

# Genetic Covariances Between Animals

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# 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
- $\beta$  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  $\beta$  and  $X$  links observations to components in  $\beta$

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

## 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  $x$ .

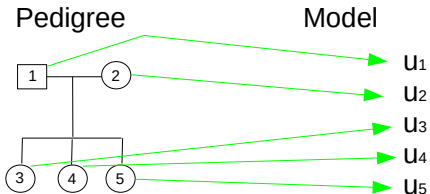
## Meaning of $\text{var}()$ for a vector $u$

- ▶ Assume that  $u$  is a vector with  $q$  elements

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

- ▶ Then  $\text{var}(u)$  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

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