration affects the structure of plant breeding populations. After the passage of the plant variety protection act, plant breeders working in the commercial sector began to keep breeding records for purposes of protecting intellectual property. An unintended consequence has been the application of mixed linear models to produce predictors of performance, originally developed by animal breeders. These methods are predicated on use of coefficients of relationship among cultivars with known performance and progeny with unknown or limited information on performance.

Fig. 1 Plant breeding specimens in a lab at Makerere University in Uganda. Photo by Iowa State University.

Background

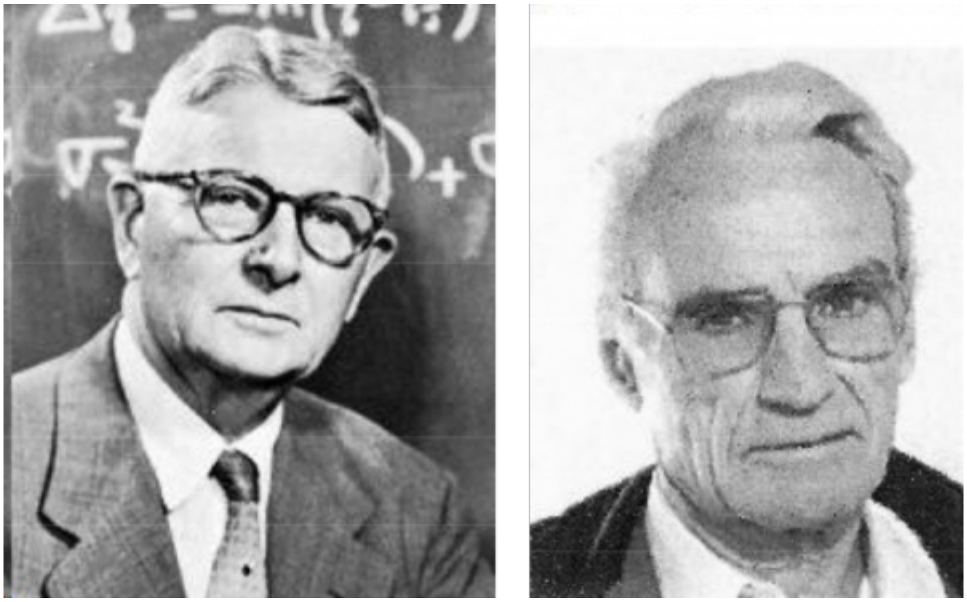


Fig. 2 Sewall Wright (top) and Gustave Malécot laid the groundwork for calculation of coefficients of relationships and inbreeding.

The calculation of coefficients of relationships and inbreeding were originally developed as path coefficients by Sewall Wright and identity by descent by Gustave Malécot. The calculations were simplified by Emik and Terrill (1949) and extended to all possible measures of identity by Cockerham (1971).

Herein we introduce inbreeding and parentage as deviations (disequilibrium) from Hardy Weinberg Equilibrium. In other words the calculation of all of these measures are based on a reference population and the reference population must be defined or else the calculated values have no meaning.

Coefficient of Inbreeding

Coefficient of Inbreeding - Definition

Let’s consider a random mating diploid population consisting of N individuals: Because there are 2N gametes the probability that two mating gametes are identical by descent is $\frac{1}{2N}$. Therefore $F_1 = \frac{1}{2N}$.

The remaining proportion of zygotes $1 - \frac{1}{2N}$ carry genes that are independent in origin from generation 1.

Therefore the probability of identical homozygotes in generation 2 is:

$$F_2 = \frac{1}{2N} + (1 - \frac{1}{2N})F_1$$

Where F_1 and F_2 are the inbreeding coefficients of generations 1 and 2. The same arguments apply to future generations, so we can write the recurrence equation:

$$F_t = \frac{1}{2N} + (1 - \frac{1}{2N})F_{t-1}$$

The inbreeding of any generation is composed of two components: New inbreeding, which arises from self-fertilization and the “old” that was already there.

