

Additional Aspects of BLUP



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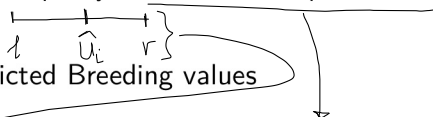
- * Prediction of breeding values using linear mixed effects models.
- * Examples: Sire model, animal model
- * Solutions for fixed effects estimates and for predicted breeding values can be obtained using Mixed Model equations. In MME, A^{-1} required ==> efficient computations shown

Aspects

- ▶ Accuracy
 - ▶ 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



True value for u_i is with probability
 $(1-\alpha)$ between l and r

0.99
0.95

With estimates and predictions,
there are always errors associated
==> quantify error

Accuracy

fixed effects $\beta - \hat{\beta}$

breeding values $u - \hat{u}$

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

fixed $\Rightarrow \text{var}(\beta) = 0$
 $\text{cov}(\beta, \hat{\beta}) = 0$

\uparrow

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

$\hookrightarrow \text{eg: } (X^T X)^{-1} \sigma_e^2$

- ▶ Random effects

$\hookrightarrow \text{var}(u) \neq 0$

$\text{var}(u - \hat{u}) = \text{var}(u) - 2 * \text{cov}(u, \hat{u}) + \text{var}(\hat{u}) = \text{var}(u) - \text{var}(\hat{u}) = \overbrace{PEV(\hat{u})}^{\min}$

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

Aim: predicted breeding values should be as close as possible to the true breeding values $\Rightarrow PEV \Rightarrow 0$

PEV

In practise: Coefficient matrix of MME cannot be inverted, hence
PEV are always approximation

- ▶ PEV depends on inverse of coefficient matrix of MME

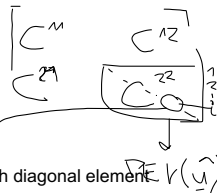
$$\begin{bmatrix} X^T R^{-1} X & X^T R^{-1} Z \\ Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{bmatrix}^{-1} = \begin{bmatrix} C^{11} & C^{12} \\ C^{21} & \underline{C^{22}} \end{bmatrix}$$

- ▶ For predicted breeding values \hat{u}

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

Single Animal i

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



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

► Accuracy measured by correlation

of the predicted breeding value for animal i

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

$$\text{BLUP: } \text{cov}(u_i, \hat{u}_i) = \text{var}(\hat{u}_i)$$

$$\sqrt{\frac{\text{var}(\hat{u}_i)}{\text{var}(u_i)}}$$

► Combining

Ref $r()$

$$r^2 = \frac{\text{var}(\hat{u}_i)}{\text{var}(u_i)}$$

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

$$(1 - r^2) \text{var}(u_i)$$

Accuracy B_i

Bestimmtheitsmass

Reliability

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

Handwritten notes: $PEV \rightarrow 0$
SMA ||: $\Rightarrow B \rightarrow 1$

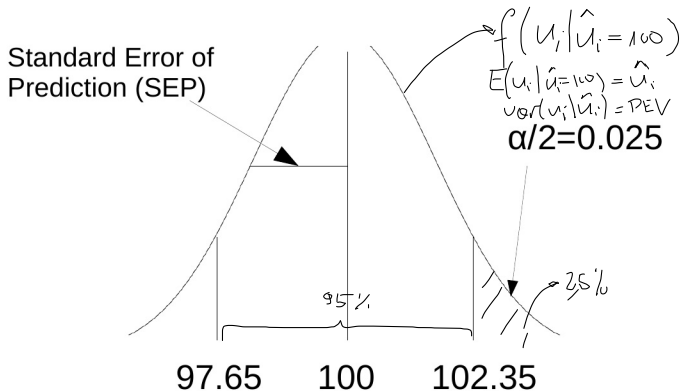
- ▶ B_i is large for small $PEV(\hat{u}_i)$
- ▶ In the limit $B_i \rightarrow 1$ for $PEV(\hat{u}_i) \rightarrow 0$
- ▶ For $PEV(\hat{u}_i) \rightarrow 0$ we must have $\text{var}(\hat{u}_i) \rightarrow \text{var}(u_i)$
- ▶ Therefore, the closer $\text{var}(\hat{u}_i)$ is to $\text{var}(u_i)$, the more 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: Standard error of prediction

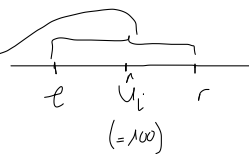


$$SEP(\hat{u}_i) = \sqrt{PEV(\hat{u}_i)} = \sqrt{(1 - \underbrace{r^2_{u_i, \hat{u}_i}}_{\Lambda^2}) * \underbrace{var(u_i)}_{\Lambda^2}}$$

Widths Of Confidence Intervals

Table 1: Widths of Confidence Intervals for Given Accuracies

Accuracy	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

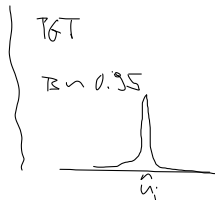
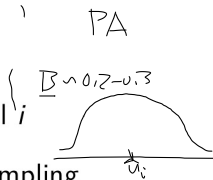


with $\hat{u}_i = 100$, $\text{var}(u_i) = 144$ and $\alpha = 0.05 \Rightarrow 95\% \text{ CI}$

Selection Response

Correlation r_{u_i, \hat{u}_i} for a single animal i

- ▶ across conceptual repeated sampling
- ▶ change of a predicted breeding value for animal i with increasing information
- ▶ related to standard error of prediction (SEP) → measure of risk of using i as parent



Accuracies also important for selection response

$$R = i \cdot r \cdot \sqrt{g}$$

- ▶ correlation between true and predicted breeding values in selection candidates
- ▶ characteristic of population not of single animal
- ▶ estimation with cross-validation

population accuracy

→ use correlation between predicted breeding values with whole and partial data

Decomposition of Predicted Breeding Value

BLUP uses all info

- Write MME as

$$M \cdot s = r$$

with

$$s = \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix}$$

- $\hat{\beta}$ has length p
- \hat{u} has length q

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
 - ▶ n progeny k_j (with $j = 1, \dots, n$)
 - ▶ n mates l_j (with $j = 1, \dots, n$).
- ▶ 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

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

$$X^T X = [5], X^T Z = [1 \quad 1 \quad 1 \quad 1 \quad 1]$$

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

Right-hand Side

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

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

$$A^{-1}$$

`## 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 \hat{u}_4

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

- ▶ \hat{u}_4 depends on
 - ▶ own performance record y_4
 - ▶ estimate of fixed effect $\hat{\mu}$ - environment
 - ▶ predicted breeding value of parents 1 and 2, mate 3 and progeny 5

General Equation

$$\hat{u}_i = \frac{1}{1 + \alpha\delta^{(i)} + \frac{\alpha}{4} \sum_{j=1}^n \delta^{(k_j)}} [y_i - \hat{\mu} + \frac{\alpha}{2} \left\{ \delta^{(i)}(\hat{u}_s + \hat{u}_d) + \sum_{j=1}^n \delta^{(k_j)}(\hat{u}_{k_j} - \frac{1}{2}\hat{u}_{l_j}) \right\}]$$

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