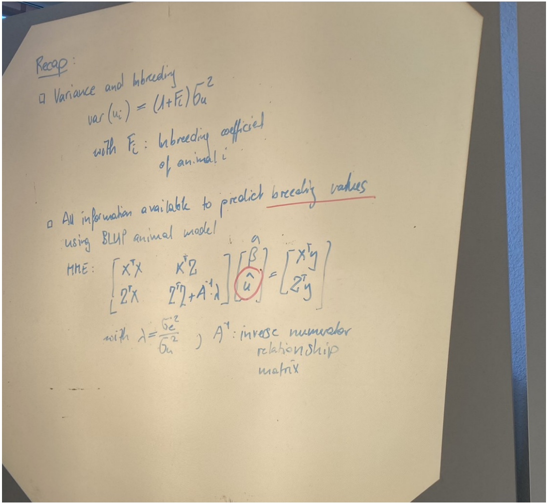
OHP Picture 1



Recap:

☐ Variance and Inbreeding

$$\mathrm{var}(u_i) = (1+F_i)\,\sigma_u^2$$

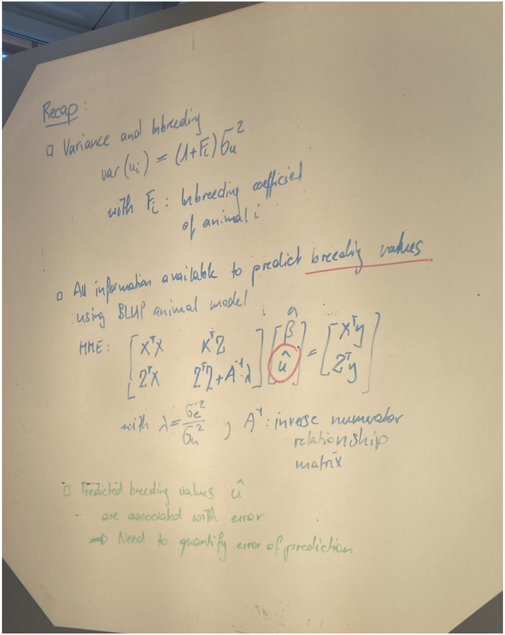
with F_i: Inbreeding coefficient of animal i

☐ All information available to predict breeding values using BLUP animal model

$$\text{MME: } \begin{bmatrix} X^T X & X^T Z \\ Z^T X & Z^T Z + A^{-1}\lambda \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \enclose{circle}{\hat{u}} \end{bmatrix} = \begin{bmatrix} X^T y \\ Z^T y \end{bmatrix}$$

with $\lambda = \frac{\sigma_e^2}{\sigma_u^2}$; A^{-1}: inverse numerator relationship matrix

OHP Picture 2



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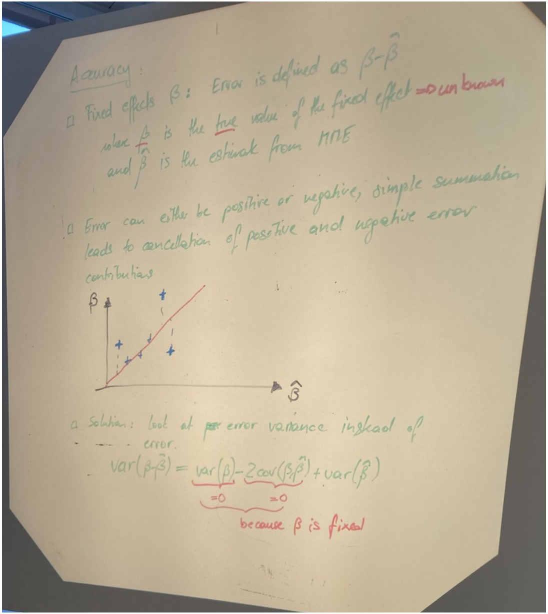
MME: $$\begin{bmatrix} X^TX & X^TZ \\ Z^TX & Z^TZ+A^{-1}\lambda \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^Ty \\ Z^Ty \end{bmatrix}$$

with $\lambda = \frac{\sigma_e^2}{\sigma_u^2}$, A^{-1} : inverse numerator relationship matrix

☐ Predicted breeding values $\hat{u}$ are associated with error

⇒ Need to quantify error of prediction

OHP Picture 3



Accuracy:

☐ Fixed effects β: Error is defined as $\beta - \hat{\beta}$

where β is the true value of the fixed effect $\Rightarrow$ unknown

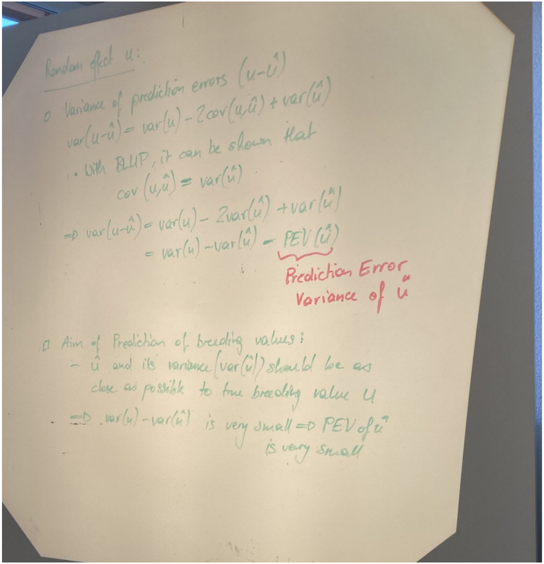
and $\hat{\beta}$ is the estimate from MME

☐ Error can either be positive or negative, simple summation leads to cancellation of positive and negative error contributions

☐ Solution: look at ~~per~~ error variance instead of error.

$$\mathrm{var}(\beta - \hat{\beta}) = \underbrace{\underbrace{\mathrm{var}(\beta)}_{=0} - \underbrace{2\,\mathrm{cov}(\beta, \hat{\beta})}_{=0}}_{\text{because } \beta \text{ is fixed}} + \mathrm{var}(\hat{\beta})$$

OHP Picture 4



Random effect u:

☐ Variance of prediction errors $(u-\hat{u})$

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

- With BLUP, it can be shown that

$$cov(u,\hat{u}) = var(\hat{u})$$

$$\Rightarrow var(u-\hat{u}) = var(u) - 2var(\hat{u}) + var(\hat{u})$$

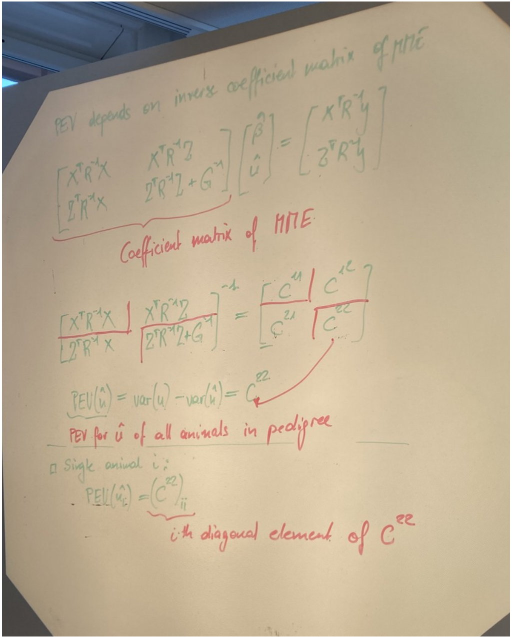
$$= var(u) - var(\hat{u}) = \underbrace{PEV(\hat{u})}_{\text{Prediction Error Variance of } \hat{u}}$$

☐ Aim of Prediction of breeding values:

- $\hat{u}$ and its variance $(var(\hat{u}))$ should be as close as possible to true breeding value u

$\Rightarrow var(u) - var(\hat{u})$ is very small $\Rightarrow$ PEV of $\hat{u}$ is very small

OHP Picture 5



PEV depends on inverse coefficient matrix of MME

$$\underbrace{\begin{bmatrix} X^T R^{-1} X & X^T R^{-1} Z \\ Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{bmatrix}}_{\text{Coefficient matrix of MME}} \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix} = \begin{bmatrix} X^T R^{-1} y \\ Z^T R^{-1} y \end{bmatrix}$$

$$\left[\begin{array}{c|c} X^T R^{-1} X & X^T R^{-1} Z \\ \hline Z^T R^{-1} X & Z^T R^{-1} Z + G^{-1} \end{array}\right]^{-1} = \left[\begin{array}{c|c} C^{11} & C^{12} \\ \hline C^{21} & C^{22} \end{array}\right]$$

