

Approximating individual animal reliabilities in single-step genomic model

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Introduction

- Calculation of individual animal reliabilities of genomic breeding values from single-step genomic BLUP (ssGBLUP) requires an inversion of the coefficient matrix of the mixed model equations (MME).
- When the MME coefficient matrix is small, reliability can be computed by direct inversion of the matrix. When the matrix is large, the inversion is not possible, and reliability needs to be approximated.

Introduction

- Several approximation methods for animal models have been developed for the non-genomic evaluations.
- Only few approximation methods have been developed in ssGBLUP genomic evaluation ([Misztal et al. 2013](#); [Edel et al. 2019](#)).

Aims

- Approximate the reliabilities separately for genotyped and non-genotyped animals.
- Compare the approximated reliabilities with corresponding reliabilities obtained from the inverse of the MME coefficient matrix (Exact animal and ssGBLUP models).

Models

Consider a univariate ssGBLUP model

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{W}\mathbf{u} + \mathbf{e},$$

MME are

$$\begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{W} \\ \mathbf{W}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{W}'\mathbf{R}^{-1}\mathbf{W} + \mathbf{H}^{-1}\sigma_u^{-2} \end{bmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{u}} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{W}'\mathbf{R}^{-1}\mathbf{y} \end{bmatrix},$$

Where $\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$, and $\mathbf{G}_w = (1 - w)\mathbf{G} + w\mathbf{A}_{22}$

Denote the MME coefficient matrix by \mathbf{C} and its inverse matrix elements as

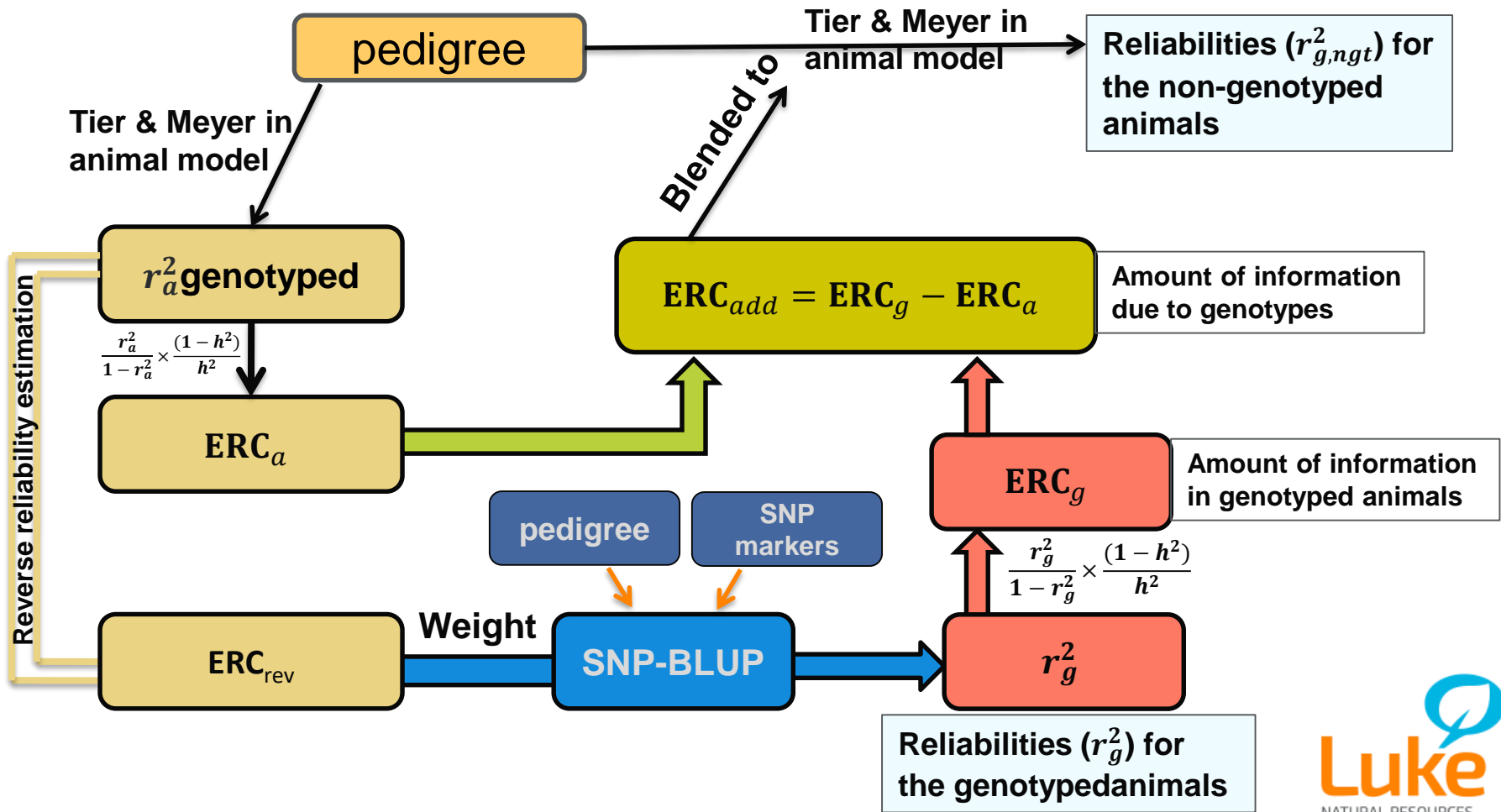
$$\mathbf{C}^{-1} = \begin{bmatrix} \mathbf{C}^{bb} & \mathbf{C}^{bu} \\ \mathbf{C}^{ub} & \mathbf{C}^{uu} \end{bmatrix},$$

