



Decomposition of the Genotypic Value

Partitioning of Phenotypic Values



- We introduced the general model of $Y = G + E$ in the first lecture, where Y is the phenotypic value, G is the genotypic value, and E is the environmental deviation.
- G is the combination of all genetic loci that influence the phenotypic value and the E consists of all non-genetic factors that influence the phenotype
- The mean environmental deviation E is generally taken to be 0 so that the mean genotypic value is equal to the mean phenotypic value
- Thus the term "population mean" can refer to either the mean phenotypic or genotype value.

Decomposition of Genotypic Values



- Now G can potentially be a very complicated and nonlinear function of numerous trait loci.
- It is useful to decompose G into additive components and components that deviate from an additive model such that individuals with alleles A_i and A_j at a locus have a mean genotypic value of

$$G_{ij} = G_{ij}^A + \delta_{ij} = \mu_G + \alpha_i + \alpha_j + \delta_{ij}$$

where

- ▶ μ_G is the overall genotypic mean (or equivalently the phenotypic mean) in the population
- ▶ α_i and α_j are the mean additive effects for alleles i and j , respectively
- ▶ δ_{ij} is a dominance effect, i.e., genetic deviation from additivity at the locus for an individual with alleles A_i and A_j

Decomposition of Genotypic Values



- So, for a trait locus with only two allelic types, A_1 and A_2 , we would have

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

- We will now focus on calculating the average effect of each allele for a quantitative phenotype

Representation of Genotypic Values



- We previously showed the genotype values can be represented relative to the average of the mean genotype values for the two homozygotes:

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

- We will use this representation of the genotypic values as it will make the interpretation of the additive effects for the alleles a bit easier. We will let that A_1 be the allele that increases the phenotype value.

Representation of Genotypic Values



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

- The point of origin, zero, on this scale is the mid-way point between the two homozygotes genotype values.
- $d = 0$ when there is no dominance effect, d is positive if A_1 exhibits dominance over A_2 , and d is negative if A_2 exhibits dominance over A_1 .
- If the frequency of the A_1 and A_2 alleles is p and q in this population, what is the mean genotypic value, μ_G , on this scale? You can assume Hardy Weinberg Equilibrium (HWE).

Population Mean Genotype Value



$$\begin{aligned}\mu_G &= -a(q^2) + d(2pq) + ap^2 = a(p^2 - q^2) + d(2pq) \\ &= a(p + q)(p - q) + 2dpq = a(p - q) + 2dpq\end{aligned}$$

- So, the contribution of a locus to the population mean of a phenotype (which is the same as the mean of the genotype values) has two terms:
 - ▶ the first term, $a(p - q)$, is attributable to the homozygotes (since a is based only on the homozygotes genotype values)
 - ▶ the second term, $2dpq$, is attributable to the heterozygotes.
- If there is no dominance, the mean genotype value is proportional to the allele frequency: $\mu_G = a(1 - 2q)$
- If there is complete dominance of the A_1 allele, i.e., $d = a$, then the mean is proportional to the square of the allele frequency:
 $\mu_G = a(1 - 2q^2)$

Population Mean Genotype Value



$$\mu_G = a(p - q) + 2dpq$$

- The total range of values attributed to this locus is $2a$ assuming no overdominance, i.e., from $-a$ to a .
- What would the contribution of this locus be to the phenotype if the population was monomorphic (allele frequency is 1 in the population) for the A_1 allele? What about for a monomorphic A_2 allele in the population?

Mean Allele Effects



- The mean allelic effect, which is different from a mean genotypic effect, is the average effect associated with an allele carried by an individual.
- Allelic effects in a population are of importance in characterizing the trait in the population since parents transmit one of their alleles at a locus to offspring in a population and not their genotypes
- The term "breeding value" is often used in quantitative genetics. It is the sum of the mean effects of the alleles carried by an individual to be transmitted to offspring.

Average Allelic Effects



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

- α_i , the mean effect of allele A_i , can be viewed as the mean deviation from the population mean of individuals who receive the allele from one parent, while the allele received from the other parent is drawn at random from the population.
- As before, let alleles A_1 and A_2 have frequencies p and q , respectively.
- If A_1 randomly unites with gametes in the population, what is the average effect of the genotypes that are created with this allele?
What is α_1 ?
- What is α_2 ?

