Estimation of genomic breeding values for traits with high and low heritability in Brown Swiss bulls

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Outline

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  - Different G matrices
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  - Accuracy of gEBVs with different G matrices
- Conclusions

Introduction

- GBLUP is a common approach for estimation of genomic breeding values (gEBVs)
  - Regression on SNP effects
  - Use of genomic relationship matrix (G matrix)

- Several methods are well known in animal breeding for setting up G matrices from SNP data
  - Hayes and Goddard (2008)
  - Van Raden (2008)

Aim of the Study

- The method of Astle and Balding (2009) has not been applied to animal breeding so far

⇒ Comparison of G matrix by Astle and Balding (2009) to widely used algorithms

→ logL as a measurement of how well the model fits the data

→ Accuracy of gEBVs form different G matrices compared by cross validation

Material

- 1,138 Brown Swiss bulls
- 54,001 SNP genotypes (Illumina 54k SNP Chip)

- Conventional EBVs (April 2010):
  - Milk yield (MY)
  - Somatic cell score (SCS)
  - Non-return rate (NRR)
  - Interval from calving to first insemination (CFI)

Filtering and imputation

- Elimination of SNP markers:
  - Unknown position
  - Callrate < 95%
  - MAF < 5%

  ⇒ 34,474 SNP used for analysis

- Imputing with BEAGLE 3.2 (Browning and Browning, 2009)

Statistical model

- GBLUP in ASReml:

$$\mathbf{y} = \mathbf{1}\boldsymbol{\mu} + \mathbf{Z}\mathbf{u} + \mathbf{e}$$

y vector of EBVs

$$\mathbf{u} \sim N(0, \mathbf{G}\sigma_u^2)$$

$$\mathbf{e} \sim N(0, \mathbf{I}\sigma_e^2)$$

Cross validation

- 5 fold cross validation with 10 replicates
- Random distribution of animals to validation and calibration set

  → All accuracies are means of 50 replicates

- Calculation of accuracy (Legarra et al. 2008):

$$r\left(g,\hat{g}\right)=\frac{r\left(y,\hat{g}\right)}{\sqrt{h^2}}$$

Different G matrices

- **Hayes and Goddard (2008):**

$$\overline{S}_{xy} = \frac{S_{xy} - \min}{1 - \min}$$

- Where S_{xy} is the average **similarity index** (Eding and Meuwissen, 2001) over all loci

$$S_{xy,l} = \frac{I_{11} + I_{12} + I_{21} + I_{22}}{4}$$

Different G matrices

- **Van Raden (2008):**

$$\mathbf{G}_{\mathbf{VR}} = \frac{\mathbf{ZZ}'}{2\sum p_l(1-p_l)}$$

relationship

- **Astle and Balding (2009):**

$$\mathbf{G}_{\mathbf{AB}} = \frac{1}{L}\sum\frac{(\mathbf{Z}_{.,\mathbf{l}})(\mathbf{Z}_{.,\mathbf{l}})'}{4p_l(1-p_l)}$$