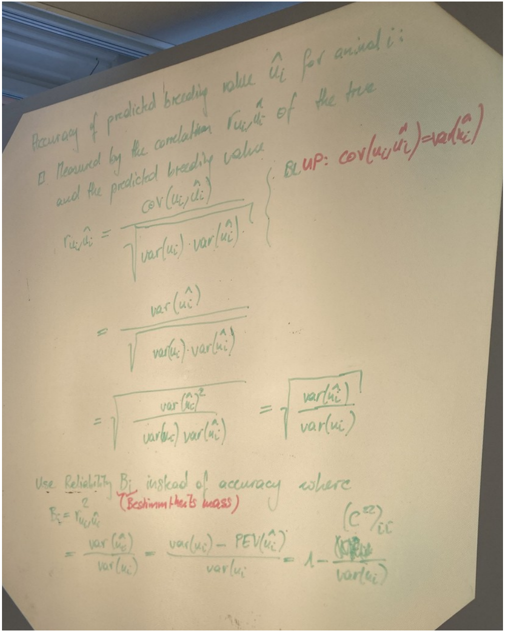
$$\underbrace{PEV(\hat{u})} = var(u) - var(\hat{u}) = C^{22}$$

PEV for $\hat{u}$ of all animals in pedigree

☐ Single animal i:

$$PEV(\hat{u}_i) = \underbrace{(C^{22})_{ii}}_{i\text{th diagonal element of } C^{22}}$$

OHP Picture 6



Accuracy of predicted breeding value $\hat{u}_i$ for animal i:

☐ Measured by the correlation $r_{u_i,\hat{u}_i}$ of the true and the predicted breeding value

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

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

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

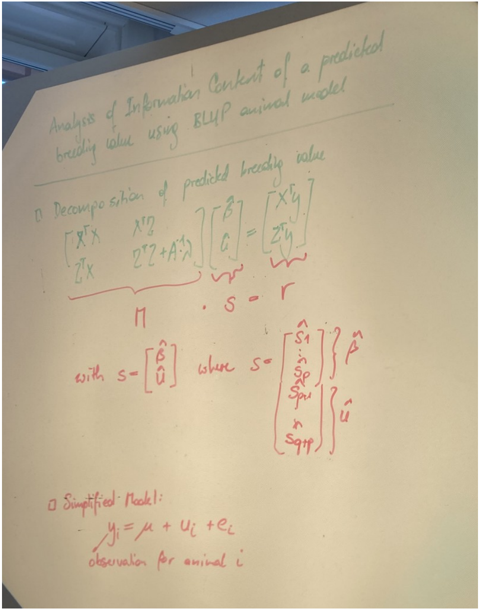
$$= \sqrt{\frac{\text{var}(\hat{u}_i)^2}{\text{var}(u_i)\,\text{var}(\hat{u}_i)}} = \sqrt{\frac{\text{var}(\hat{u}_i)}{\text{var}(u_i)}}$$

Use Reliability B_i instead of accuracy where (Bestimmtheitsmass)

$$B_i = r^2_{u_i,\hat{u}_i}$$

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

OHP Picture 7



Analysis of Information Content of a predicted breeding value using BLUP animal model

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☐ Decomposition of predicted breeding value

$$\underbrace{\begin{bmatrix} X^TX & X^TZ \\ Z^TX & Z^TZ + A^{-1}\lambda \end{bmatrix}}_{M} \cdot \underbrace{\begin{bmatrix} \hat{\beta} \\ u \end{bmatrix}}_{s} = \underbrace{\begin{bmatrix} X^Ty \\ Z^Ty \end{bmatrix}}_{r}$$

$$M \cdot s = r$$

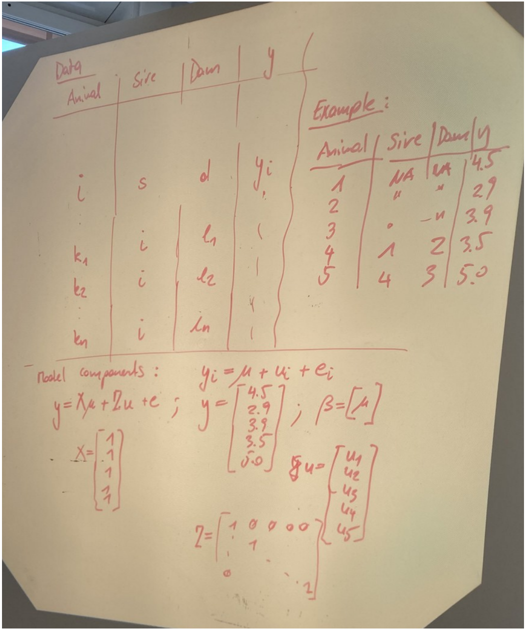
with $s = \begin{bmatrix} \hat{\beta} \\ \hat{u} \end{bmatrix}$ where $s = \begin{bmatrix} \hat{s}_1 \\ \vdots \\ \hat{s}_p \\ \hat{s}_{p+1} \\ \vdots \\ \hat{s}_{q+p} \end{bmatrix} \begin{matrix} \left.\vphantom{\begin{matrix}a\\a\\a\end{matrix}}\right\} \hat{\beta} \\ \left.\vphantom{\begin{matrix}a\\a\\a\end{matrix}}\right\} \hat{u} \end{matrix}$