Note that inbreeding is cumulative and that the absence of inbreeding in generation t does not change the fact that a population may be inbred relative to prior generations.

General Principle

Rather than considering a random mating population, let's consider a population that is experiencing a systematic inbreeding process. In this case F refers to the proportionate reduction in heterozygosity (relative to a population that is in HWE) through inbreeding processes. For example, let's consider self-pollination. Begin with an F_1 from a cross of two homozygous lines. We can self the F_1; we get an F_2. How about if we random mate F_1? Does this create a population in HWE? What is the reference population?

If F is the proportionate decrease in heterozygosity due to an inbreeding process, then with self-pollination F can be easily calculated for any generation of selfing.

$$F_n = 1 - (\frac{1}{2})^{n-2}$$

Impact on Disequilibrium

The impact on deviations, i.e., disequilibrium, relative to HWE can be summarized as:

Table 1

	HWE Frequencies	**Change due to inbreeding**
AA	p_o^2	$+p_0q_0F$
Aa	$2p_0q_0$	$-2p_0q_0F$
Aa	q_o^2	$+p_0q_0F$

Alternatively, we can think of the coefficient of inbreeding at the probability of identity by descent. In this case the coefficient of inbreeding is the probability that two alleles at a locus in an individual are IBD. For two individuals $X_{(ab)}$ and $Y_{(cd)}$

$$F_x = P(a \equiv b))(F_y = P(c \equiv d)$$

Coefficient of Parentage

Coefficient of Parentage - Definition

What if two homozygous parents of an F_1 used to create an F_2 population are related? Let’s think about the relationship, parentage, and co-ancestry between two individual people, dogs, corn plants, soybean plants, etc. Refer to these individuals as X and Y. Also, let’s use a short hand for a quantitative measure of this relationship. This relationship is also known as the coefficient of parentage and is defined as the probability that a random gene from an individual X is identical by descent (IBD) with a random allele at the same locus from an individual Y.

$$XabYcd(r_{xy} = \frac{1}{4}[P(a \equiv c) + P(a \equiv d) + P(b \equiv c) + P(b \equiv d)]$$

Historically, this measure has been denoted $\Theta_{X,Y}$ or $f_{X,Y}$.

Calculations

$\Theta_{X,Y} = 1$ means that X and Y have the same identical alleles by decent across all loci. What is another name for this condition? (twins). $\Theta_{X,Y} = 0$ means what? Is it possible that you and I have no alleles that are identical by descent?

There is a relationship between F_n and $\Theta_{X,Y}$. In an individual, if two alleles at a single locus are identical by descent then this is a special case of $\Theta_{X,Y}$, where X and Y are the same individual, i.e., $F_X = \Theta_{X,X}$. To return to the original question "What if two homozygous parents of an F_1 used to create an F_2 population are related?"

$$F_n = 1 - (\frac{1}{2})^{n-2}\{1 - \theta_{X,Y}\}$$

Example Calculations

Example Calculations - Inbreeding Coefficient

Consider the following pedigree:

$$(X_{ab)}|Y_{cd}) \implies Z)i.e., Zisaprogenyofthematingbetween XandY.$$

Individual Z has the following probabilities of containing the various alleles:

$$\frac{1}{4}ac + \frac{1}{4}ad + \frac{1}{4}bc + \frac{1}{4}bd)(F_z = r_{xy} = \frac{1}{4}[P(a \equiv c) + P(a \equiv d) + P(b \equiv c) + P(b \equiv d)]$$

The inbreeding coefficient of the progeny is the coefficient of parentage of the parents.

