

Bavarian State Research Center for Agriculture



## 66<sup>th</sup> EAAP Annual Meeting Equivalence of genomic breeding values and reliabilities estimated with SNP-BLUP and GBLUP

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GBLUP (VanRaden, 2008) is one of the most common procedures to estimate genomic breeding values

An alternative to estimate genomic breeding values is the so called SNP-BLUP (Meuwissen et al., 2001)

The equivalence of both model has been shown (e.g. Goddard, 2008; VanRaden, 2008)

But: there have been some irritations in the literature (Strandén and Christensen, 2011)
Christensen, 2011)

Demonstrate the identity of DGVs and reliabilities by a practical example



Why did we do that?

- Check the practicability and feasibility in real life applications
- Preliminary investigation: methods
- Current studies: enhance the reference population by a large number of genotyped cows



Phenotypes and genotypes of 11 852 Fleckvieh sires

Genotyped with the Illumina BovineSNP50 BeadChip

DGVs and their reliabilities for milk yield

Total of 41 266 SNPs retained after filtering

Genotype coding: 2q, (q-p), -2p



## **G-BLUP**

y = Xb + Za + e

#### **SNP-BLUP**

### y = Xb + Mg + e

$$\begin{pmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z}+\mathbf{G}^{-1}/\sigma_{a}^{2} \end{pmatrix} \begin{bmatrix} \hat{\mathbf{b}} \\ \hat{\mathbf{a}} \end{bmatrix} = \begin{pmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{y} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{y} \end{pmatrix}$$

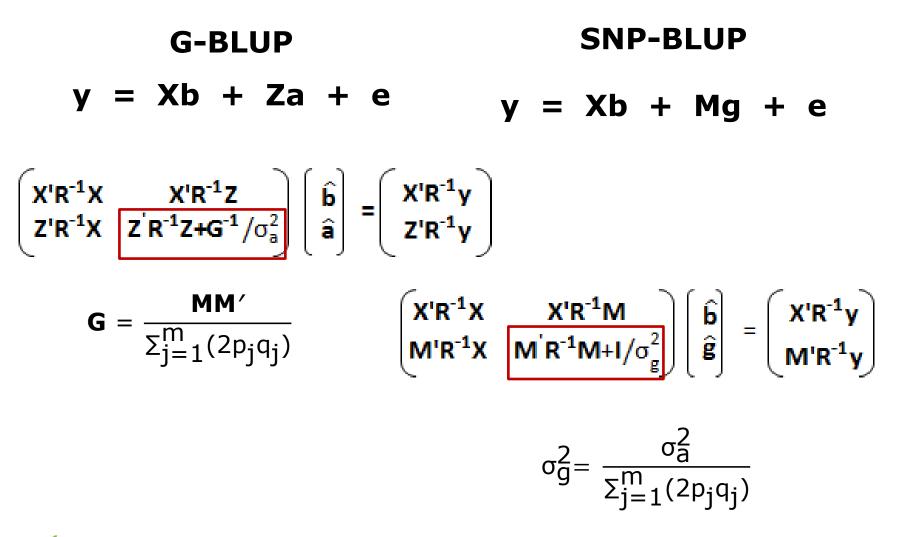
X'R <sup>-1</sup> X	X'R <sup>-1</sup> M	<b>6</b> ]	(X'R <sup>-1</sup> y)	
M'R <sup>-1</sup> X	$X'R^{-1}M$ $M'R^{-1}M+I/\sigma_g^2$	) [ ĝ	_	M'R <sup>-1</sup> y

y b	
а	
Х,	Ζ
R	
G	
Μ	
g	
Ι	
е	

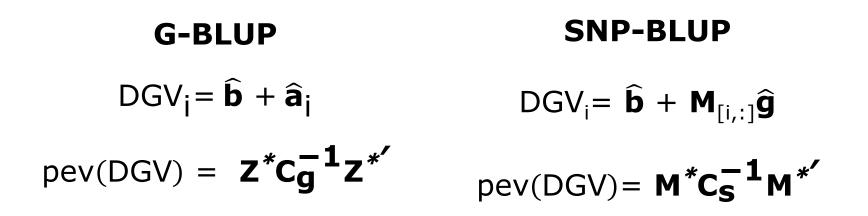
- vector of observations (DYD)
  vector of fixed effects (mean)
  vector of random animal effects
  design matrices
  - = residual co-variance matrix
  - = genomic relationship matrix
  - = coefficient matrix of marker genotypes
  - = vector of random marker effects
  - = identity matrix
  - = vector of residual effects



Models



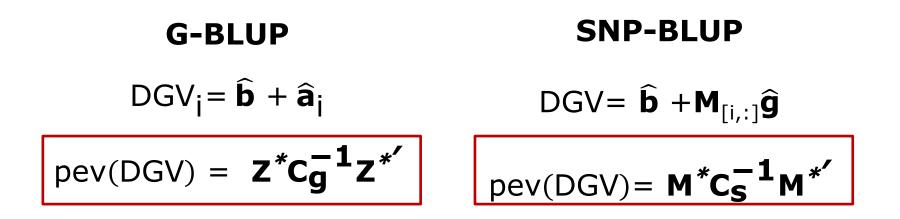




$$r_{i}^{2}=1-\frac{\text{diag}(\text{pev}(\text{DGV}))_{i}}{\text{diag}(\mathbf{G})_{i}\sigma_{a}^{2}}$$

 $C^{-1}$  = Inverse of the left-hand-side of the MME

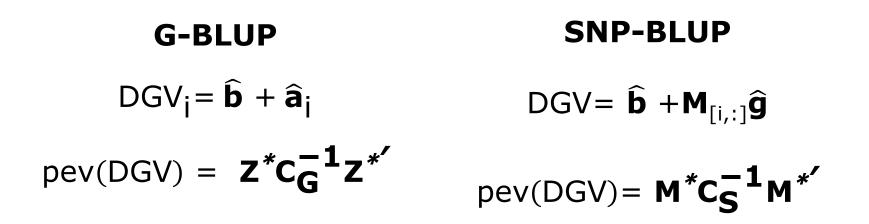




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DGVs obtained with both models were the same

models are **equivalent in DGVs** 

Reliabilities of DGVs from both models were also the same, when genomic inbreeding was taken into account

models are equivalent in reliabilities of DGVs



- For both methods we can imagine advantages and disadvantages in different scenarios
- This is primarily due to the structure of data:
  - If number of markers >> number of animals: GBLUP would be preferable
  - If number of markers << number of animals: SNP-BLUP would be preferable



- SNP-BLUP and GBLUP lead to equivalent results for DGVs and their reliabilities
- Prerequisites for identical and meaningful reliabilities in both cases:
  - Error variance of the intercept
  - Genomic inbreeding coefficient
  - Genotype coding
- The model of choice should mainly depend on the structure of the dataset



# Thank you for your attention

We gratefully acknowledge:

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Contributors of the genotype pool Germany-Austria

