Comparison of model reliabilities from single-step and bivariate blending methods

Matti Taskinen¹
Esa A. Mäntysaari¹  Martin H. Lidauer¹  Timo Knürr¹
Jukka Pösö²  Guosheng Su³  Gert P. Aamand⁴
Ismo Strandén¹

¹MTT Agrifood Research Finland, ²FABA, ³Aarhus University, ⁴Nordisk Avlsværdivurdering

2013 Interbull Meeting - Nantes, France
Background

- Increasing interest on estimation of **model reliability in genomic evaluations**:
  - Differences exist: range from pedigree accuracy to accuracy of full progeny test
  - Reliability is needed as weights for international genomic evaluations

- **GBLUP**: the model based reliability is computed through inversion of MME
  - If $G^{-1}$ can be formed then also $(MME)^{-1}$ can be done ($MME$ is size `genotyped animals`)

- In the future genomic evaluations are mostly based on **single-step BLUP (ssGBLUP)**
  - Exact model based reliability estimation requires to invert a matrix of size `all animals`
  - approximations have been suggested by Misztal et al. 2013 based on added genomic information into MME
Background

- Increasing interest on estimation of **model reliability in genomic evaluations:**
  - Differences exist: range from pedigree accuracy to accuracy of full progeny test
  - Reliability is needed as weights for international genomic evaluations
- **GBLUP:** the model based reliability is computed through inversion of MME
  - If $G^{-1}$ can be formed then also $(MME)^{-1}$ can be done (MME is size genotyped animals)
- In the future genomic evaluations are mostly based on **single-step BLUP** (ssGBLUP)
  - Exact model based reliability estimation requires to invert a matrix of size all animals
  - approximations have been suggested by Misztal et al. 2013 based on added genomic information into MME
Background

• Increasing interest on estimation of **model reliability in genomic evaluations**:
  • Differences exist: range from pedigree accuracy to accuracy of full progeny test
  • Reliability is needed as weights for international genomic evaluations

• **GBLUP**: the model based reliability is computed through inversion of MME
  • If $G^{-1}$ can be formed then also $(MME)^{-1}$ can be done (MME is size genotyped animals)

• In the future genomic evaluations are mostly based on **single-step BLUP** (ssGBLUP)
  • Exact model based reliability estimation requires to invert a matrix of size all animals
  • approximations have been suggested by Misztal et al. 2013 based on added genomic information into MME
Background
Estimation of reliability for single-step model

- Nordic genomic evaluations: DGV\(^1\) and pedigree are combined using bivariate blending
  - Bivariate blending (Mäntysaari and Strandén, 2010) treats DGV as a correlated trait with 100% accuracy, with a correlation of \(\sqrt{R^2_{DGV}}\) to “trait”
  - Original bivariate blending was revised for this study (as will be presented)

- We wanted to compare model-based reliability computed from the full inverse of MME using models:
  - animal model BLUP (AM-BLUP)
  - single-step BLUP (ssGBLUP)
  - bivariate blending using GBLUP (bbGBLUP)

\(^1\)Direct Genomic Value
Background

Estimation of reliability for single-step model

- Nordic genomic evaluations: DGV\(^1\) and pedigree are combined using bivariate blending
  - **Bivariate blending** (Mäntysaari and Strandén, 2010) treats DGV as a correlated trait w. 100% accuracy, with a correlation of \(\sqrt{R^2_{DGV}}\) to “trait”
  - Original bivariate blending was **revised** for this study (as will be presented)

- We wanted to compare model based **reliability** computed from the **full inverse of MME** using models:
  - animal model BLUP (AM-BLUP)
  - single-step BLUP (ssGBLUP)
  - bivariate blending using GBLUP (bbGBLUP)

\(^{1}\)Direct Genomic Value
Background

Estimation of reliability for single-step model

- Nordic genomic evaluations: DGV\textsuperscript{1} and pedigree are combined using bivariate blending
  - Bivariate blending (Mäntysaari and Strandén, 2010) treats DGV as a correlated trait w. 100% accuracy, with a correlation of $\sqrt{R_{DGV}^2}$ to “trait”
  - Original bivariate blending was revised for this study (as will be presented)
- We wanted to compare model based reliability computed from the full inverse of MME using models:
  - animal model BLUP (AM-BLUP)
  - single-step BLUP (ssGBLUP)
  - bivariate blending using GBLUP (bbGBLUP)

\textsuperscript{1}Direct Genomic Value
Background
Estimation of reliability for single-step model

• Nordic genomic evaluations: DGV\(^1\) and pedigree are combined using bivariate blending
  
  • **Bivariate blending** (Mäntysaari and Strandén, 2010) treats DGV as a correlated trait w. 100% accuracy, with a correlation of \(\sqrt{R^2_{DGV}}\) to “trait”
  
  • Original bivariate blending was revised for this study (as will be presented)

• We wanted to compare model based reliability computed from the full inverse of MME using models:
  
  • animal model BLUP (AM-BLUP)
  
  • single-step BLUP (ssGBLUP)
  
  • bivariate blending using GBLUP (bbGBLUP)

\(^1\)Direct Genomic Value
Model reliability: \( y = Xb + Zu + e \)