Self Pollination

$F_z = r_{xx} = \frac{1}{4}[P(a \equiv a) + P(a \equiv b) + P(b \equiv a) + P(b \equiv b)])(P(a \equiv a) = P(b \equiv b) = 1)(P(a \equiv b) = P(b \equiv a) = F_x)(F_z = r_{xx} = \frac{1}{4}[2 + 2F_x])(= \frac{1}{2}[1 + F_x]$

Panmictic Index

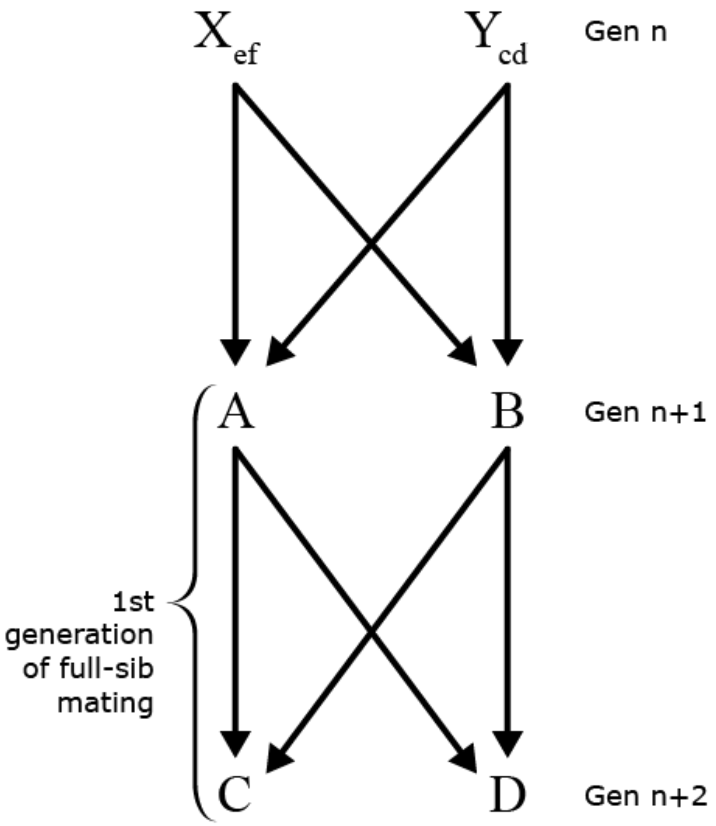
P = 1 - F = **Panmictic Index** — probability that two alleles at a locus are not IBD.

Substituting

$$1 - P_z = \frac{1}{2}[1 + 1 - P_x])(P_z = \frac{1}{2}P_x)(P_1 = \frac{1}{2}P_0)(P_2 = \frac{1}{2}P_1 = \frac{1}{2} \cdot \frac{1}{2}P_0 = (\frac{1}{2})^2 P_0)(P_n = (\frac{1}{2})^n P_0$$

For diploids this is also the percent of heterozygotes at a locus

Full-Sib Mating (1)



Probability that A & B both receive *e* from X =

$$(\frac{1}{2})(\frac{1}{2}) = \frac{1}{4}$$

Probability that A & B both receive *f* from X =

$$(\frac{1}{2})(\frac{1}{2}) = \frac{1}{4}$$

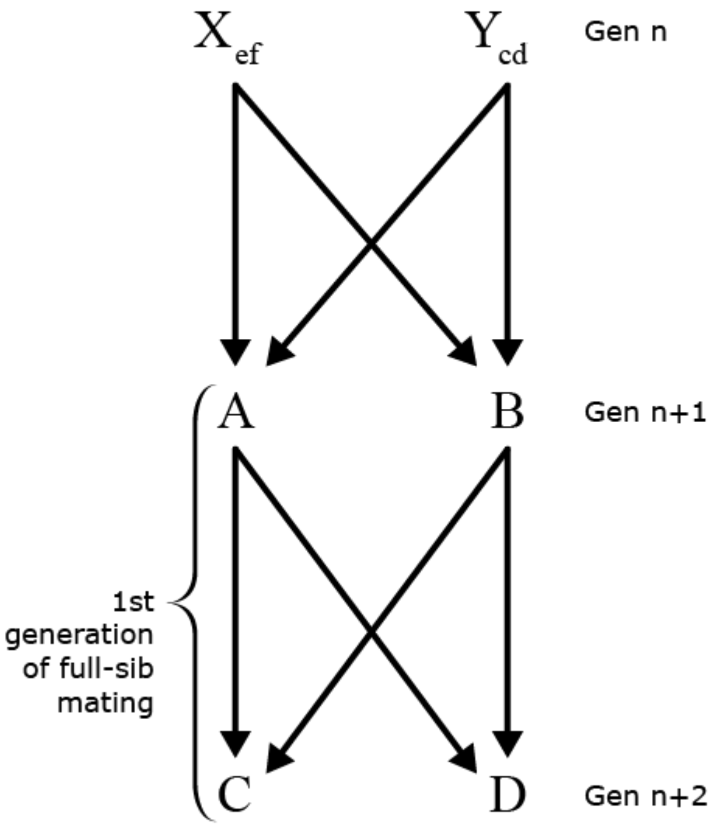
Probability that *e* and *f* are not IDB =

