BIOB480/BIOE548 notes 10/17/2024

Introduction:

- Reminders: HW7 due Thursday next week. Bring questions Tuesday. Exam 3 a week from Tuesday. Will have grading done over the weekend so you can use HW and Exam 2 as study material.

Inbreeding without pedigrees

In most cases we will have no pedigree to use to calculate F. We therefore need a way to infer inbreeding from genotype frequency data. Because F is equivalent to the probability two alleles are identical by descent, the genotype frequency of homozygotes in a fully inbred population is 0 (0% * $2pq$), while the frequency of each homozygote is equivalent to its respective allele frequency, as the probability of an individual being homozygous is 100% once you account for the frequency of the allele in the population. A partially inbred population will see a reduction in heterozygosity proportional to F, leaving a frequency of $2pq$ heterozygotes multiplied by the complement of the inbreeding coefficient. The frequency of the two homozygotes will be a mixture of the predicted frequencies under random mating and those under full inbreeding, weighted by the inbreeding coefficient:

	F	$A_1 A_1$	$A_1 A_2$	$A_2 A_2$
random mating	0	p^2	$2pq$	q^2
fully inbred	1	p	0	q
partially inbred	0<F<1	$p^2(1-F) + p*1*F = p^2 + Fpq$	$2pq(1-F)$	$q^2(1-F) + q*1*F = q^2 + Fqp$

(Above, note that I have shortened the derivations for $p^2(1-F) + p*1*F = p^2(1-F) + p*1*F = p^2 - Fp^2 + pF = p^2 + Fp(1-p) = p^2 + Fpq$ and $q^2(1-F) + q*1*F = q^2(1-F) + q*1*F = q^2 - Fq^2 + qF = q^2 + Fq(1-q) = q^2 + Fqp$).

We can therefore understand the reduction in heterozygosity of an inbred population as $\frac{H_{inbred}}{H_e} = \frac{2pq(1-F)}{2pq} = 1 - F$. Simplifying, we get:

$$\frac{H_{inbred}}{H_e} + F = 1$$

$$F = 1 - \frac{H_{inbred}}{H_e}$$

$$F = 1 - \frac{H_o}{H_e}$$

In other words, the inbreeding coefficient is equal to 1 minus the ratio of observed to expected heterozygosity.

Lastly, we derive a model for relating the inbreeding coefficient to population size to predict the increase in F across generations. Recall that F is defined as the probability of sampling two alleles that are identical by descent. This can happen two ways: by new inbreeding (at rate $\frac{1}{2N}$), and by sampling alleles that are

already IBD from previous inbreeding (at frequency $(1 - \frac{1}{2N})F_{t-1}$, where F_{t-1} is the inbreeding coefficient of the parental generation):

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

This tells us that the increase in the inbreeding coefficient each generation is $\Delta F = \frac{1}{2N}$: equivalent to the *loss* of homozygosity each generation. From this, we can develop a general relationship between expected inbreeding at generation t and the initial inbreeding coefficient:

$$F_t = 1 - [(1 - \frac{1}{2N})^t (1 - F_0)]$$

You should notice our model for the exponential decay of heterozygosity through time embedded within, and recall that $1 - F_0$ is the reduction in in heterozygosity below expected values under random mating caused by inbreeding. F therefore grows larger with smaller population sizes, greater initial inbreeding values, and a greater number of generations.

Inbreeding depression

In a vaccuum, inbreeding itself would not be particularly interesting. It is its effects on expected trait values— particularly fitness traits—that make it important for conservation biologists to consider. We now develop a model to understand its impacts on mean trait values using simple quantitative genetics. Remember that $+a$ is the deviation of the trait value for A_1A_1 away from the mean of the two homozygotes, d is the trait value deviation for the heterozygote, and $-a$ is deviation of the trait value for A_2A_2. The average trait value for the population will require weighting these deviations by the frequency of the genotype they are associated with. The table below lays out these weightings for different mating schemes:

	A_1A_1	A_1A_2	A_2A_2
random mating	$p^2 a$	$2pqd$	$-q^2 a$
fully inbred	pa	0	$-qa$
partially inbred	$p^2 a + Fpqa$	$2pqd(1 - F)$	$-q^2 a + Fqpa$

From this, we can determine that the mean trait value deviation of a randomly mating population (M_0) from the midpoint of the two homozygotes is:

$$M_O = p^2 a + 2pqd - q^2 a = p^2 a - q^2 a + 2pqd = a(p^2 - q^2) + 2pqd = a(p + q)(p - q) + 2pqd = a(p - q) + 2pqd$$

(Note the substitution of 1 for $p + q$.)

Similarly, the mean trait value deviation of an inbred population (M_F) from the midpoint of the two homozygotes is:

$$M_F = p^2 a + Fpqa + 2pqd(1 - F) - q^2 a - Fpqa = p^2 a - q^2 a + Fpqa - Fpqa + 2pqd - 2pqdF$$

$$M_F = a(p^2 - q^2) + 2pqd - 2pqdF = a(p + q)(p - q) + 2pqd - 2pqdF = a(p - q) + 2pqd - 2pqdF$$

Because $a(p - q) + 2pqd = M_0$, $M_F = M_0 - 2pqdF$. In this equation, the term $2pqdF$ represents inbreeding depression, which we denote as δ. Inbreeding depression is thus the degree to quick the average trait value of the poulation is depressed below random mating expectations.

This tells us a few other things too:

1) if there is no dominance (i.e., $d = 0$, there can be no inbreeding depression;
2) if there is no inbreeding (i.e., $F = 0$), there can be no inbreeding depression;
3) the degree of inbreeding depression (δ) is a linear function of F;
4) we can estimate δ as $1 - \frac{\text{fitness of inbred offspring}}{\text{fitness of outbred offspring}}$