Basics of Quantitative Genetics (Part 2)

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05 Oktober 2018

Variances

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

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

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 $E\left[X\right]$ of X

Variation of Genotypic Values

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

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

Additive Genetic Variance

$$
\begin{aligned}
\sigma_A^2 = Var\left[BV\right] &= BV_{11}^2 * f(G_1G_1) + BV_{12}^2 * f(G_1G_2) + BV_{22}^2 * f(G_2G_2) \\
&= (2q\alpha)^2 * p^2 + ((q-p)\alpha)^2 * 2pq + (-2p\alpha)^2 * q^2 \\
&= 4p^2q^2\alpha^2 + \left(q^2\alpha^2 - 2pq\alpha^2 + p^2\alpha^2\right) * 2pq + 4p^2q^2\alpha^2 \\
&= 8p^2q^2\alpha^2 + 2pq^3\alpha^2 - 4p^2q^2\alpha^2 + 2p^3q\alpha^2 \\
&= 4p^2q^2\alpha^2 + 2pq^3\alpha^2 + 2p^3q\alpha^2 \\
&= 2pq\alpha^2\left(2pq + q^2 + p^2\right) \\
&= 2pq\alpha^2
\end{aligned}
$$

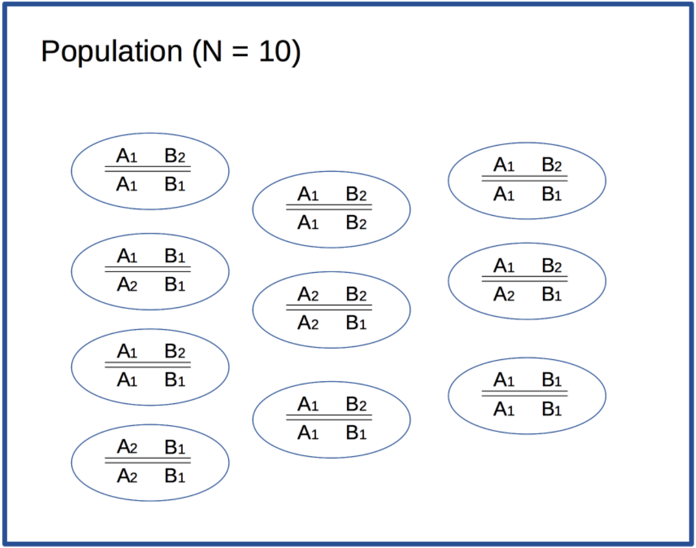
because $E\left[BV\right] = 0$

Dominance Variance

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

because $E\left[D\right] = 0$

Extension To More Loci



Population (N = 10)

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

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

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

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

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

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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

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

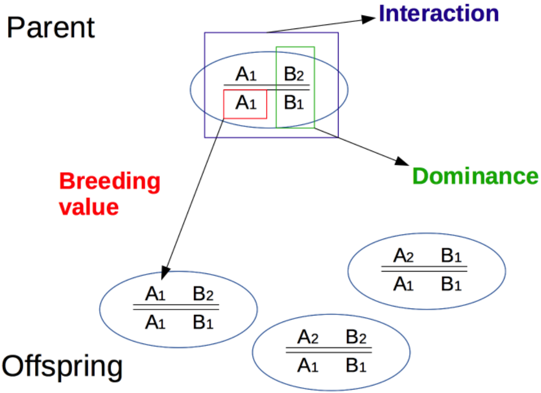
where A : breeding values and D: Dominance deviations

Interaction Variance

- Interaction deviation lead to new variance component σ_I^2

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

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 allels 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

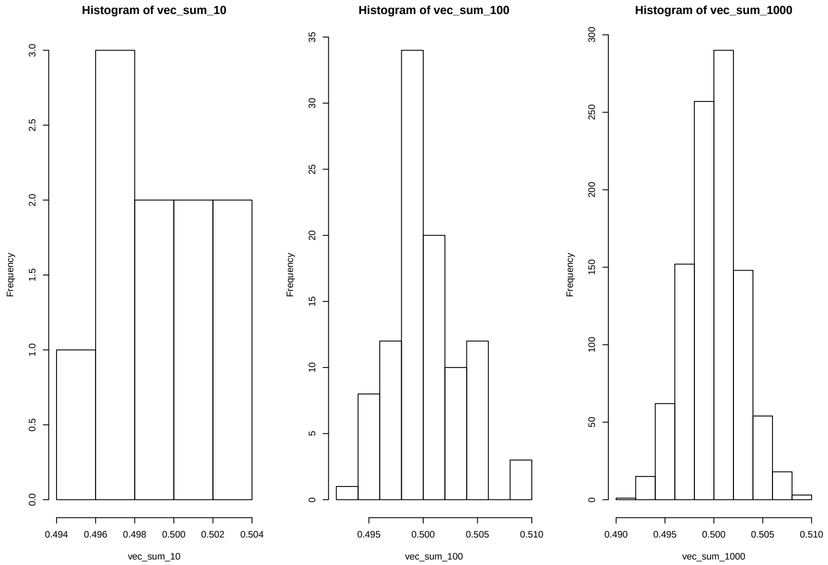


Figure 1: Distribution of Sums of Different Numbers of Components