and PEV_i = diagonal i in the prediction error variance (PEV) matrix \mathbf{C}^{uu} . Reliability is

$$Rel_i = 1 - \frac{PEV_i}{H_{i,i}\sigma_u^2}$$

A recipe to approximate reliability in ssGBLUP

1. Calculate the amount of the non-genomic information in the GEBV of the genotyped animals:
 1. calculate the approximate reliability (r_a^2) in non-genomic animal model
 2. use r_a^2 to approximate effective record contributions (ERC_a), i.e., amount of non-genomic information
 3. Use reverse reliability estimation to calculate $ERC_{rev|} r_a^2$ for the genotyped animals
2. Calculate the total amount of information for the genotyped animals
 1. calculate **reliability (r_g^2) of genomic breeding values** by SNP-BLUP with weight ERC_{rev}
 2. calculate amount of information using ERC_g : $ERC_g = \frac{r_g^2}{1-r_g^2} \times \frac{(1-h^2)}{h^2}$
3. Increased information due to genomics for the genotyped animals: $ERC_{add} = ERC_g - ERC_a$
4. **Reliabilities ($r_{g,ngt}^2$) for the non-genotyped animals** can be approximated by blending the increased genomic information of the genotyped animals (ERC_{add}) in animal model.



Computational details

- Exact reliabilities by inverting the MME matrix were calculated using exa99 from MiX99
- Animal model reliabilities by Tier&Meyer (2004) were calculated using apax99 in MiX99
- Reverse reliability estimates of ERCs were calculated using apax99 in MiX99
- SNP-BLUP reliabilities were calculated using snp_blup_rel program



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**Using Monte Carlo method to include polygenic effects
in calculation of SNP-BLUP model reliability**

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Snp_blup_rel: software for calculating individual animal
SNP-BLUP model reliabilities



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Data

- 19,757 genotyped animals in the Finnish Red dairy cattle
- Pedigree for the genotyped animals: 136,593 animals
- A set of 11,729 SNP markers which were selected from those used in the joint Nordic genomic evaluations
- We assumed the heritability of the trait to be 0.43

Comparison of reliabilities from exact ssGBLUP to

A) animal model with no-genomic information

B) approximations by weighted SNP-BLUP

Genotyped animals

Methods	correlation	max	MSE	b0	b1
Animal Model	0.945	0.51	0.0406	0.48	0.48
SNP-BLUP	0.988	0.08	0.0003	0.04	0.93

MSE: mean squared error

b0, b1 regression of exact ssGBLUP reliabilities on AM and weighted-SNP-BLUP reliabilities

