NON-RANDOM MATING AND INBREEDING

DEFINITIONS

Nonrandom mating: Mating individuals are more closely related or less closely related than those drawn by chance from a random mating population (Hedrick, 2005, p. 238).

Inbreeding: Consanguineous mating or mating between relatives (e.g., sibs, cousins, etc.). Affects all gene loci simultaneously.

Outbreeding: Opposite of inbreeding; mating are between individuals that are more distantly related than those drawn by chance from a random mating population. Affects all gene loci simultaneously.

Assortative mating: mating between individuals that share a particular phenotype (positive assortative mating). Negative assortative mating involves avoidance of mating between individuals that share a particular phenotype. Affects only the loci (and linked genes) involved in expression of the phenotypic trait used for mate choice.

INBREEDING IN NATURAL POPULATIONS

Inbreeding results in increased homozygosity of alleles that are **identical by descent (IBD)**.

Define **f** (the **inbreeding coefficient**) as the probability that two homologous alleles in an individual are IBD.

Let p represent the frequency of allele A_1. Homozygosity from alleles that are IBD and alleles that are identical in state. Combining these probabilities, the frequency of A_1A_1 is:

$$P(A_1A_1) \quad = \quad \boxed{P(\text{identity by descent})} \; + \; \boxed{P(\text{identity in state})}$$
$$= \quad \boxed{pf} \; + \; \boxed{p^2(1\text{-}f)}$$

$$= pf + p^2(1-f) = pf + p^2 - p^2f = f(p - p^2) + p^2 = fp(1-p) + p^2$$

$$P(A_1A_1) = p^2 + fpq, \qquad \text{and similarly}$$
$$H(A_1A_2) = 2pq - 2fpq$$
$$Q(A_2A_2) = q^2 + fpq$$

$$\text{If } f = 0, \; P(A_1A_1) = p^2 + 0pq = p^2$$
$$\text{If } f = 1, \; P(A_1A_1) = p^2 + 1pq = p^2 + p(1-p) = p^2 + p - p^2 = p$$

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Thus, inbreeding and random mating terms are summarized as follows:

Frequency	$f = 0$	$f = 1$
$P(A_1A_1)$	p^2	p
$H(A_1A_2)$	$2pq$	0
$Q(A_2A_2)$	q^2	q

Note from the table that **inbreeding changes genotypic frequencies but not allelic frequencies**.

Note also that rare recessive alleles are more likely to occur as homozygotes in populations that have some degree of inbreeding. If q is small (say 0.01) the frequency of homozygotes would be very small in a randomly mating population, $q^2 = 0.0001$.

But inbreeding will increase the proportion of homozygotes by fpq, so if $f = 0.125$ and $q = 0.01$, the frequency of homozygotes will be $q^2 + fpq$, which is $0.0001 + (0.125)(0.99)(0.01)$, or $0.0001 + 0.00124$, which is about 0.00134, a 13.4–fold increase (see Hedrick, 2005, Table 5.1).

Finally, note that the frequency of heterozygotes, $H = 2pq - 2fpq$, can be rewritten as

$$H = 2pq(1 - f),$$

which gives us a way to solve for f.

$$\frac{H}{2pq} = 1 - f$$

By rearrangement

$$f = 1 - \frac{H}{2pq}$$

So observed (H_{obs}) and expected (H_{exp}) heterozygosities in a population can provide an estimate of f, assuming alleles are selectively neutral. We will see relationship this again when we study hierarchical population structure.

SELFING

Heterozygosity is lost at the rate of 1/2 per generation as the inbreeding coefficient, f, increases at the rate of 1/2 per generation.

$$H_t = \left(\frac{1}{2}\right)^t H_0 \text{ , so } \frac{H_t}{H_0} = \left(\frac{1}{2}\right)^t = 1 - f_t, \text{ note also that } f_t = 1 - \frac{H_t}{H_0}$$
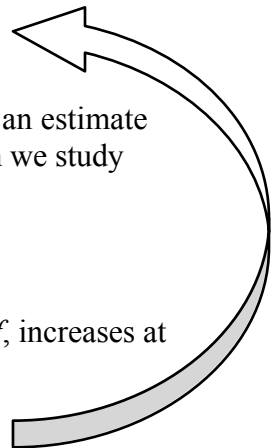
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Generation	Frequency of			$\dfrac{H_t}{H_0}$	f_t
	AA	*Aa*	*aa*		
0	p^2	$2pq$	q^2	1	0
1	$p^2 + pq/2$	pq	$q^2 + pq/2$	1/2	1/2
2	$p^2 + 3pq/4$	$pq/2$	$q^2 + 3pq/4$	1/4	3/4
3	$p^2 + 7pq/8$	$pq/4$	$q^2 + 7pq/8$	1/8	7/8
∞	p	0	q	0	1

In a more general sense, the increase in f_t under inbreeding is inversely correlated to the number of breeding adults, N, and the number of generations, t:

$$f_0 = 0$$

$$f_1 = \frac{1}{2N}$$

$$f_2 = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right)f_1$$

$$f_t = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right)f_{t-1}$$

which can be stated more generally as:

$$f_t = 1 - \left(1 - \frac{1}{2N}\right)^t$$

Under selfing, $N = 1$, so in $t = 3$ generations $f_t = 1 - (1-1/2)^3 = 1 - (1/2)^3 = 1 - 1/8 = 7/8$.

