Additional Aspects of BLUP

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Aspects

- Accurracy
 - Results from MME are estimates of fixed effects and predictions of breeding values
 - ▶ Need statement about quality of estimates and predictions
- Confidence Intervals
- Decomposition of Predicted Breeding values

Accurracy

- One property of BLUP was that variance of prediction error is minimal
- How can we measure the variance of the prediction error
- Fixed effects

$$var(\beta - \hat{\beta}) = var(\hat{\beta})$$

Random effects

$$\mathit{var}(\mathit{u}-\hat{\mathit{u}}) = \mathit{var}(\mathit{u}) - 2*\mathit{cov}(\mathit{u},\hat{\mathit{u}}) + \mathit{var}(\hat{\mathit{u}}) = \mathit{var}(\mathit{u}) - \mathit{var}(\hat{\mathit{u}}) = \mathit{PEV}(\hat{\mathit{u}})$$

because with BLUP: $cov(u, \hat{u}) = var(\hat{u})$

PEV

▶ PEV depends on inverse of coefficient matrix of MME

$$\begin{bmatrix} X^T R^{-1} X & X^T R^{-1} Z \\ Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} \\ C^{21} & C^{22} \end{bmatrix}$$

ightharpoonup For predicted breeding values \hat{u}

$$PEV(\hat{u}) = var(u) - var(\hat{u}) = C^{22}$$

Single Animal i

$$PEV(\hat{u}_i) = (C)_{ii}^{22}$$

where $(C)_{ii}^{22}$ is the *i*-th diagonal of C^{22}

Accuracy measured by correlation

$$r_{u_i,\hat{u}_i} = \frac{cov(u_i,\hat{u}_i)}{\sqrt{var(u_i) * var(\hat{u}_i)}} = \sqrt{\frac{var(\hat{u}_i)}{var(u_i)}}$$

Combining

$$PEV(\hat{u}_i) = (C)_{ii}^{22} = var(u_i) - var(\hat{u}_i) = var(u_i) - r_{u_i,\hat{u}_i}^2 var(u_i)$$

Accuracy B_i

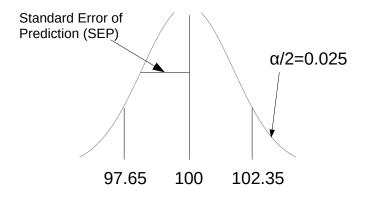
$$B_i = r_{u_i, \hat{u}_i}^2 = \frac{var(u_i) - (C)_{ii}^{22}}{var(u_i)} = 1 - \frac{PEV(\hat{u}_i)}{var(u_i)} = 1 - \frac{(C)_{ii}^{22}}{var(u_i)}$$

- $ightharpoonup B_i$ is large for small $PEV(\hat{u}_i)$
- ▶ In the limit $B_i \rightarrow 1$ for $PEV(\hat{u}_i) \rightarrow 0$
- ▶ For $PEV(\hat{u}_i) \rightarrow 0$ we must have $var(\hat{u}_i) \rightarrow var(u_i)$
- ▶ Therefore, the closer $var(\hat{u}_i)$ is to $var(u_i)$, the more accurate the predicted breeding value

Confidence Intervals of \hat{u}_i

- ▶ Predicted breeding value (\hat{u}_i) is a function of the data (y)
- ▶ Hence \hat{u}_i is a random variable with a distribution

Distribution



$$SEP(\hat{u}_i) = \sqrt{PEV(\hat{u}_i)} = \sqrt{(1 - r_{u_i,\hat{u}_i}^2) * var(u_i)}$$

Widths Of Confidence Intervals

Table 1: Widths of Confidence Intervals for Given Accuracies

| Accurracy | Interval Width |
|-----------|----------------|
| 0.40 | 36.44 |
| 0.50 | 33.26 |
| 0.60 | 29.75 |
| 0.70 | 25.76 |
| 0.80 | 21.04 |
| 0.90 | 14.88 |
| 0.95 | 10.52 |
| 0.99 | 4.70 |
| | |

with $\hat{u}_i = 100$, $var(u_i) = 144$ and $\alpha = 0.05$

Decomposition of Predicted Breeding Value

Write MME as

$$M \cdot s = r$$

with

$$s = \left[egin{array}{c} \hat{eta} \ \hat{u} \end{array}
ight]$$

- \triangleright $\hat{\beta}$ has length p

Simplified Model

$$y_i = \mu + u_i + e_i$$

where y_i Observation for animal i u_i breeding value of animal i with a variance of $(1+F_i)\sigma_u^2$ e_i random residual effect with variance σ_e^2 μ single fixed effect

Data

- all animals have an observation
- ▶ animal *i* has
 - parents s and d
 - ightharpoonup n progeny k_j (with $j = 1, \ldots, n$)
 - ightharpoonup n mates l_i (with $j = 1, \ldots, n$).
- **Progeny** k_j has parents i and l_j .