Comparison of reliabilities from exact ssGBLUP to

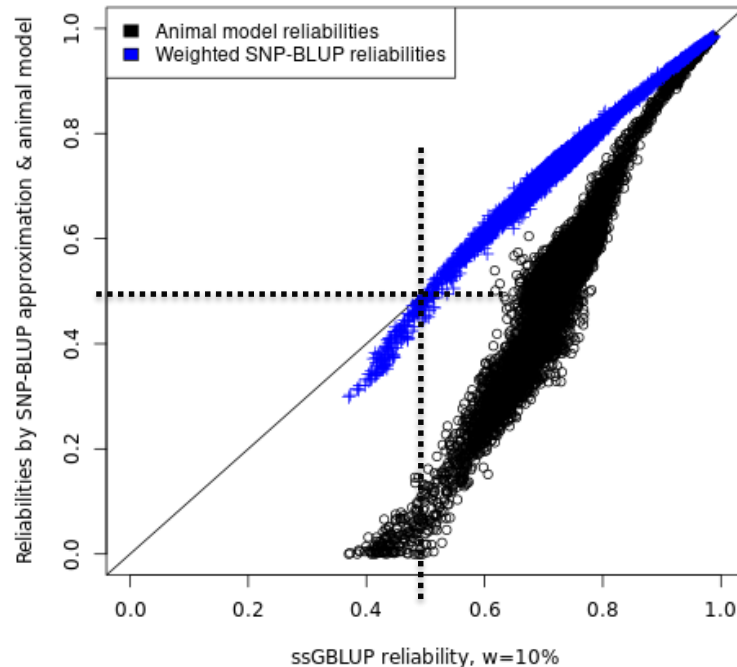
A) animal model with no-genomic information

B) SNP-BLUP blended to animal model

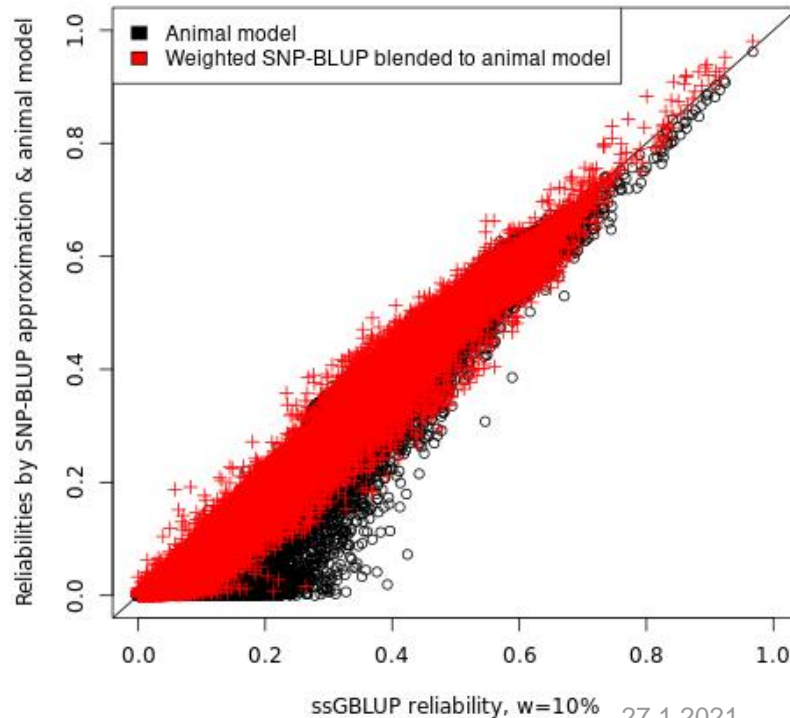
Non-genotyped animals

Methods	correlation	max	MSE	b0	b1
Animal Model	0.989	0.37	0.0014	0.03	0.96
SNP-BLUP blended to AM	0.995	0.25	0.0006	0.02	0.99

Exact ssGBLUP versus approximate SNP-BLUP reliabilities for the genotyped animals



Exact ssGBLUP compared with genomic reliability by SNP-BLUP blended to AM and AM reliabilities for the non-genotyped animals



Computing times

Methods	Peak memory (GB)	Wall clock time (h)
Animal Model	161.1	6.7
Exact ssGBLUP	161.1	6.8
ssGBLUP approximation	17.91	0.16

Conclusions

- The SNP-BLUP approximation gave a high correlation with ssGBLUP model reliability
- Results show good agreement between approximate and true values both for the genotyped and non-genotyped animals, although the approximate reliabilities deviated from the truth to both directions.
- The upward and downward biases could result from several approximations and assumptions inherent in multi-step procedure.
- The weighted SNP-BLUP method shows a good fit for the genotyped animals.
- The fit is likely dependent on the population structure.
- Testing the approximation in the multiple trait models is required.

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Thank you!