What will f_t be after 10 generations of selfing? $f_t = 1 - (1-1/2)^{10} = 1 - (1/2)^{10} = 1 - 0.00098 = 0.999$

What will f_t be after 10 gen. of sib-mating? $f_t = 1 - (1-1/4)^{10} = 1 - (3/4)^{10}\ 1 - 0.0563 = 0.947$

How many generations of sib-mating are required to produce a mouse strain that is 99% homozygous?

$$0.99 = 1 - \left(1 - \frac{1}{2(2)}\right)^t = 1 - \left(1 - \frac{1}{4}\right)^t = 1 - \left(\frac{3}{4}\right)^t$$

By rearrangement

$$\left(\frac{3}{4}\right)^t = 1 - 0.99$$

$$t \log(0.75) = \log(1 - 0.99) = \log(0.01)$$

$$t = \frac{\log(0.01)}{\log(0.75)} = 16.008$$

It takes 16 generations of sib-mating to produce what mouse breeders call a congenic strain ($f = 0.99$).

For small populations, the inbreeding coefficient grows as a function of the number of breeding adults, N.

$$f_t = 1 - \left(1 - \frac{1}{2N}\right)^t$$

Heterozygosity decreases according to a related function
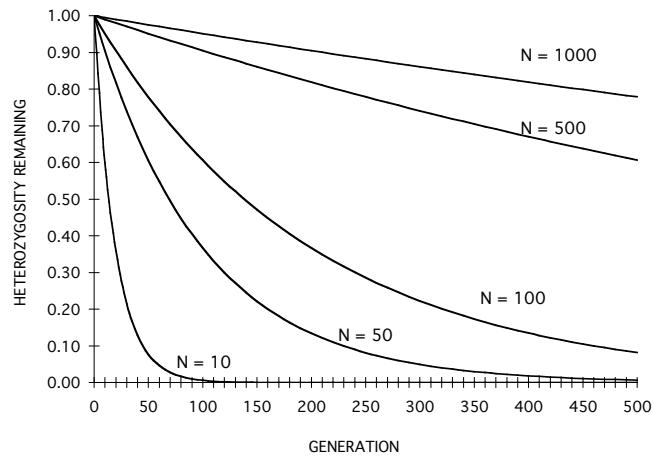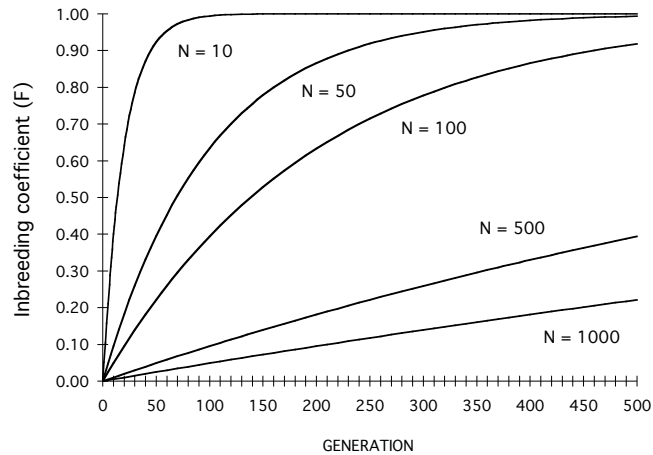
$$H_t = H_0(1 - f_t)$$

Substituting the equation for f_t gives

$$H_t = H_0\left(1 - \frac{1}{2N}\right)^t$$

and

$$\frac{H_t}{H_0} = \left(1 - \frac{1}{2N}\right)^t$$

These are very important relationships for plant and animal breeders and conservation geneticists.

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INBREEDING AND KINSHIP COEFFICIENTS (FROM CROW, 1983)

We define the **kinship coefficient** (F_{JK}) for individuals J and K as the probability that two homologous alleles (one allele chosen at random from individual J and K) are **identical by descent**. Note that **kinship coefficient** is synonymous with **coefficient of consanguinity**. The **coefficient or relatedness** of parents is twice the inbreeding coefficient of offspring, $r = 2f$.