Average Allelic Effects



- The average effects of genotypes created with A_1 randomly uniting with gametes in the population is:

$$a \times P(A_1 \text{ unites with another } A_1 \text{ in population})$$

$$+ d \times P(A_1 \text{ unites with } A_2 \text{ in population}) = pa + qd$$

- So,

$$\begin{aligned}\alpha_1 &= pa + qd - \mu_G = pa + qd - [a(p - q) + 2dpq] \\ &= q[a + d(1 - 2p)] = q[a + d(q - p)]\end{aligned}$$

- Take a moment and calculate α_2 , the mean effect of allele A_2
- What is the expected value of the average allelic effects?

Average Allelic Effects



- Similarly can show that $\alpha_2 = -qa + pd - \mu_G = -p[a + d(q - p)]$
- The expected value of the average allelic effects is 0.

Allele Substitution



- When a locus has only two alleles, the average effect is often expressed in terms of the average effect of **allele substitution**
- That is, the average effect in genotype values when one allele is substituted for the other allele.
- For example, what would be the average effect if an A_2 allele was substituted with A_1 ?
- For A_2 alleles chosen at random, a proportion p of them would be found in the A_1A_2 genotypes, and changing genotype A_1A_2 to A_1A_1 would change the genotype value from d to a , so the effect will therefore be $a - d$.
- Similarly, a proportion q will be found in the A_2A_2 genotypes, and changing one of the A_2 alleles in genotype A_2A_2 such that the new genotype is A_1A_2 would change the genotypic value from $-a$ to d , so the effect is $d + a$
- What is the average effect of allele substitution then of an A_2 allele with an A_1 allele?

Allele Substitution



- Thus the average effect of allele substitution, which is often written as α (without subscripts) is $p(a - d) + q(d + a)$, which can be shown to be

$$\alpha = a + d(q - p) = \alpha_1 - \alpha_2$$

- So the average effect of allele substitution is the difference between the average effects of the two alleles
- One can also show that
 - ▶ $\alpha_1 = q\alpha$
 - ▶ $\alpha_2 = -p\alpha$

Decomposition of Genotypic Values



- We previously decomposed the genotypic value at a locus into additive effects and dominant deviations:

$$G_{ij} = G_{ij}^A + \delta_{ij} = \mu_G + \alpha_i + \alpha_j + \delta_{ij}$$

- For a locus with only two allelic types, the model is essentially:

$$G_{ij} = \mu_G + \alpha_1 X_1^{ij} + \alpha_2 X_2^{ij} + \delta_{ij}$$

where X_1^{ij} and X_2^{ij} are the number of type A_1 and A_2 alleles, respectively, in genotype G_{ij}

- Alternatively, since $X_1^{ij} = 2 - X_2^{ij}$, we could rewrite this in terms of a single effect:

$$G_{ij} = \beta_0 + \beta_1 X_1^{ij} + \delta_{ij}$$

- What would β_0 and β_1 be in this univariate model in terms of α_1 and α_2 ?

Decomposition of Genotypic Values



- $\beta_0 = \mu_G + 2\alpha_2$
- $\beta_1 = \alpha_1 - \alpha_2$. This is the average effect of allele substitution!
- This result has implications for linear regression.
- Average allele effects can be estimated using the slope of a linear regression line.

Multi-locus Traits



- Alleles at several loci can contribute to the genotype mean
- A question of interest is how do alleles at different loci combine to produce a joint effect on the trait
- Let consider the case when the bi-allelic loci are unlinked with no epistasis (no interaction) and the effects combine by addition
- In this case, the population mean of the trait resulting from the joint effects of L loci on the trait is the sum of the contributions from each of the separate loci:

$$\mu_G = \sum_{i=1}^L a_i(p_i - q_i) + 2 \sum_{i=1}^L d_i p_i q_i$$

where a_i and d_i are the genotypic values for the upper homozygotes and the heterozygotes at locus i , respectively, and p_i and q_i are the two allele frequencies at locus i .