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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• Material and methods
  – Data, Filtering, imputing
  – Different G matrices
• Results
  – logL with different G matrices
  – 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:

\[ y = 1\mu + Zu + e \]

- \( y \) vector of EBVs

- \( u \sim N(0, G\sigma_u^2) \)

- \( e \sim N(0, I\sigma_e^2) \)
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):

\[ r(g, \hat{g}) = \frac{r(y, \hat{g})}{\sqrt{h^2}} \]
Different G matrices

- Hayes and Goddard (2008):

\[ \bar{S}_{xy} = \frac{S_{xy} - \min}{1 - \min} \]

- 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):

\[ G_{VR} = \frac{ZZ'}{2 \sum p_l(1 - p_l)} \]

relationship

• Astle and Balding (2009):

\[ G_{AB} = \frac{1}{L} \sum \frac{(Z_{..l})(Z_{..l})'}{4 p_l(1 - p_l)} \]

kinship
Different G matrices

• Van Raden (2008):

\[ G_{VR} = \frac{ZZ'}{2 \sum p_l (1 - p_l)} \]

• Astle and Balding (2009):

\[ G_{AB} = \frac{1}{L} \sum \frac{(Z_{.,l}) (Z_{.,l})'}{4 p_l (1 - p_l)} \]

Average over all loci

Each locus individually
### Results -logL of the model

<table>
<thead>
<tr>
<th>G matrix</th>
<th>logL MY</th>
<th>logL SCS</th>
<th>logL NRR</th>
<th>logL CFI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Astle &amp; Balding</td>
<td>-7218.55</td>
<td>-2917.51</td>
<td>-2706.86</td>
<td>-3050.14</td>
</tr>
<tr>
<td>VanRaden</td>
<td>-7227.55</td>
<td>-2921.61</td>
<td>-2710.88</td>
<td>-3052.30</td>
</tr>
<tr>
<td>Hayes &amp; Goddard</td>
<td>-7227.92</td>
<td>-2921.61</td>
<td>-2709.76</td>
<td>-3052.30</td>
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</tbody>
</table>
Results - accuracy of gEBVs

<table>
<thead>
<tr>
<th>Trait</th>
<th>Astle and Balding</th>
<th>VanRaden</th>
<th>Hayes and Goddard</th>
</tr>
</thead>
<tbody>
<tr>
<td>MY</td>
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<tr>
<td>SCS</td>
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<td>NRR</td>
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<td>CFI</td>
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</tbody>
</table>
Conclusion

- G matrix 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
Acknowledgement

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