

Basics of Quantitative Genetics (Part 2)

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Variances

- ▶ selection can only be done with variation
- ▶ variation is assessed by variance

$$\text{Var} [X] = \sum_{x_i \in \mathcal{X}} (x_i - \mu_X)^2 * f(x_i)$$

where \mathcal{X} : set of all possible x -values
 $f(x_i)$ probability that x assumes the value of x_i
 μ_X expected value $E [X]$ of X

Variation of Genotypic Values

$$\begin{aligned}\sigma_G^2 &= \text{Var}[V] = (V_{11} - \mu)^2 * f(G_1 G_1) \\ &\quad + (V_{12} - \mu)^2 * f(G_1 G_2) \\ &\quad + (V_{22} - \mu)^2 * f(G_2 G_2) \\ &= (BV_{11} + D_{11})^2 * f(G_1 G_1) \\ &\quad + (BV_{12} + D_{12})^2 * f(G_1 G_2) \\ &\quad + (BV_{22} + D_{22})^2 * f(G_2 G_2) \\ &= 2pq\alpha^2 + (2pqd)^2 \\ &= \sigma_A^2 + \sigma_D^2\end{aligned}$$

where $\mu = (p - q)a + 2pqd$ the population mean and
 $V_{ij} - \mu = BV_{ij} + D_{ij}$

Additive Genetic Variance

$$\begin{aligned}\sigma_A^2 &= \text{Var}[BV] = BV_{11}^2 * f(G_1 G_1) + BV_{12}^2 * f(G_1 G_2) + BV_{22}^2 * f(G_2 G_2) \\ &= (2q\alpha)^2 * p^2 + ((q - p)\alpha)^2 * 2pq + (-2p\alpha)^2 * q^2 \\ &= 4p^2 q^2 \alpha^2 + (q^2 \alpha^2 - 2pq\alpha^2 + p^2 \alpha^2) * 2pq + 4p^2 q^2 \alpha^2 \\ &= 8p^2 q^2 \alpha^2 + 2pq^3 \alpha^2 - 4p^2 q^2 \alpha^2 + 2p^3 q \alpha^2 \\ &= 4p^2 q^2 \alpha^2 + 2pq^3 \alpha^2 + 2p^3 q \alpha^2 \\ &= 2pq\alpha^2 (2pq + q^2 + p^2) \\ &= 2pq\alpha^2\end{aligned}$$

because $E[BV] = 0$

Dominance Variance

$$\begin{aligned}\sigma_D^2 &= D_{11}^2 * f(G_1 G_1) + D_{12}^2 * f(G_1 G_2) + D_{22}^2 * f(G_2 G_2) \\ &= (-2q^2d)^2 * p^2 + (2pqd)^2 * 2pq + (-2p^2d)^2 * q^2 \\ &= 4p^2q^4d^2 + 8p^3q^3d^2 + 4p^4q^2d^2 \\ &= 4p^2q^2d^2 (q^2 + 2pq + p^2) \\ &= 4p^2q^2d^2\end{aligned}$$

because $E[D] = 0$

Extension To More Loci

Population (N = 10)

$$\frac{A_1 \quad B_2}{A_1 \quad B_1}$$
$$\frac{A_1 \quad B_2}{A_1 \quad B_2}$$
$$\frac{A_1 \quad B_2}{A_1 \quad B_1}$$
$$\frac{A_1 \quad B_1}{A_2 \quad B_1}$$
$$\frac{A_2 \quad B_2}{A_2 \quad B_1}$$
$$\frac{A_1 \quad B_2}{A_2 \quad B_1}$$
$$\frac{A_1 \quad B_2}{A_1 \quad B_1}$$
$$\frac{A_1 \quad B_2}{A_1 \quad B_1}$$
$$\frac{A_1 \quad B_1}{A_1 \quad B_1}$$
$$\frac{A_2 \quad B_1}{A_2 \quad B_1}$$

