Breeding Values and Inbreeding

Genotypic Values

- For the bi-allelic single locus case, we previously defined the mean genotypic (or equivalently the mean phenotypic values) to be

$$G_{ij} = \begin{cases} -a & \text{if genotype is } A_2A_2 \\ d & \text{if genotype is } A_1A_2 \\ a & \text{if genotype is } A_1A_1 \end{cases}$$

and $\mu_G = a(p-q) + d(2pq)$. The additive genetic values are

$$G_{ij}^A = \begin{cases} \mu_G + 2\alpha_2 & \text{if genotype is } A_2A_2 \\ \mu_G + \alpha_1 + \alpha_2 & \text{if genotype is } A_1A_2 \\ \mu_G + 2\alpha_1 & \text{if genotype is } A_1A_1 \end{cases}$$

- where the additive effects α_i were defined by Fisher to be the least-squares regression coefficients of genotypic values on allele counts at a locus.

Breeding Values

- For the bi-allelic case, we showed that additive effects are $\alpha_1 = q[a + d(q - p)]$ and $\alpha_2 = -p[a + d(q - p)]$, where p and q be the allele frequencies of the A_1 and A_2 allele, respectively, in the population.
- The usefulness of the concept of additive effects arises from the fact that parents pass on their alleles and not their genotypes to their progeny, as previously mentioned.
- The "value" of an individual, as judged the the mean value of the individual's progeny, is called the individuals **breeding value**.
- The breeding value for an individual at a locus is defined to be the sum of the additive effects of the alleles at the locus.
- For a single locus trait with two alleles, the breeding values are $2\alpha_1$ for homozygous genotype A_1A_1, $\alpha_1 + \alpha_2$ for heterozygous genotype A_1A_2, and $2\alpha_2$ for homozygotes genotype A_2A_2.

Breeding Values

- Consider the expected genotypic values of progeny produced by the parental genotypes.
- If an individual with the A_1A_1 genotype is mated to a number of individuals taken at random from the population, what would be the mean genotypic value of the progeny? What is the deviation of the expected progeny mean from the population mean?
- Similarly, what is the mean genotypic progeny values and the deviation of the expected progeny values from the population mean for individuals with the A_1A_2 and A_2A_2 genotypes?

Mean Progeny Breeding Values

- $E[\text{progeny genotypic value}|\text{one parent is } A_1A_1]$

$$= a \times P(\text{progeny has genotype } A_1A_1|\text{one parent is } A_1A_1\ )$$

$$+d \times P(\text{progeny has genotype } A_1A_2|\text{one parent is } A_1A_1\ ) = pa + qd$$

- The mean deviation of the progeny from the population mean is

$$pa + qd - \mu_G = pa + qd - [a(p-q) + 2dpq]$$

$$= q[a + d(1-2p)] = q[a + d(q-p)] = \alpha_1$$

- A parent with a breeding value of $2\alpha_1$ has progeny with an average deviation from the population mean equal to α_1!

Mean Progeny Breeding Values

- $E[\text{progeny genotypic value} | \text{one parent is } A_2A_2]$

$$-a \times P(\text{progeny has genotype } A_2A_2 | \text{one parent is } A_2A_2\ )$$

$$+d \times P(\text{progeny has genotype } A_1A_2 | \text{one parent is } A_2A_2\ )$$

$$= -qa + pd$$

- The mean deviation of the progeny from the population mean is

$$-qa + pd - \mu_G = -qa + pd - [a(p-q) + 2dpq]$$

$$= -p[a + d(2q-1)] = -p[a + d(q-p)] = \alpha_2$$

- So a parent with a breeding value of $2\alpha_2$ has progeny with an average deviation from the population mean equal to α_2!

