

Prediction of breeding values for mean and environmental variance with an iterative BLUP-procedure

Han Mulder, Lars Rönnegård, Roel Veerkamp



Acknowledgement

- This work was carried out as part of the RobustMilk project that is financially supported by the European Commission under the Seventh Research Framework Programme, Grant Agreement KBBE-211708.
- These results are part of the SABRE research project that has been co-financed by the European Commission, within the 6th Framework Programme, contract No. FOOD-CT-2006-016250.
- The content of this paper is the sole responsibility of the authors, and it does not necessarily represent the views of the Commission or its services.



LIVESTOCK RESEARCH
WAGENINGEN UR



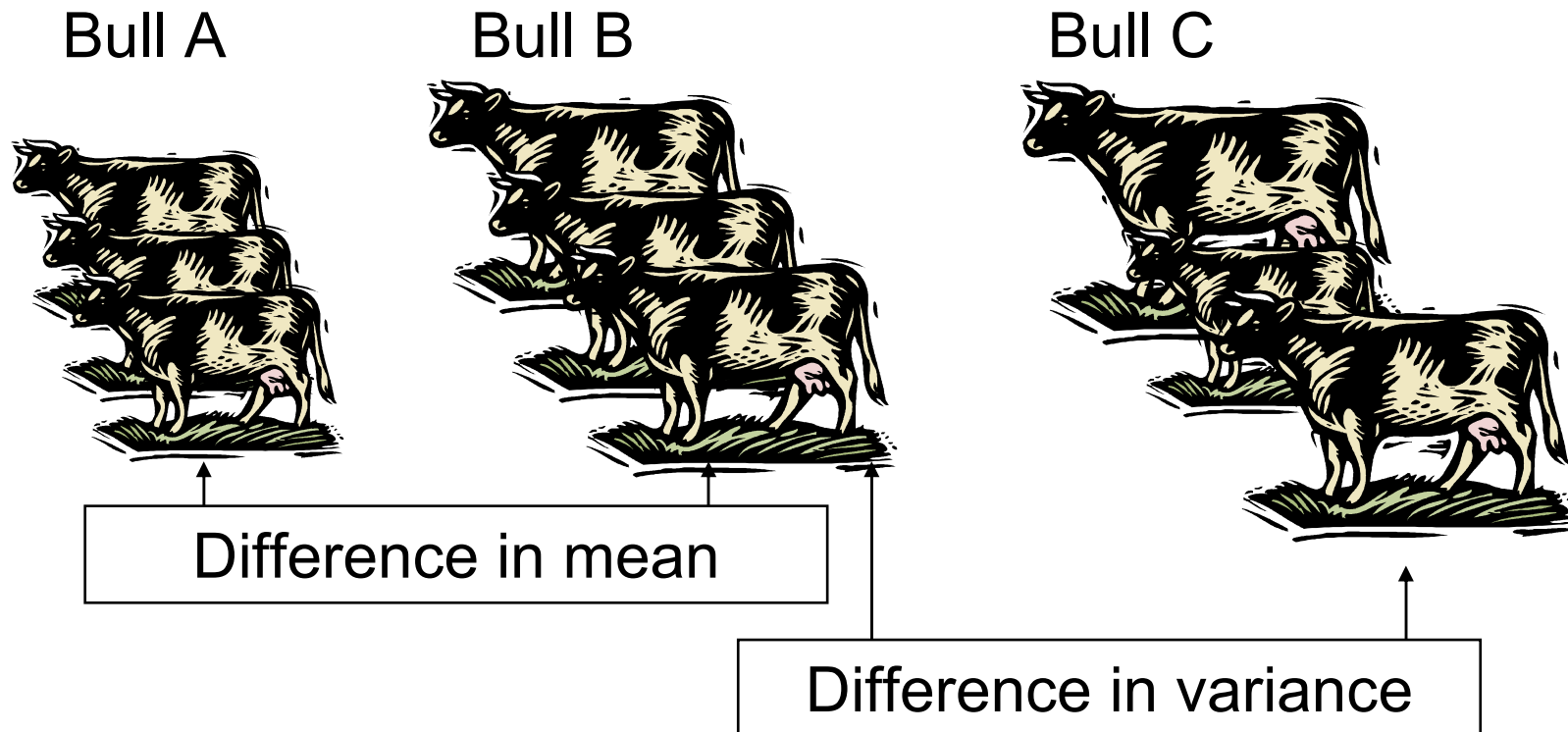
ROBUSTMILK

S A B R E

Animal Breeding &
Genomics Centre

Introduction

- Prediction of EBV for mean and environmental variance requires genetic variation in mean and environmental variance