$$1 - F_x$$

Probability that A & B contain an identical allele from X by chance (given that *e* and *f* are not IBD) =

$$(\frac{1}{4} + \frac{1}{4})(1 - F_x)$$

Full-Sib Mating (2)



Probability that (*e*) and (*f*) are identical =

$$F_x$$

Probability A & B receive an identical allele from X (given that (*e*) and (*f*) are IBD) = 1

Total probability that A & B receive an identical allele from X =

$$F_x + \frac{1}{2}(1 - F_x) = \frac{1}{2}(1 + F_x) = r_{xx}$$

Total probability that A & B receive an identical allele from Y =

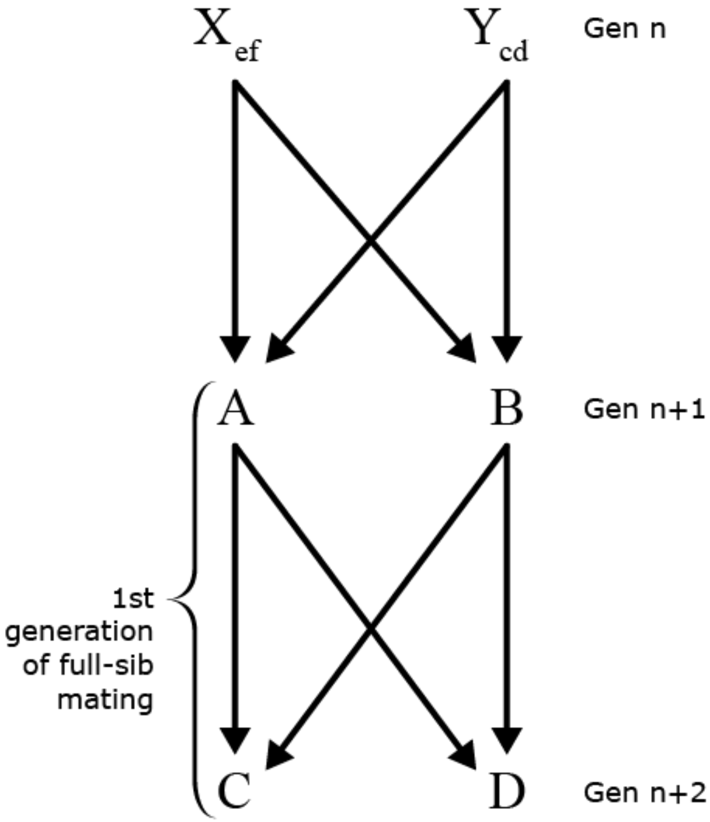
$$F_y + \frac{1}{2}(1 - F_y) = \frac{1}{2}(1 + F_y) = r_{yy}$$

Full-Sib Mating (3)

