BLUP

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Recap: Prediction of Breeding Values

Own Performance Records (h²: Heritability)

$$\hat{u}_i = h^2 * (y_i - \mu)$$

► Repeated Measurements

$$\hat{u}_i = \frac{nh^2}{1 + (n-1)t} * (\bar{y}_i - \mu)$$

with n: number of records, t: repeatability

Progeny Records

$$\hat{u}_i = \frac{2n}{n+k} * (\bar{y}_i - \mu) \text{ with } k = \frac{4-h^2}{h^2}$$

with *n*: number of progeny

General Principle

- ► All methods to predict breeding values follow the same principle
- 1. Correct information sources for some population mean
- 2. Multiply corrected information source by an appropriate factor
- Regression Method

$$\hat{u} = b(y - \mu)$$

- Selection Index
 - uses all available information combined into an index

Selection Index

- will be presented later to estimate aggregate genotype
- ▶ Idea: all available information about an animals breeding value is combined into an index of merit (1)
- corresponds to multiple regression approach

$$\hat{u} = I = b_1 * y_1^* + b_2 * y_2^* + ... + b_k * y_k^* = b^T y^*$$

where b the regression coefficients are computed such that the variance $(var(u - \hat{u}))$ of the error is minimal.

Index Weights

▶ Minimization of the variance of the errors means

$$PEV = var(u - \hat{u}) = var(u - I) = var(u - b^{T}y^{*})$$

$$= var(u) + var(b^{T}y^{*}) - 2cov(u, (y^{*})^{T}b)$$

$$= \sigma_{u}^{2} + b^{T} * var(y^{*}) * b - 2 * b^{T} * cov(u, (y^{*})^{T})$$

$$= \sigma_{u}^{2} + b^{T} * P * b - 2 * b^{T} * G$$

Solution

► Compute $\frac{\partial PEV}{\partial b} = 0$

$$\frac{\partial PEV}{\partial b} = 2 * P * b - 2 * G = 0$$

$$\rightarrow b = P^{-1} * G$$

Problem with Correction

Population mean is ideal as correction

$$y = \mu + u + e$$
 \rightarrow $\bar{y} = \bar{\mu} + \bar{u} + \bar{e} = \mu$

- Because performances are observed in different
 - environments and
 - time points
- ► Formation of comparison groups where animals are exposed to the same environments
- ► The more groups, the better the correction of environmental effects
- ► The more groups, the smaller the single groups

Bias

- ▶ With small comparison groups, it is more likely that mean breeding value of animals in a single group is not 0
- Average performance of all animals in a comparison group

$$\bar{y}_{CG} = \mu + \bar{u}_{CG} + \bar{e}_{CG}$$

* If \bar{u}_{CG} is not 0, the predicted breeding value \hat{u}_i of animal i is

$$\hat{u}_i = I = b(y_i - (\mu + \bar{u}_{CG}))$$

$$= b(y_i - \mu) - b\bar{u}_{CG}$$

$$= \hat{u}_i - b\bar{u}_{CG}$$

where $b\bar{u}_{CG}$ is called bias.

Solution - BLUP

- Solution to correction problem in selection index: BLUP
- ► Estimates environmental effects at the same time as breeding values are predicted
- Linear mixed effects model
- ► Meaning of BLUP
 - **B** stands for **best** \rightarrow correlation between true (u) and its prediction (\hat{u}) is maximal or the prediction error variance $(var(u-\hat{u}))$ is minimal.
 - L stands for linear → predicted breeding values are linear functions of the observations (y)
 - U stands for unbiased → expected values of the predicted breeding values are equal to the true breeding values
 - P stands for prediction

Example

Animal	Sire	Dam	Herd	Weaning Weight
12	1	4	1	2.61
13	1	4	1	2.31
14	1	5	1	2.44
15	1	5	1	2.41
16	1	6	2	2.51
17	1	6	2	2.55
18	1	7	2	2.14
19	1	7	2	2.61
20	2	8	1	2.34
21	2	8	1	1.99
22	2	9	1	3.10
23	2	9	1	2.81
24	2	10	2	2.14
25	2	10	2	2.41
26	3	11	2	2.54
27	3	11	2	3.16

Linear Models

► Simple linear model

$$y_{ij} = \mu + herd_j + e_{ij}$$

- ► Result: Estimate of effect of herd j
- ► Try with given dataset

Linear Mixed Effects Model

- ▶ What about breeding value u_i for animal i?
 - Problem: breeding values have a variance σ_{μ}^2
 - Cannot be specified in simple linear model
- → Linear Mixed Effects Model (LME)

$$y_{ijk} = \mu + \beta_j + u_i + e_{ijk}$$

Matrix-Vector Notation

- ► LME for all animals of a population
- → use matrix-vector notation

$$y = X\beta + Zu + e$$

where

- y vector of length n of all observations
- β vector of length p of all fixed effects
- X $n \times p$ design matrix linking the fixed effects to the observations
- u vector of length n_u of random effects
- $Z = n \times n_u$ design matrix linking random effect to the observations
- e vector of length n of random residual effects.

Expected Values and Variances

Expected values

$$E(u) = 0$$
 and $E(e) = 0 \rightarrow E(y) = X\beta$

Variances

$$var(u) = G$$
 and $var(e) = R$

with $cov(u, e^T) = 0$,

$$var(y) = Z * var(u) * Z^T + var(e) = ZGZ^T + R = V$$

Estimates of unknown Parameters

$$\hat{u} = E(u|y) = GZ^TV^{-1}(y - X\hat{\beta})$$

$$\hat{\beta} = (X^T V^{-1} X)^- X^T V^{-1} y$$

Mixed Model Equations

- ▶ Problem: V^{-1}
- Same solutions obtained with following set of equations

$$\begin{bmatrix} X^T R^{-1} X & X^T R^{-1} Z \\ Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T R^{-1} y \\ Z^T R^{-1} y \end{bmatrix}$$

Sire Model

▶ Breeding value of sire as random effect:

$$y = X\beta + Zs + e$$

Example

[2.61]]	Γ1	0]		Γ1	0	0]		$\lceil e_1 \rceil$
2.31		1	0		1	0	0		<i>e</i> ₂
2.44		1	0		1	0	0	$egin{bmatrix} s_1 \ s_2 \ s_3 \end{bmatrix} +$	<i>e</i> ₃
2.41		1	0	$\begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix} +$	1	0	0		e ₄
2.51		0	1		1	0	0		<i>e</i> ₅
2.55		0	1		1	0	0		<i>e</i> ₆
2.14		0	1		1	0	0		e ₇
2.61		0	1		1	0	0		<i>e</i> ₈
2.34	-	1	0		0	1	0		<i>e</i> ₉
1.99		1	0		0	1	0		e ₁₀
3.1		1	0		0	1	0		e_{11}
2.81		1	0		0	1	0		e ₁₂
2.14		0	1		0	1	0		e ₁₃
2.41		0	1		0	1	0		e ₁₄
2.54		0	1		0	0	1		e ₁₅
3.16]	0	1		0	0	1		$\lfloor e_{16} floor$

Animal Model

▶ Breeding value for all animals as random effects

$$y = X\beta + Zu + e$$