☐ Simplified Model:

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

observation for animal i

OHP Picture 8



Data

Animal	Sire	Dam	y
i	s	d	y_i
⋮			
k_1	i	l_1	
k_2	i	l_2	
⋮			
k_n	i	l_n	

Example:

Animal	Sire	Dam	y
1	NA	NA	4.5
2	"	"	2.9
3	"	"	3.9
4	1	2	3.5
5	4	3	5.0

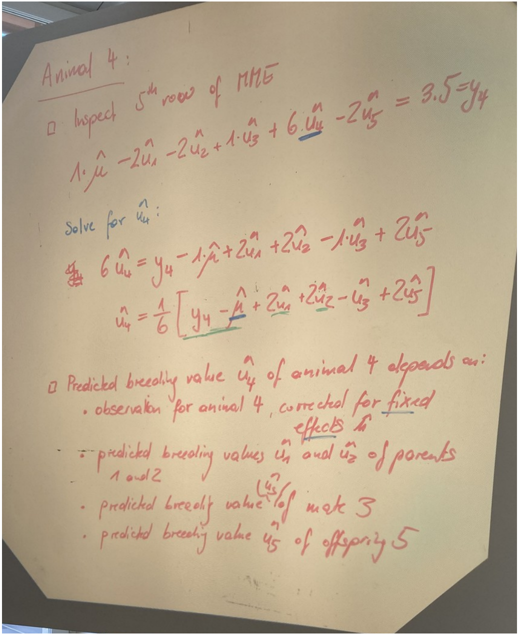
Model components: $y_i = \mu + u_i + e_i$

$y = X\mu + Zu + e$; $y = \begin{bmatrix} 4.5 \\ 2.9 \\ 3.9 \\ 3.5 \\ 5.0 \end{bmatrix}$; $\beta = [\mu]$

$X = \begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \\ 1 \end{bmatrix}$ $u = \begin{bmatrix} u_1 \\ u_2 \\ u_3 \\ u_4 \\ u_5 \end{bmatrix}$

$Z = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 \\ \vdots & 1 & & & \\ \vdots & & \ddots & & \\ 0 & & & \ddots & 1 \end{bmatrix}$

OHP Picture 9



Animal 4:

☐ Inspect 5th row of MME

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

Solve for $\hat{u}_4$:

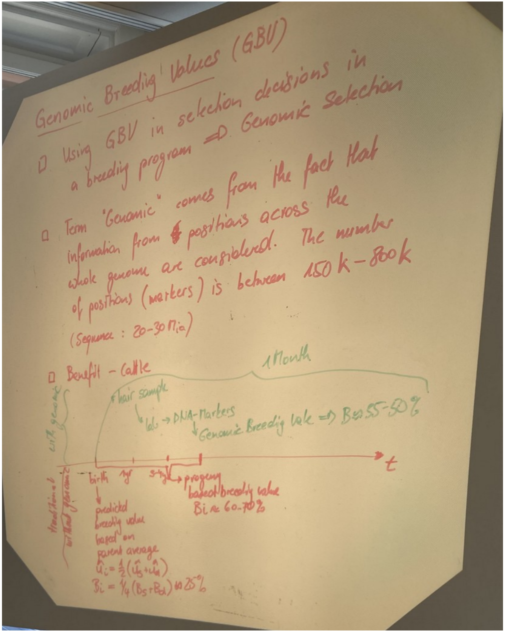
$$6\hat{u}_4 = y_4 - 1\cdot\hat{\mu} + 2\hat{u}_1 + 2\hat{u}_2 - 1\cdot\hat{u}_3 + 2\hat{u}_5$$

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

☐ Predicted breeding value $\hat{u}_4$ of animal 4 depends on:

- observation for animal 4, corrected for fixed effects $\hat{\mu}$
- predicted breeding values $\hat{u}_1$ and $\hat{u}_2$ of parents 1 and 2
- predicted breeding value $\hat{u}_3$ of mate 3
- predicted breeding value $\hat{u}_5$ of offspring 5

OHP Picture 10



Genomic Breeding Values (GBV)