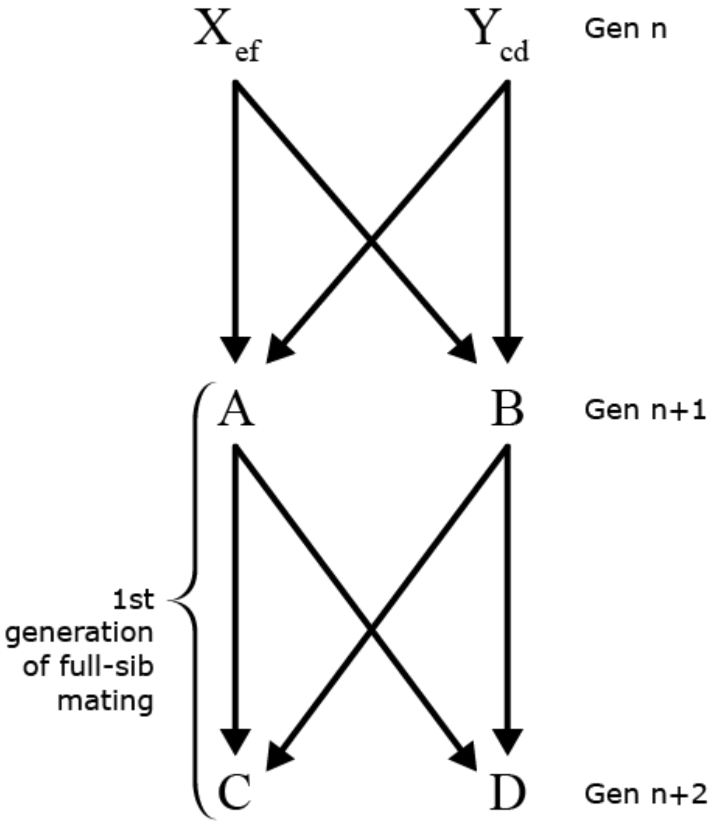
$$r_{AB} = \frac{1}{4}[r_{xx} + 2r_{xy} + r_{yy}]$$

Probability that a gene from X to A and one from Y to B are IBD is r_{xy}

Probability that a gene from Y to A and one from X to B are IBD is r_{xy}



Full-Sib Mating (4)



$$F_x = F_y = F_n)(r_{xy} = r_n)(r_{n+1} = \frac{1}{4}[r_{xx}+r_{yy}+2r_{xy}])(= \frac{1}{4}[\frac{1}{2}(1+F_n)+\frac{1}{2}(1+F_n)+2r_n])(r_{n+1} = F_{n+2})(r_n = F_{n+1})(F_{n+2} = r_{n+1} = \frac{1}{4}[\frac{1}{2}(1+F_n)+\frac{1}{2}(1+F_n)+2F_{n+1}])(= \frac{1}{4}[1 + F_n + 2F_{n+1}])(P_{n+2} = \frac{1}{2}P_{n+1} + \frac{1}{4}P_n)(F_n = 1 - (\frac{1}{2})^n(1 - F_0)$$

Self Pollination

Assume original population is non-inbred (by definition = F_2)

$$P_n = (\frac{1}{2})^n P_0$$

Table 2

Generation	**P**	**F**
0	1.00000000	0.00000000
1	0.50000000	0.50000000
2	0.25000000	0.75000000
3	0.12500000	0.87500000
4	0.06250000	0.93750000
5	0.03125000	0.98437500
6	0.01562500	0.98437500
7	0.00781250	0.99218750
8	0.00390625	0.99609375
9	0.00195313	0.99804688
10	0.00097656	0.99902344
∞	0.00000000	1.00000000

Full-Sibing

$$P_{n+2} = \frac{1}{2}P_{n+1} + \frac{1}{4}P_n$$

Table 3

Generation	P	F
0	1.00000000	0.00000000
1	1.00000000	0.00000000
2	0.75000000	0.25000000
3	0.62500000	0.37500000
4	0.50000000	0.50000000
5	0.40625000	0.59375000
6	0.32812500	0.73437500
7	0.26562500	0.78515625
8	0.21484375	0.78515625
9	0.17382813	0.82617188
10	0.14062500	0.85937500
∞	0.00000000	1.00000000

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