Introduction

- Existence of genetic variation in environmental variance
 - Pigs (Sorensen and Waagepeetersen, 2003; Ibanez-Escriche et al., 2008)
 - Chickens (Rowe et al., 2006, Wolc et al., 2009; Mulder et al., 2009)
 - Mice (Gutierrez et al., 2006; Ibanez-Escriche et al., 2008)
 - Drosophila (Mackay and Lyman, 2005)
 - Snail (Ros et al., 2004)
 - Rabbit (Ibanez-Escriche et al., 2008; Garreau et al., 2008)

- Focus has been mainly on estimation of variance components and less on estimation of breeding values

Objective

- To develop an iterative BLUP-procedure to estimate breeding values for mean and environmental variance
 - Bivariate versus univariate breeding value estimation
 - Homogeneous versus heterogeneous residual variance
 - With or without use of leverages

Quantitative genetic model

- Genetic differences in environmental variance
 - Additive model

$$P = \mu + A_m + \chi \sqrt{\sigma_E^2 + A_v}$$

$$G = \begin{bmatrix} \sigma_{A_m}^2 & r_A \sigma_{A_m} \sigma_{A_v} \\ r_A \sigma_{A_m} \sigma_{A_v} & \sigma_{A_v}^2 \end{bmatrix}$$

Bivariate EBV-model: heterogeneous variance

$$\begin{bmatrix} \mathbf{p} \\ \mathbf{e}_{e^2}^2 \end{bmatrix} = \begin{bmatrix} \mathbf{X}\mathbf{b}_p \\ \mathbf{X}\mathbf{b}_{e^2} \end{bmatrix} + \begin{bmatrix} \mathbf{Z}\hat{\mathbf{a}}_m \\ \mathbf{Z}\hat{\mathbf{a}}_v \end{bmatrix} + \begin{bmatrix} \mathbf{e}_p \\ \mathbf{e}_{e^2} \end{bmatrix}$$

$$\begin{bmatrix} \hat{\mathbf{a}}_m \\ \hat{\mathbf{a}}_v \end{bmatrix} \sim N(\mathbf{0}, \mathbf{A} \otimes \mathbf{G}) \quad \mathbf{G} = \begin{bmatrix} \sigma_{a_m}^2 & r_a \sigma_{a_m} \sigma_{a_v} \\ r_a \sigma_{a_m} \sigma_{a_v} & \sigma_{a_v}^2 \end{bmatrix}$$

$$\begin{bmatrix} \mathbf{e}_p \\ \mathbf{e}_{e^2} \end{bmatrix} \sim N(\mathbf{0}, \mathbf{R} \otimes \mathbf{I}) \quad \mathbf{R} = \begin{bmatrix} \sigma_{e_{p,i}}^2 & 0 \\ 0 & \sigma_{e_{e^2}}^2 \end{bmatrix} \quad \sigma_{e_{p,i}}^2 = \sigma_{e_p}^2 + \hat{a}_{v,i}$$

Bivariate EBV-model: with leverages

- Leverage (l): Effect of an observation on the predicted value
= diagonal element of hat-matrix
→ $1-l \sim$ accuracy of residual

$$\begin{bmatrix} \mathbf{p} \\ \mathbf{e}_p^2 / (1-l_i) \end{bmatrix} = \begin{bmatrix} \mathbf{Xb}_p \\ \mathbf{Xb}_{e^2} \end{bmatrix} + \begin{bmatrix} \mathbf{Z}\hat{\mathbf{a}}_m \\ \mathbf{Z}\hat{\mathbf{a}}_v \end{bmatrix} + \begin{bmatrix} \mathbf{e}_p \\ \mathbf{e}_{e^2} \end{bmatrix}$$

$$\mathbf{R} = \begin{bmatrix} \sigma_{e_p,i}^2 & 0 \\ 0 & \sigma_{e^2}^2 / (1-l_i) \end{bmatrix} \quad l_i = (1 - r_{a_m}^2 \sigma_{a_m}^2) / \sigma_{e_p}^2$$

Similar to Rönnegård et al. (2010); without GLM

Implementation

- MiXBLUP software to solve mixed model equations (Lidauer and Strandén, 1999)
- True variance components were used
- Iterative updating of squared residuals; 10 iterations
- Approximated reliabilities (Tier and Meyer, 2004)

- Four models
 - 2 univariate runs: on phenotype and squared residuals
 - Homogeneous variance
 - Heterogeneous variance
 - Heterogeneous variance with leverages

Simulation

- Simulation according to simplified genetic model
 - No fixed effect yet on mean or environmental variance

- Structured population
 - 5 discrete generations
 - 50 bulls with each 50 daughters, bulls are sired by 10 randomly selected bull-sires
 - No selection