Here we see two individuals that are homozygous for *AA* (I and J), but only I has *A* alleles that are **IBD**. J is **identical in state**.
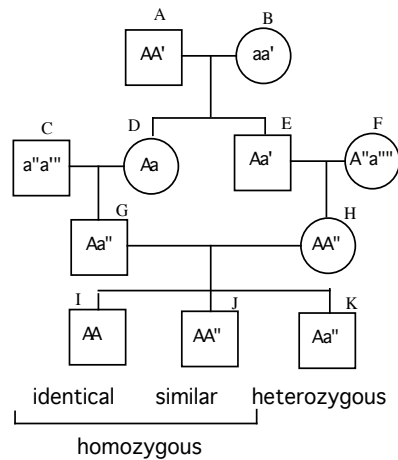
For the adjacent pedigree, we determine the kinship coefficient of individuals D and E very simply. They are siblings. Assuming that A and B are not inbred, the probability of D drawing a particular allele A^1 from A is 1/2. The probability of E drawing A^1 from A also is 1/2, so the joint probability of D and E drawing A^1 is (1/2)(1/2) = 1/4. Thus, the kinship coefficient of D and E (F_{DE}) is 1/4.
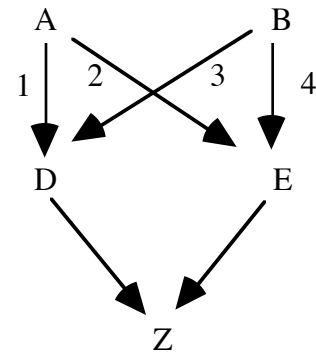
Note that the **inbreeding coefficient** of an individual (F_Z) equals the **kinship coefficient** of its parents (F_{DE}). Thus, the inbreeding coefficient of a child produced by D and E would equal 1/4. In other words, a child of sib-mating is *expected* to be homozygous (identical by descent) for 1/4 of its gene loci, on average. Remember, this is an expectation that is associated with a binomial sampling variance. The realized F_Is would range from 0 to 0.5 with a mean of 0.25.

The common method of determining inbreeding coefficients from pedigrees is **path analysis**, which was developed by Sewell Wright in the early 1900s. Your textbook refers to these as **chain counting** techniques (Hedrick, 2005, p. 266). Look at the example in Fig. 5.14 on p. 268.

Let's examine the sib-mating case with path analysis. We are interested in determining the inbreeding coefficient of individual Z (F_Z). We simply need to count the number of paths (and individuals in the paths that lead to common ancestors. Path 1-2 leads through common ancestor A. Path 3-4 leads through common ancestor B. The general rule for any pedigree is

$$F_I = F_{JK} = \sum \left[(1/2)^n (1 + F_A) \right]$$

Path 1-2 goes through three ancestors (D-A-E), as does path 3-4 (D-B-E). Assuming that A and B were not inbred (F_A and F_B = 0), then

$$F_I = (1/2)^3(1 + F_A) + (1/2)^3(1 + F_B)$$
$$= (1/8)(1) + (1/8)(1) = 1/4$$

You should rely primarily on the text by Hedrick for information on inbreeding. He does a fair job with this.

Try a more complicated pedigree involving first cousins (right). Assume that the common ancestors R and S are themselves not inbred ($F_R = F_S = 0$). The inbreeding coefficient of individual Z (F_Z) the sum of two paths 1-2-3-4 and 1-5-6-4, or $(1/2)^5+(1/2)^5 = 1/16$.
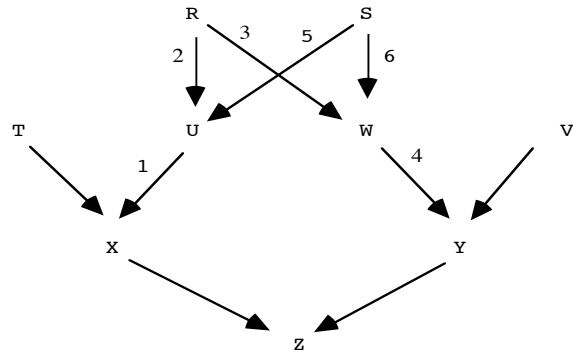
Things can get a lot more complicated fast in pedigree analysis. Some sophisticated computer programs have been written to do this. One of the most useful methods employed in conservation genetics and animal breeding is the **gene dropping method**, which uses a Monte Carlo simulation approach to assess relatedness in pedigrees.

The issue of relatedness, *r*, is central to theories about kin-selection. More later.

REFERENCES

Crow JF (1983) *Genetics Notes: an Introduction to Genetics* Burgess Publ., Minneapolis, MN.

Hedrick PW (2005) *Genetics of Populations*, 3rd edn. Jones and Bartlett Publishers, Sudbury, MA.