

Inbreeding

1. The coefficient of kinship (f_{xy}) between two individuals is the probability that a gene copy taken at random from one of them is identical by descent with a gene copy taken at random from the other one. Thus the inbreeding coefficient (F_I) of an individual is equal to its parents' coefficient of kinship. (See Gillespie, pp 121-125.) Show by direct probability calculations that the inbreeding coefficient of an individual whose parents are first cousins (but not inbred) is $1/16$. This is the chance that at any given locus, the offspring will be homozygous for a gene copy derived from one of its grandparents. You will want to draw a pedigree diagram similar to those in Gillespie or in Alan's lecture, to keep track of all the paths and their associated probabilities of transmission.
2. Consider a deleterious recessive allele at a frequency of $q = 0.001$ in the population. How many times more likely is the offspring of a cousin mating to suffer its effects (that is, to be homozygous for it) than is an outbred individual? Start by calculating the probabilities of being a homozygote, for both kinds of offspring ($F = 0$, and $F = 1/16$). Now do the same analysis for recessive alleles at lower ($q = 0.0001$) and higher ($q = 0.01$) frequencies. For which kinds of alleles does inbreeding most strongly increase the probability (absolutely, and relatively) of being affected by the mutation?

Population structure

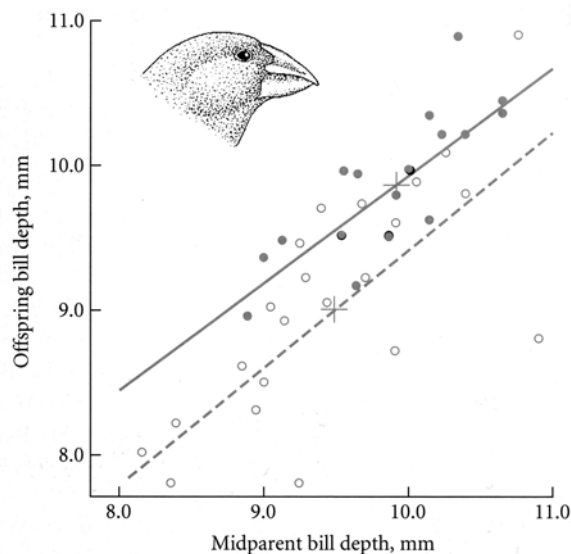
3. F_{ST} can be expressed in terms of gene diversity $[(H_T - H_S)/H_T]$, or homozygosity $[(G_S - G_T)/(1 - G_T)]$, or the variance of allele frequencies among the subdivisions $[V/(pq)]$. Demonstrate algebraically that all three formulas are equivalent. (Hint: Look closely at Gillespie's pages 132-133.)
4. In 1978, Sewall Wright (then 89 years old, with a decade of productive work still ahead of him) published a paper on genetic variation among the human racial groups. He included a table of allele frequencies at six loci, from which the following is extracted. Both of these loci are biallelic. The numbers are observed frequencies of the P^1 allele at the P locus, and the Fy allele at the *Duffy* locus.

Population	P^1	Fy
African	0.734	0.037
European	0.496	0.436
Australian	0.330	1.000
East Asian	0.259	0.901
Average	0.455	0.593

- 4a. What is F_{ST} at the P locus? At the *Duffy* locus?
- 4b. What is the average of the two estimates? How does your overall estimate compare with the value of 0.12, which has been found in many other studies of genetic differentiation among the major racial groups? Are these loci typical, or unusual in some way? If so, how?
- 4c. Consider a population divided into several groups within which mating is random. Suppose the frequency of allele A is 0.25 in the population as a whole, and that $F_{ST} = 1/3$. Within the population as a whole, what are the observed frequencies of the three genotypes AA , Aa and aa ?

Quantitative traits

5. Two completely inbred varieties of tobacco are crossed and the variance of leaf number among F_1 plants is 3.5. In the F_2 generation the variance is 14.0. What are the genotypic and environmental variance components and the broad-sense heritability in the F_2 generation?
6. In a population of the flour beetle *Tribolium* the mean weight of pupae is 2 mg (2000 μg). The phenotypic variance is 400 μg^2 and the additive genetic variance is 100 μg^2 . If individuals with a *mean* pupal weight that is two phenotypic standard deviations above the population-wide mean are selected as parents, what is the expected average pupal weight among their progeny?
7. Five generations of selection for decreased plasma cholesterol in a population of semi-wild mice changed the mean from 2.15 mg/100 ml to 2.01 mg/100 ml. The selection differential (S) was -0.07 mg/100 ml. Estimate the heritability of plasma cholesterol levels in this population.
8. The average bill depth of *Geospiza fortis* (Darwin's medium ground finch) increased by 0.5 mm in one generation (1976 to 1978) in the population on Isla Daphne Major that has been studied by Peter and Rosemary Grant and their students and colleagues since the early 1970s. The phenotypic standard deviation of this trait is around 1 mm, and its heritability has been estimated (from the correlations among relatives) to be around $h^2 = 0.90$.
 - 8a. Given these numbers, what was the selection gradient (β) during the drought of 1977? (The drought was caused by a severe El Niño event that forced the birds to feed on large, hard seeds that they otherwise wouldn't eat.)
 - 8b. What were the *relative* fitnesses of two otherwise equivalent birds with 9-mm and 10-mm bill depths?



The figure shows bill-depth heritability data for *G. fortis* in 1976 (before the drought, open circles and dashed regression line) and in 1978 (after the drought, filled circles and solid line). The crosses are the mean midparent and offspring values in each of these two years.