Mean Progeny Breeding Values

- $E[\text{progeny genotypic value}|\text{one parent is } A_1A_2]$

$$a \times P(\text{progeny has genotype } A_1A_1|\text{one parent is } A_1A_2\ )$$

$$+d \times P(\text{progeny has genotype } A_1A_2|\text{one parent is } A_1A_2\ )$$

$$-a \times P(\text{progeny has genotype } A_2A_2|\text{one parent is } A_1A_2\ )$$

$$= \frac{pa}{2} + \frac{d}{2} - \frac{qa}{2}$$

- The mean deviation of the progeny from the population mean is

$$\frac{pa}{2} + \frac{d}{2} - \frac{qa}{2} - \mu_G$$

$$= \frac{1}{2}(pa + qd - \mu_G) + \frac{1}{2}(-qa + pd - \mu_G) = \frac{\alpha_1 + \alpha_2}{2}$$

- So a parent with a breeding value of $\alpha_1 + \alpha_2$ has progeny with average deviation from population mean equal to $\frac{\alpha_1+\alpha_2}{2}$!

Mean Progeny Breeding Values

- So, when mating is random, the breeding value of a genotype for an individual is equivalent to twice the expected deviation if its offspring mean phenotype from the population mean.
- The deviation is multiplied by two since only of one the two parental genes is passed on to each offspring (which is why the average allelic effect is so important!)
- Thus, we can estimate the breeding value of an individual by mating it to randomly chosen individuals from the population and taking twice the deviation of its offspring mean from the population mean
- These types of experiments are often performed in animal genetics

Kinship Coefficients and Inbreeding

- Two alleles that are inherited copies of a common ancestral allele are said to be identical by descent (IBD). The term IBD is generally used for referring to recent, rather than ancient, common ancestry.
- Two individuals that have IBD alleles are said to be related.
- Inbreeding occurs when individuals who are related to each other by ancestry mate.
- If two parents are related, then the probability that two parents transmit IBD alleles to an offspring is the inbreeding coefficient F of the child.
- The degree of Inbreeding in a population depends on the size of the population and the number of ancestors that the population is derived from

Kinship Coefficients and Inbreeding

- The probability that an allele taken at random from one individual is IBD to an allele taken at random from another individual is the kinship coefficient or coancestry coefficient, ϕ, of those two individuals.
- The inbreeding coefficient of an individual is the coancestry of its parents.
- What is the inbreeding coefficient for an offspring that is a product of a mating between outbred siblings?
- What is the kinship coefficient of a parent and an offspring?

Genotype Frequencies for Inbred Individuals

- Consider once again a bi-allelic genetic marker with alleles A_1 and A_2. Let p be the frequency of allele A_1 and $q = 1 - p$ the frequency of allele A_2 in the population.
- Consider an individual with inbreeding coefficient F. What are the genotype frequencies for this individual at the marker?

Genotype	A_1A_1	A_1A_2	A_2A_2
Frequency			

Genotype Frequencies for Inbred Individuals

- We have that

$$
\begin{aligned}
P(A_1A_1|F) &= P(A_1A_1 \text{ and alleles are IBD}|F) \\
&+ P(A_1A_1 \text{ and alleles are not IBD}|F) \\
&= P(A_1A_1|\text{alleles are IBD}, F)P(\text{alleles are IBD}|F) \\
&+ P(A_1A_1|\text{alleles are not IBD}, F)P(\text{alleles are not IBD}|F) \\
&= pF + p^2(1-F) = p^2 + Fp(1-p)
\end{aligned}
$$

Generalized Hardy-Weinberg Deviations

- The table below gives genotype frequencies at a marker for an inbred individual with inbreeding coefficient F

Genotype	A_1A_1	A_1A_2	A_2A_2
Frequency	$p^2 + Fp(1-p)$	$2pq(1-F)$	$q^2 + Fq(1-q)$

  where $q = 1 - p$
- $F = 0$ corresponds to outbred populations and with genotype frequencies in HWE.
- The parameters p and F are sufficient to describe the genotype frequencies at a single locus for an inbreed individual.