kinship

Different G matrices

- **Van Raden (2008):**

$$\mathbf{G}_{\mathbf{VR}} = \frac{\mathbf{ZZ}'}{2\sum p_l\left(1-p_l\right)}$$

Average over **all** loci

- **Astle and Balding (2009):**

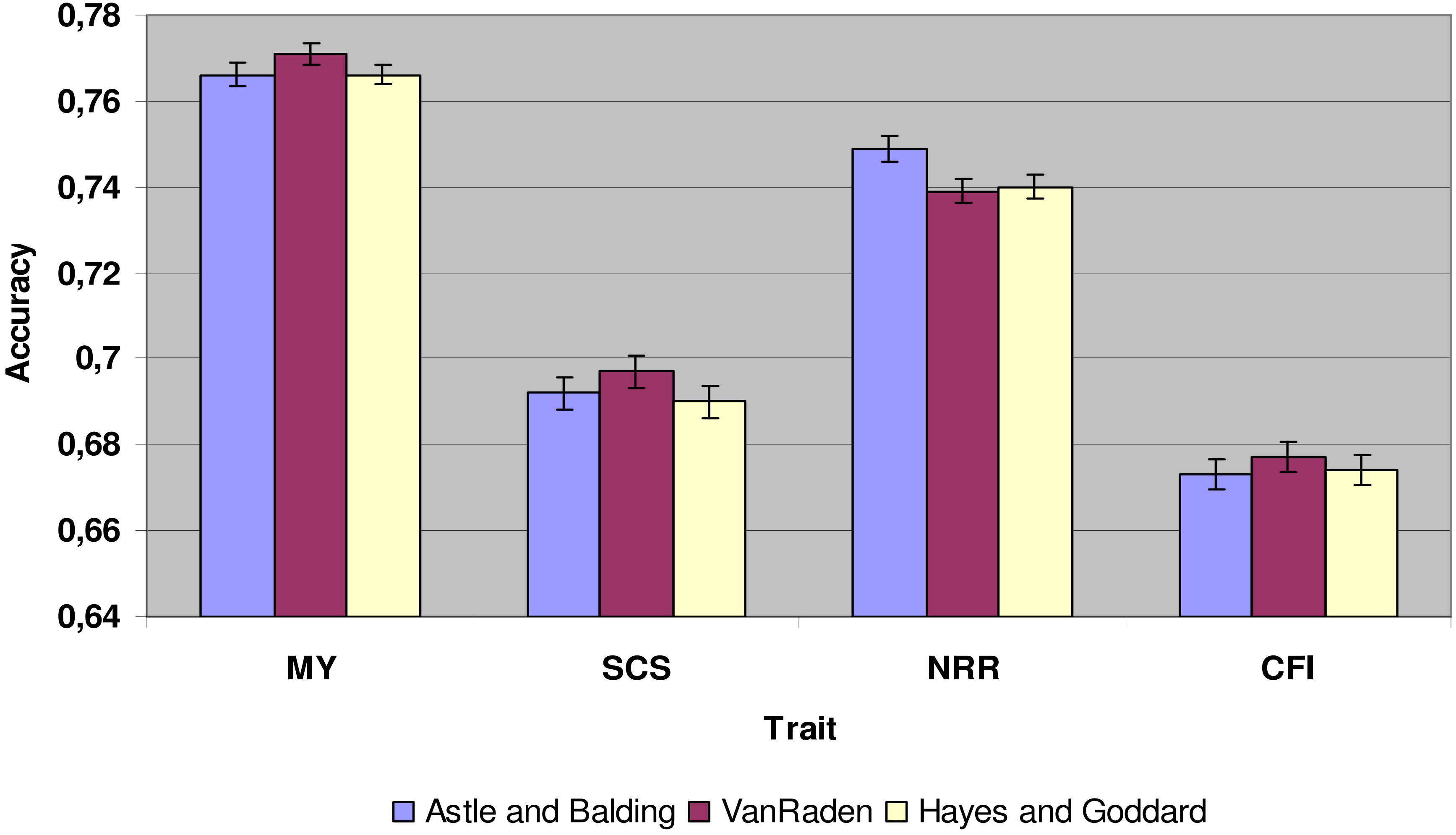
$$\mathbf{G}_{\mathbf{AB}} = \frac{1}{L}\sum \frac{\left(\mathbf{Z}_{\mathbf{.,l}}\right)\left(\mathbf{Z}_{\mathbf{.,l}}\right)'}{4p_l\left(1-p_l\right)}$$

Each locus **individually**

Results -logL of the model

G matrix	logL MY	logL SCS	logL NRR	logL CFI
Astle & Balding	-7218.55	-2917.51	-2706.86	-3050.14
VanRaden	-7227.55	-2921.61	-2710.88	-3052.30
Hayes & Goddard	-7227.92	-2921.61	-2709.76	-3052.30

Results -accuracy of gEBVs



Conclusion

- G matirx by Astle and Balding can be used to estimate gEBVs.
- G matrix by Astle and Balding delivers higher logL than G matrix by VanRaden or G Matrix by Hayes and Goddard

  → Fitting of the model with G matrix by Astle and Balding is the best
- Accuracies of gEBVs are equivalent with all three G matrices

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