Epistatic Interaction

- ▶ Decomposition of overall genotypic value V

$$V = V_A + V_B + I_{AB}$$

where I_{AB} : deviation from additively combining A and B

- ▶ Decomposition of V_A and V_B as before and re-grouping additive and dominance terms

$$V = \mu + U + D + I_{AB}$$

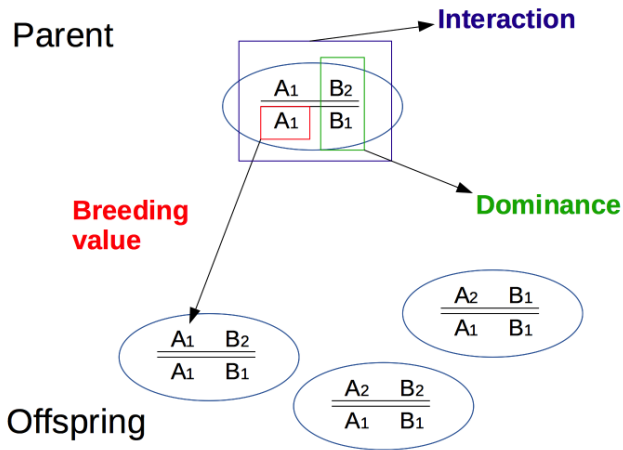
where U : breeding values and D : Dominance deviations

Interaction Variance

- ▶ Interaction deviation lead to new variance component σ_I^2

$$\begin{aligned}\sigma_G^2 &= \text{var}(V) = \text{var}(\mu + U + D + I_{AB}) \\ &= \text{var}(U) + \text{var}(D) + \text{var}(I_{AB}) \\ &= \sigma_U^2 + \sigma_D^2 + \sigma_I^2\end{aligned}$$

Summary of Effects



Importance for Livestock Breeding

- ▶ Breeding values measure effects of alleles
- ▶ Dominance deviations measure effects of genotypes
- ▶ Interaction deviations measure effects of different loci

→ for livestock breeding

- ▶ parents pass random sample of alleles to offspring

→ **breeding value** and associated **genetic additive variance** are important

→ dominance and interaction deviations and associated variance components rarely considered

Genetic Models

- ▶ **polygenic model**

- ▶ large but finite number of loci affect phenotype
- ▶ used in genomic selection

- ▶ **infinitesimal model**

- ▶ infinite number of loci affect phenotype
- ▶ breeding value is the sum of infinitely small single locus breeding values
- ▶ breeding value converges to normal distribution (Central Limit Theorem)
- ▶ used in traditional breeding value estimation

Central Limit Theorem

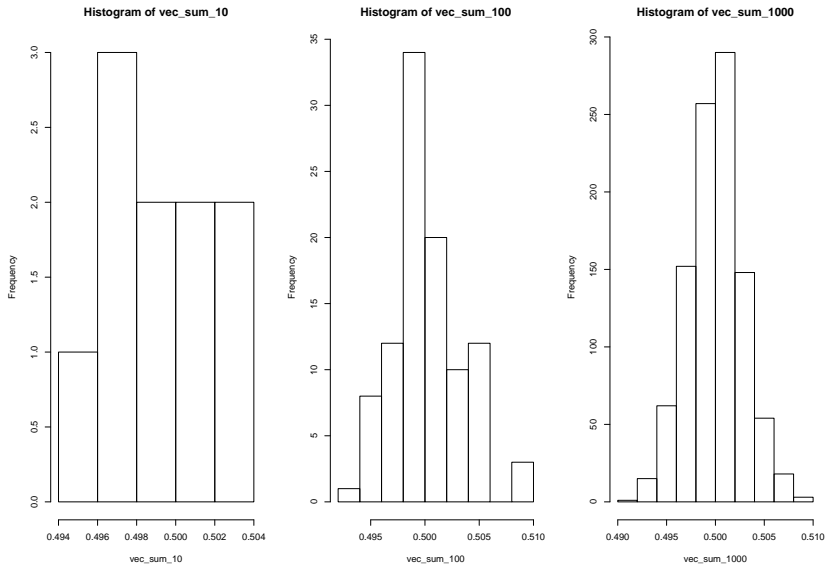


Figure 1: Distribution of Sums of Different Numbers of Components