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
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

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

$$\left[\begin{array}{lr} X^TR^{-1}X & X^TR^{-1}Z \\ Z^TR^{-1}X & Z^TR^{-1}Z + G^{-1} \end{array}\right] \left[\begin{array}{c} \hat{\beta} \\ \hat{u} \end{array}\right] = \left[\begin{array}{c} X^TR^{-1}y \\ Z^TR^{-1}y \end{array}\right]$$

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

$$\left[\begin{array}{lr} X^TX & X^TZ \\ Z^TX & Z^TZ + \lambda * A^{-1} \end{array}\right] \left[\begin{array}{c} \hat{\beta} \\ \hat{u} \end{array}\right] = \left[\begin{array}{c} X^Ty \\ Z^Ty \end{array}\right]$$

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

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

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.

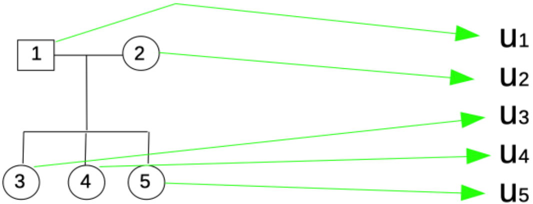
Meaning of *var*() for a vector *u*

- 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



Pedigree

Model

Variance-Covariance

	u_1	u_2	u_3	u_4	u_5
u_1	var(u_1)	cov(u_1,u_2)	cov(u_1,u_3)	cov(u_1,u_4)	cov(u_1,u_5)
u_2		var(u_2)	cov(u_2,u_3)	cov(u_2,u_4)	cov(u_2,u_5)
u_3			var(u_3)	cov(u_3,u_4)	cov(u_3,u_5)
u_4				var(u_4)	cov(u_4,u_5)
u_5					var(u_5)

Elements of A

- Remember: $var(u) = G = A * \sigma_u^2$
- Diagonal elements $(A)_{ii} = 1 + F_i$ where F_i: inbreeding coefficient of i
- Offdiagonal elements $(A)_{ij} = cov(u_i, u_j)/\sigma_u^2$
- 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)

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

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

$$cov(u_1, u_2) = 0$$

- Animal 3 has parents 1 and 2

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