Example

| Animal | Sire | Dam | WWG |
|--------|------|-----|-----|
| 1 | NA | NA | 4.5 |
| 2 | NA | NA | 2.9 |
| 3 | NA | NA | 3.9 |
| 4 | 1 | 2 | 3.5 |
| 5 | 4 | 3 | 5.0 |
| | | | |

Variance components $\sigma_e^2=40$ and $\sigma_u^2=20$.

Model Components

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

$$X^TX = \begin{bmatrix} 5 \end{bmatrix}, X^TZ = \begin{bmatrix} 1 & 1 & 1 & 1 \end{bmatrix}$$

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

Right-hand Side

$$X^T y = \left[\sum_{j=1}^n y_i\right] = 19.8$$

$$Z^{T}y = \begin{bmatrix} y1 \\ y2 \\ y3 \\ y4 \\ y5 \end{bmatrix} = \begin{bmatrix} 4.5 \\ 2.9 \\ 3.9 \\ 3.5 \\ 5 \end{bmatrix}$$

Δ^{-1}

 $\hbox{\tt\#\# as(<dtTMatrix>, "dtCMatrix") is deprecated since Matrix}$

$$A^{-1} = \begin{bmatrix} 1.5 & 0.5 & 0 & -1 & 0 \\ 0.5 & 1.5 & 0 & -1 & 0 \\ 0 & 0 & 1.5 & 0.5 & -1 \\ -1 & -1 & 0.5 & 2.5 & -1 \\ 0 & 0 & -1 & -1 & 2 \end{bmatrix}$$

MME

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

Insert Data

$$\begin{bmatrix} 5 & 1 & 1 & 1 & 1 & 1 \\ 1 & 4 & 1 & 0 & -2 & 0 \\ 1 & 1 & 4 & 0 & -2 & 0 \\ 1 & 0 & 0 & 4 & 1 & -2 \\ 1 & -2 & -2 & 1 & 6 & -2 \\ 1 & 0 & 0 & -2 & -2 & 5 \end{bmatrix} \begin{bmatrix} \mu \\ \hat{u}1 \\ \hat{u}2 \\ \hat{u}3 \\ \hat{u}4 \\ \hat{u}5 \end{bmatrix} = \begin{bmatrix} 19.8 \\ 4.5 \\ 2.9 \\ 3.9 \\ 3.5 \\ 5 \end{bmatrix}$$

Animal 4

- parents 1 and 2
- progeny 5
- ► mate 3
- inspection of second but last equation in MME where y_4 and \hat{u}_4 occur
- ▶ Remember from construction of A^{-1} , the variable d^{ii} can assume the following values

$$d^{ii} = \begin{cases} 2 & \text{both parents known} \\ \frac{4}{3} & \text{one parent known} \\ 1 & \text{both parents unknown} \end{cases}$$

Extract Equation

$$y_4 = 3.5 = 1 * \hat{\mu} - 2 * \hat{u}_1 - 2 * \hat{u}_2 + 1 * \hat{u}_3 + 6 * \hat{u}_4 - 2 * \hat{u}_5$$

► Solving for û₄

$$\hat{u}_4 = \frac{1}{6} \left[y_4 - \hat{\mu} + 2 * (\hat{u}_1 + \hat{u}_2) - \hat{u}_3 + 2\hat{u}_5 \right]$$

- û₄ depends on
 - \triangleright own performance record y_4
 - ightharpoonup estimate of fixed effect $\hat{\mu}$ environment
 - predicted breeding value of parents 1 and 2, mate 3 and progeny 5

General Equation

$$\hat{u}_{i} = \frac{1}{1 + \alpha \delta^{(i)} + \frac{\alpha}{4} \sum_{j=1}^{n} \delta^{(k_{j})}} \left[y_{i} - \hat{\mu} + \frac{\alpha}{2} \left\{ \delta^{(i)} (\hat{u}_{s} + \hat{u}_{d}) + \sum_{j=1}^{n} \delta^{(k_{j})} (\hat{u}_{k_{j}} - \frac{1}{2} \hat{u}_{l_{j}}) \right\} \right]$$

where α ration between variance components σ_e^2/σ_u^2 $\delta^{(j)}$ contribution for animal j to A^{-1}