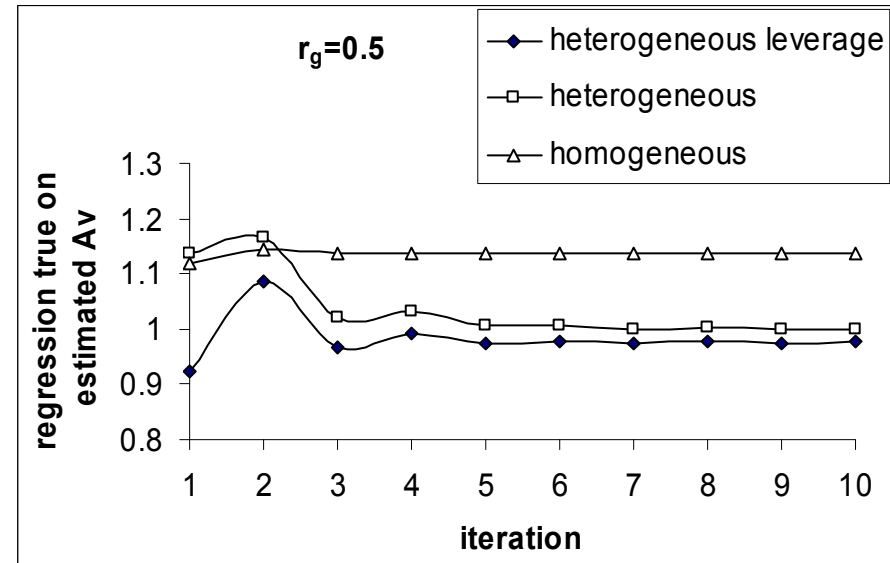
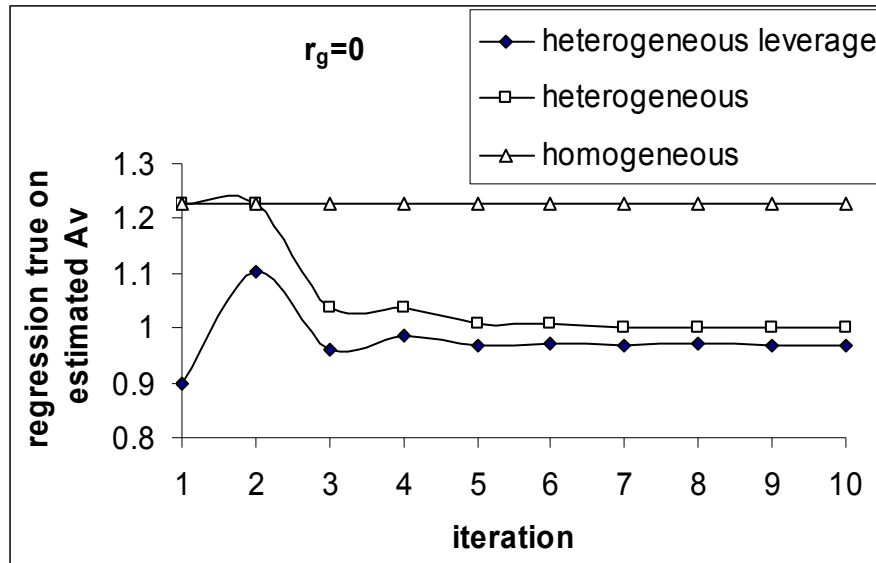
Results

Accuracy of A_v

Model		r_A			
		0.00	0.25	0.50	0.75
Bulls	Univariate	0.567	0.578	0.587	0.561
	Bivariate homogeneous	0.557	0.576	0.653	0.732
	Bivariate heterogeneous	0.553	0.575	0.652	0.728
	Bivariate heterogeneous leverage	0.553	0.575	0.652	0.728
Cows	Univariate	0.336	0.344	0.340	0.340
	Bivariate homogeneous	0.335	0.357	0.426	0.502
	Bivariate heterogeneous	0.334	0.356	0.427	0.502
	Bivariate heterogeneous leverage	0.334	0.356	0.427	0.502

→ Accuracy A_v improves with bivariate analysis when $r_a \neq 0$

Results



- Model with heterogeneous residual variance improves regression of true on estimated Av

Conclusion

- The iterative BLUP procedure works nicely and can be used in existing BLUP-software
- The iterative BLUP-procedure mainly improves the regression of true on estimated A_v
- Differences in accuracy of estimated A_v are small
- Model with heterogeneous variance and leverages is the model of choice, especially with large differences in accuracy of A_m and unbalanced data

Thank you for your attention!



S A B R E

Conclusion

- The iterative BLUP procedure works nicely and can be used in existing BLUP-software
- The iterative BLUP-procedure mainly improves the regression of true on estimated A_v
- Models differ little in accuracy of estimated A_v
- Model with heterogeneous variance and leverages is the model of choice, especially with large differences in accuracy of A_m