

Background

- ▶ Breeding value model uses genomic breeding values g as random effects
- ▶ Variance-covariance matrix of g are proposed to be proportional to matrix G

$$\text{var}(g) = G * \sigma_g^2$$

where G is called **genomic relationship matrix** (GRM)

Properties of G

q are the marker effects

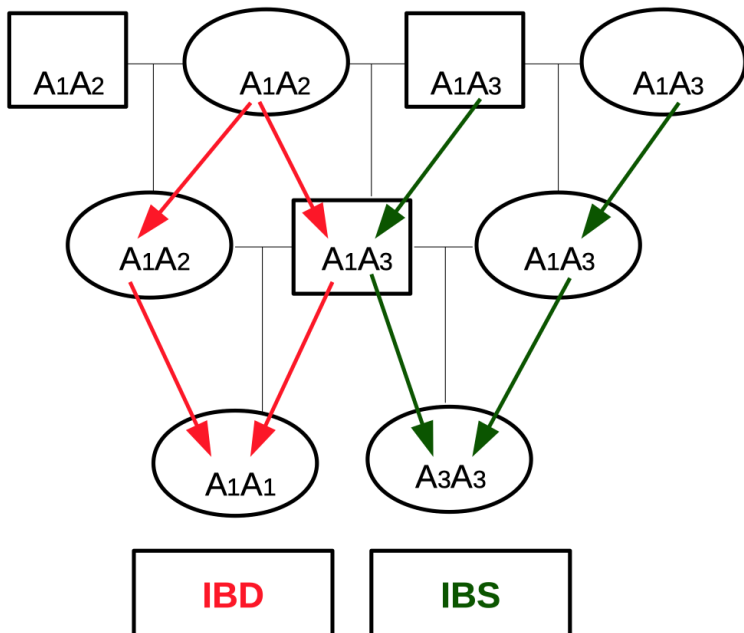
In the two-step approach: summing up q -effects to get to the genomic breeding value

- ▶ genomic breeding values g are linear combinations of q
- ▶ g as deviations, that means $E(g) = 0$
- ▶ $var(g)$ as product between G and σ_g^2 where G is the genomic relationship matrix
- ▶ G should be similar to A

Change of Identity Concept

- ▶ A is based on identity by descent
- ▶ G is based on identity by state (including ibd), assuming that the same allele has the same effect
- ▶ IBS can only be observed with SNP-genotype data

Identity



Deviation

- ▶ Genomic breeding values are defined as deviation from a certain basis

$$\rightarrow E(g) = 0$$

- ▶ How to determine matrix U such that $E(g) = 0$

Equivalence Between Models

Decomposition of phenotypic observation y_i with

- ▶ Marker effect model

$$y_i = w_i^T \cdot q + e_i$$

- ▶ Breeding value model

$$y_i = g_i + e_i$$

- ▶ g_i and $w_i^T \cdot q$ represent the same genetic effects and should be equivalent in terms of variability

Expected Values

- ▶ Required: $E(g_i) = 0$
- ▶ But: $E(w_i^T \cdot q) = q^T \cdot E(w_i)$
- ▶ Take q as constant SNP effects
- ▶ Assume w_i to be the random variable with:

$$w_i = \begin{cases} 1 & \text{with probability } p^2 \\ 0 & \text{with probability } 2p(1-p) \\ -1 & \text{with probability } (1-p)^2 \end{cases}$$

→ $E(w_i)$: For a single locus

$$E(w_i) = 1 \cdot p^2 + 0 \cdot 2p(1-p) + (-1) \cdot (1-p)^2 = p^2 - 1 + 2p - p^2 = 2p - 1 \neq 0$$

Specification of g

- Set

$$g_i = (w_i^T - s_i^T) \cdot q$$

with $s_i = E(w_i) = 2p - 1$

- Resulting in

$$g = U \cdot q = (W - S) \cdot q$$

with matrix S having columns j with all elements equal to $2p_j - 1$ where p_j is the allele frequency of the SNP allele associated with the positive effect.

Genetic Variance

- ▶ Requirement: $\text{var}(g) = G * \sigma_g^2$
- ▶ Result from Gianola et al. (2009):

$$\sigma_g^2 = \sigma_q^2 * \sum_{j=1}^k (1 - 2p_j(1 - p_j))$$

- ▶ From earlier: $g = U \cdot q$

$$\text{var}(g) = \text{var}(U \cdot q) = U \cdot \text{var}(q) \cdot U^T = UU^T \sigma_q^2$$

- ▶ Combining

$$\text{var}(g) = UU^T \sigma_q^2 = G * \sigma_q^2 * \sum_{j=1}^k (1 - 2p_j(1 - p_j))$$

Genomic Relationship Matrix

$$G = \frac{UU^T}{\sum_{j=1}^k (1 - 2p_j(1 - p_j))}$$

How To Compute G

- ▶ Read matrix W
- ▶ For each column j of W compute frequency p_j
- ▶ Compute matrix S and $\sum_{j=1}^k (1 - 2p_j(1 - p_j))$ from p_j
- ▶ Compute U from W and S
- ▶ Compute G