BLUP animal model

Why BLUP?

BLUP predicts breeding value more accurately

- BLUP corrects for environmental deviations due to fixed effects
- BLUP uses all pedigree information: accounts for selection and genetic trends etc.

BLUP EBV can be estimated for animals without phenotypes using information from their relatives
Mixed linear model

\[ y = X\beta + Za + e \]

\( y \) - Phenotypic value \( E(y) = X\beta \)
\( \beta \) - Fixed effects
\( a \) - Random genetic effects \( \sim (0, \sigma_a^2) \)
\( e \) - Residuals \( \sim (0, \sigma_e^2) \)

\( X, Z \) - Incidence matrices

BLUP animal model

Mixed linear model

\[ y = X\beta + Za + e \]

Variance covariance of \( y \) is,

\[ V = ZAZ'\sigma_a^2 + I\sigma_e^2 \]

\( A \) - numerator relationship matrix
\( I \) - identity matrix

BLUP animal model
Mixed linear model

\[ y = X\beta + Za + e \]

\[
\text{BLUP (a)} = \hat{a} = AZ'\sigma^2_a V^{-1}(y - X\hat{\beta})
\]

\[
\text{BLUE (b)} = \hat{\beta} = (X'V^{-1}X)^{-1}X'V^{-1}y
\]

These solutions are important in genetic evaluation and breeding program.
BLUP using MME

No need to invert V
  ♦ Usually computationally efficient

Can obtain \( \hat{a} \) and \( \hat{\beta} \) simultaneously

---- widely used for genetic evaluation, ----

Example

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<th>Phenotype</th>
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We want to estimate herd effects (\( \hat{\beta} \))
and random genetic animal effects (\( \hat{a} \))
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Constructing $X$

$$
\begin{bmatrix}
1 & 0 \\
0 & 1 \\
1 & 0 \\
0 & 1 \\
1 & 0
\end{bmatrix}
$$

Example

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Constructing $Z$

$$
\begin{bmatrix}
1 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1
\end{bmatrix}
$$
Example

<table>
<thead>
<tr>
<th>Herd</th>
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<th>Size</th>
<th>Dam</th>
<th>Phenytype</th>
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Constructing A (NRM)

\[
\begin{bmatrix}
1 & 0 & 0 & 0.5 & 0.25 \\
0 & 1 & 0 & 0.5 & 0.25 \\
0 & 0 & 1 & 0 & 0.5 \\
0.5 & 0.5 & 0 & 1 & 0.5 \\
0.25 & 0.25 & 0.5 & 0.5 & 1
\end{bmatrix}
\]

BLUP animal model

NRM

If both parents \( s \) and \( d \) of animal \( i \) are known

\[
r_{ij} = r_{ji} = 0.5(r_{ir} + r_{jd}) \quad j = 1 \sim (i - 1)
\]

\[
r_{ii} = 1 + 0.5(r_{sd})
\]

If only one parent \( s \) of animal \( i \) is known

\[
r_{ij} = r_{ji} = 0.5(r_{is}) \quad j = 1 \sim (i - 1)
\]

\[
r_{ii} = 1
\]

If both parents \( s \) and \( d \) of animal \( i \) are unknown

\[
r_{ij} = r_{ji} = 0 \quad j = 1 \sim (i - 1)
\]

\[
r_{ii} = 1
\]

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Example

<table>
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Constructing $V$

\[
\begin{bmatrix}
1 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1 \\
\end{bmatrix}
\times \sigma_v^2 +
\begin{bmatrix}
1 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1 \\
\end{bmatrix}
\times \sigma_e^2
\]

BLUP animal model

Example

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After constructing the matrices, it is straightforward to obtain BLUE and BLUP

\[
\hat{\beta} = (X'V^{-1}X)^{-1}X'V^{-1}y
\]

\[
\hat{a} = AZ'\sigma_v^{-2}V^{-1}(y - X\hat{\beta})
\]

BLUP animal model

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Example (using MME)