☐ Using GBV in selection decisions in a breeding program ⇒ Genomic Selection

☐ Term "Genomic" comes from the fact that information from ~~#~~ positions across the whole genome are considered. The number of positions (markers) is between 150k – 800k

(Sequence : 20-30 Mio)

☐ Benefit – Cattle

1 Month

with genomic

hair sample

lab → DNA-Markers

Genomic Breeding Value ⇒ $B \approx 55-50\%$

t

traditional

without genomic

birth

1yr

3-4yr

→ progeny based breeding value

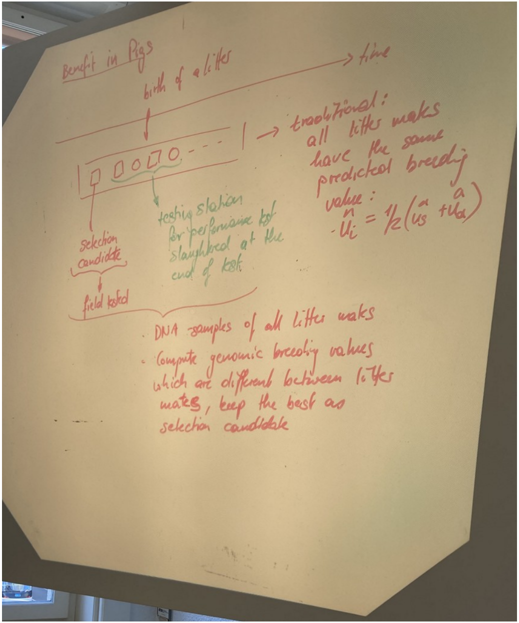
$B_i \approx 60-70\%$

predicted breeding value based on parent average

$\hat{u}_i = \frac{1}{2}(\hat{u}_s + \hat{u}_d)$

$B_i = 1/4(B_s + B_d) \approx 25\%$

OHP Picture 11

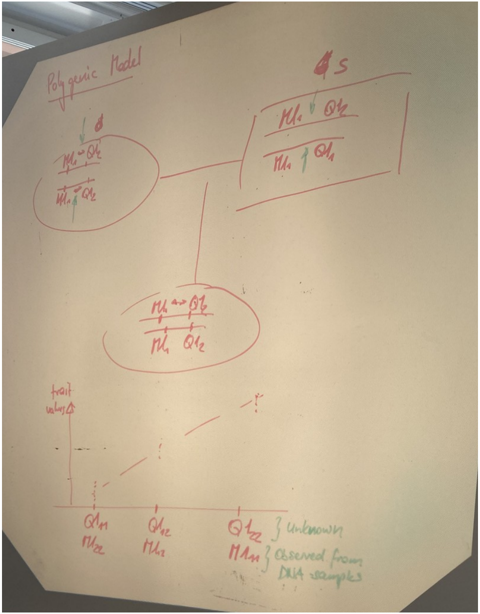


traditional: all litter mates have the same predicted breeding value:

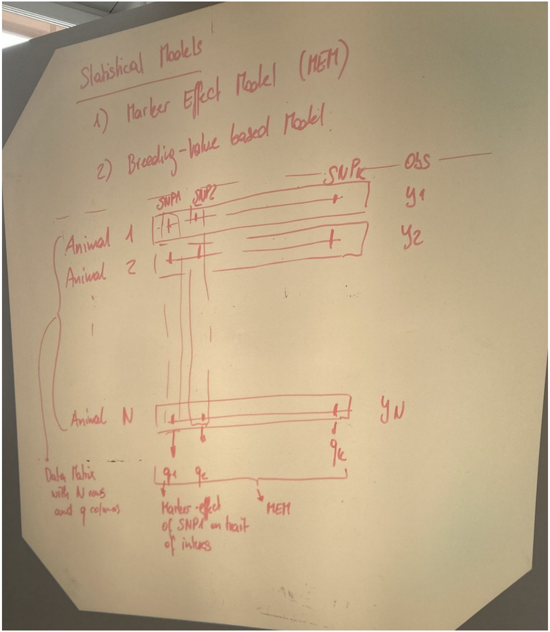
$$\hat{u}_i = 1/2(\hat{u}_s + \hat{u}_d)$$

- DNA-samples of all litter mates
- Compute genomic breeding values which are different between litter mates, keep the best as selection candidate

OHP Picture 12



OHP Picture 13



Statistical Models

1) Marker Effect Model (MEM)

2) Breeding-value based Model

Data Matrix with N rows and q columns

Marker-effect of SNP1 on trait of interest