

Genetic Covariances Between Animals

Peter von Rohr

2023-11-03

BLUP Animal Model

- ▶ Traditional prediction of breeding values
 - ▶ i.e. no genomic information available
 - ▶ de-facto standard method
- ▶ Model recap

$$y = X\beta + Zu + e$$

where

- y vector of length n of phenotypic information
- β vector of length p of unknown fixed effects
- X $n \times p$ incidence matrix
- u vector of length q of unknown random breeding values
- Z $n \times q$ incidence matrix
- e vector of length n of unknown random residuals

Example I

Calf	Sire	Dam	Herd	WWG
3	1	2	1	4.5
4	NA	NA	2	2.9
5	4	3	2	3.9
6	5	2	1	3.5

Example II

Calf	Sire	Dam	Herd	WWG
3	1	2	1	4.5
4	1	NA	2	2.9
5	4	3	2	3.9
6	5	2	1	3.5

Animal Model Setup

- ▶ Convert information from data into model
- ▶ Put observations in vector y

$$y = \begin{bmatrix} 4.5 \\ 2.9 \\ 3.9 \\ 3.5 \end{bmatrix}$$

- ▶ Fixed effects such as herd go in vector β and X links observations to components in β

$$X = \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 1 & 0 \end{bmatrix}, \beta = \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix}$$

Breeding Values As Random Effects and Residuals

$$Z = \begin{bmatrix} 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}, u = \begin{bmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \\ u_6 \end{bmatrix}, e = \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \end{bmatrix}$$

Putting Everything Together

$$\begin{bmatrix} 4.5 \\ 2.9 \\ 3.9 \\ 3.5 \end{bmatrix} = \begin{bmatrix} 1 & 0 \\ 0 & 1 \\ 0 & 1 \\ 1 & 0 \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} + \begin{bmatrix} 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix} \begin{bmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \\ u_6 \end{bmatrix} + \begin{bmatrix} e_1 \\ e_2 \\ e_3 \\ e_4 \end{bmatrix}$$

Solution with Mixed Model Equations

- ▶ General form

$$\begin{bmatrix} X^T R^{-1} X & X^T R^{-1} Z \\ Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T R^{-1} y \\ Z^T R^{-1} y \end{bmatrix}$$

- ▶ Assume $R = I * \sigma_e^2$ and we set $G = A * \sigma_u^2$

$$\begin{bmatrix} X^T X & X^T Z \\ Z^T X & Z^T Z + \lambda * A^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T y \\ Z^T y \end{bmatrix}$$

with $\lambda = \sigma_e^2 / \sigma_u^2$

Components of Mixed Model Equations

$$X^T X = \begin{bmatrix} 2 & 0 \\ 0 & 2 \end{bmatrix}, X^T Z = \begin{bmatrix} 0 & 0 & 1 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 & 1 & 0 \end{bmatrix}$$

$$Z^T Z = \begin{bmatrix} 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 & 1 \end{bmatrix}, X^T y = \begin{bmatrix} 8 \\ 6.8 \end{bmatrix}, Z^T y = \begin{bmatrix} 0 \\ 0 \\ 4.5 \\ 2.9 \\ 3.9 \\ 3.5 \end{bmatrix}$$

Numerator Relationship Matrix

- ▶ Only component missing in mixed model equations: matrix A
- ▶ A is called the **numerator relationship matrix**
- ▶ Properties of A

$$\text{var}(u) = G = A * \sigma_u^2$$

Meaning of $var()$ for scalar variable x

- ▶ Depending on type of argument to $var()$, the result is different
- ▶ Scalar argument x , that means x is just a single number

$$var(x) = \sum (x - E[x])^2 f(x)$$

for a discrete random variable x , e.g. genotypic values V in single locus model.

$$var(x) = \int (x - E[x])^2 f(x) dx$$

for a continuous random variable x .

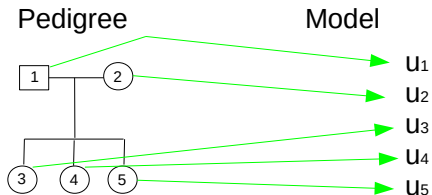
Meaning of $var()$ for a vector u

- ▶ Assume that u is a vector with q elements

$$u = \begin{bmatrix} u_1 \\ u_2 \\ \dots \\ u_q \end{bmatrix}$$

- ▶ Then $var(u)$ is a $q \times q$ variance-covariance matrix with a structure shown on the next slide

Meaning of A



Variance-Covariance

	u_1	u_2	u_3	u_4	u_5
u_1	$\text{var}(u_1)$	$\text{cov}(u_1, u_2)$	$\text{cov}(u_1, u_3)$	$\text{cov}(u_1, u_4)$	$\text{cov}(u_1, u_5)$
u_2		$\text{var}(u_2)$	$\text{cov}(u_2, u_3)$	$\text{cov}(u_2, u_4)$	$\text{cov}(u_2, u_5)$
u_3			$\text{var}(u_3)$	$\text{cov}(u_3, u_4)$	$\text{cov}(u_3, u_5)$
u_4				$\text{var}(u_4)$	$\text{cov}(u_4, u_5)$
u_5					$\text{var}(u_5)$

Elements of A

- ▶ Remember: $\text{var}(u) = G = A * \sigma_u^2$
- ▶ Diagonal elements $(A)_{ii} = 1 + F_i$ where F_i : inbreeding coefficient of i
- ▶ Offdiagonal elements $(A)_{ij} = \text{cov}(u_i, u_j) / \sigma_u^2$
- ▶ Symmetric
- ▶ Definition leads to recursive algorithm for computing components of A

Example

Elements of G are computed as

- ▶ Animal 1 has unknown parents and is assumed to show no inbreeding (parents are not related)

$$\text{var}(u_1) = (1 + F_1) * \sigma_u^2 = \sigma_u^2$$

- ▶ Animal 2 has unknown parents and is not related to animal 1

$$\text{cov}(u_1, u_2) = 0$$

- ▶ Animal 3 has parents 1 and 2

$$\text{cov}(u_1, u_3) = \text{cov} \left(u_1, \left[\frac{1}{2}(u_1 + u_2) + m_3 \right] \right) = \frac{1}{2} \sigma_u^2$$