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Constructing $X'X$

\[
\begin{bmatrix}
3 & 0 \\
0 & 2
\end{bmatrix}
\]

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Constructing $X'Z$

\[
\begin{bmatrix}
1 & 0 & 1 & 0 & 1 \\
0 & 1 & 0 & 1 & 0
\end{bmatrix}
\]

BLUP animal model
### Example (using MME)

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#### Constructing Z'X

\[
\begin{bmatrix}
1 & 0 \\
0 & 1 \\
1 & 0 \\
0 & 1 \\
1 & 0
\end{bmatrix}
\]

---

### Example (using MME)

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#### Constructing Z'Z

\[
\begin{bmatrix}
1 & 0 & 0 & 0 & 0 \\
0 & 1 & 0 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 \\
0 & 0 & 0 & 1 & 0 \\
0 & 0 & 0 & 0 & 1
\end{bmatrix}
\]
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Constructing MME

\[
\begin{bmatrix}
3 & 0 \\
2 & 0 \\
1 & 0 \\
0 & 0 \\
1 & 0 \\
0 & 0 \\
0 & 0 \\
1 & 0 \\
\end{bmatrix}
\begin{bmatrix}
1 & 0 & 1 & 0 & 1 \\
0 & 1 & 0 & 1 & 0 \\
1 & 0 & 0 & 0 & 1 \\
0 & 1 & 0 & 0 & 1 \\
1 & 0 & 0 & 0 & 0 \\
\end{bmatrix}
\]

\[\begin{bmatrix}
A^{-1} \alpha
\end{bmatrix}
\]

BLUP animal model

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After constructing the MME, it is straightforward to obtain BLUE and BLUP

\[
\begin{bmatrix}
\hat{\beta} \\
\hat{\alpha}
\end{bmatrix}
= \begin{bmatrix}
X'X & X'Z \\
Z'X & Z'Z + A^{-1} \alpha
\end{bmatrix}
\begin{bmatrix}
X'y \\
Z'y
\end{bmatrix}
\]

\[
(\hat{\alpha} = \frac{\sigma_a^2}{\sigma^2} \left(1 - \frac{h^2}{h^2}\right))
\]
BLUP accuracy and response

\[ C = \begin{bmatrix} XX & XZ \\ ZX & ZZ + A' \alpha \end{bmatrix}^{-1} \quad (\alpha = \frac{\sigma_a^2}{\sigma_e^2} \cdot \frac{1 - h^2}{h^2}) \]

Let the diagonal for animal \( i \) be \( C_{ii} \)

The accuracy of the EBV = \( \sqrt{1 - C_{ii} \alpha} \)

The selection response \( R = i \sigma_{EBV} \)

Practical session

We will try

1. Simulating pedigree and phenotypic data
2. Estimating GLS and BLUP solutions with true \( h^2 \)

Compare TBV and EBV
- with varying herd effects
- without pedigree
- without herd record
- with wrong pedigree

Compare MME method and iterative BLUP

Selection response from BLUP or from phenotypes
Practical session

If you are keen to learn more genetic analysis,

※ Estimate $V_A$, $V_E$ and $h^2$ with simulated data
  * Standard error of estimates

※ Compare EBV with estimated and true $h^2$

※ Family design for better estimating $h^2$
  * A few large families or many small families

※ More replicates would give more reliable results

Simulation study:
Correlation between TBV and EBV (phenotypes)

When herd effect is 0
Simulation study: Correlation between TBV and EBV (phenotypes)

When herd effect is $\sim 2\sigma_p$

Simulation study: Correlation between TBV and EBV

Herd effect should be corrected for BLUP estimation. Otherwise, they are confounded.
Simulation study:
Correlation between TBV and EBV

Correct pedigree ($r=0.82$)  Wrong pedigree ($r=0.63$)

Pedigree record is important for BLUP estimation

Estimated $h^2$ and true $h^2$ for BLUP solution

Correlation of BLUP solutions with estimated $h^2$
and true $h^2$ is very high