Inverse of the coefficient matrix of the MME:

\[
C^{-1} = \begin{bmatrix}
C_{b,b} & C_{b,u} \\
C_{u,b} & C_{u,u}
\end{bmatrix}
= \begin{bmatrix}
X' R^{-1} X & X' R^{-1} Z \\
Z' R^{-1} X & Z' R^{-1} Z + V_u^{-1}
\end{bmatrix}^{-1}
\]

AM-BLUP: \( V_u^{-1} = \frac{1}{\sigma_u^2} A^{-1} \)

ssGBLUP: \( V_u^{-1} = \frac{1}{\sigma_u^2} \left[ A^{-1} + \begin{bmatrix}
0 & 0 \\
0 & G^{-1} - (A_{22})^{-1}
\end{bmatrix} \right] \)

where

- \( A = \) pedigree based relationship matrix
- \( G = \) genomic relationship matrix
- \( A_{22} = \) pedigree based relationships of genotyped animals

Reliability for animal \( i \):

\[
r_i^2 = 1 - \frac{\{C_{u,u}\}_i}{\sigma_u^2}
\]

where \( \{C_{u,u}\}_i \) is diagonal element corresponding to animal \( i \).
Model reliability: \( y = Xb + Zu + e \)

Inverse of the coefficient matrix of the MME:

\[
C^{-1} = \begin{bmatrix}
C^{b,b} & C^{b,u} \\
C^{u,b} & C^{u,u}
\end{bmatrix} = \begin{bmatrix}
X'R^{-1}X & X'R^{-1}Z \\
Z'R^{-1}X & Z'R^{-1}Z + V_u^{-1}
\end{bmatrix}^{-1}
\]

AM-BLUP: \( V_u^{-1} = \frac{1}{\sigma_u^2} A^{-1} \)

ssGBLUP: \( V_u^{-1} = \frac{1}{\sigma_u^2} \left[ A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G^{-1} - (A_{22})^{-1} \end{bmatrix} \right] \)

where

- \( A = \) pedigree based relationship matrix
- \( G = \) genomic relationship matrix
- \( A_{22} = \) pedigree based relationships of genotyped animals

**Reliability for animal** \( i \):

\[
r_i^2 = 1 - \frac{\{C^{u,u}\}_i}{\sigma_u^2}
\]

where \( \{C^{u,u}\}_i \) is diagonal element corresponding animal \( i \).
Steps in bivariate blending bbGBLUP

- **Step 1:** get reliabilities from AM-BLUP \( \Rightarrow r^2_{EBV} \)

- **Step 2:** reliability increase due to genotypes
  - \( EDC^2 \) for all genotyped animals:
    - bull EDC based on non-genotyped daughters
    - cow EDC is \( \sigma^2_e r^2_o / \sigma^2_e (1 - r^2_o) \) where \( r^2_o = \) individual Interbull reliability
  - get reliabilities from GBLUP \( \Rightarrow r^2_{DGV} \)
  - use EDC from as weight in GBLUP
  - calculate relative increase in evaluation accuracy due to GBLUP for genotyped animals:
    \[
    EDC_G = \frac{r^2_{DGV}}{1 - r^2_{DGV}} - \frac{r^2_{EBV}}{1 - r^2_{EBV}}
    \]
  - calculate accuracy of added value due to DGV:
    \[
    r_a = \sqrt{1 - \frac{1}{EDC_G + 1}}
    \]

\(^2\)Effective Daughter Contribution
Steps in bivariate blending bbGBLUP

- **Step 1**: get reliabilities from AM-BLUP ⇒ \( r_{EBV}^2 \)
- **Step 2**: **reliability increase** due to genotypes
  - EDC\(^2\) for all genotyped animals:
    - bull EDC based on non-genotyped daughters
    - cow EDC is \( \frac{\sigma_e^2 r_o^2}{\sigma_u^2 (1-r_o^2)} \) where \( r_o^2 = \) individual Interbull reliability
  - get reliabilities from GBLUP ⇒ \( r_{DGV}^2 \)
    - use EDC from as weight in GBLUP
  - calculate **relative increase in evaluation accuracy** due to GBLUP for genotyped animals:
    \[
    EDC_G = \frac{r_{DGV}^2}{1 - r_{DGV}^2} - \frac{r_{EBV}^2}{1 - r_{EBV}^2}
    \]
  - calculate accuracy of added value due to DGV:
    \[
    r_a = \sqrt{1 - \frac{1}{EDC_G + 1}}
    \]

\(^2\)Effective Daughter Contribution
Steps in bivariate blending bbGBLUP

• **Step 1**: get reliabilities from AM-BLUP ⇒ $r^2_{EBV}$

• **Step 2**: **reliability increase** due to genotypes
  
  • $EDC^2$ for all genotyped animals:
    - bull EDC based on non-genotyped daughters
    - cow EDC is $\frac{\sigma^2_e r^2_o}{\sigma^2_o (1 - r^2_o)}$ where $r^2_o = $ individual Interbull reliability

  • get reliabilities from GBLUP ⇒ $r^2_{DGV}$
  
  • use EDC from as weight in GBLUP

• calculate **relative increase in evaluation accuracy** due to GBLUP for genotyped animals:

  \[ EDC_G = \frac{r^2_{DGV}}{1 - r^2_{DGV}} - \frac{r^2_{EBV}}{1 - r^2_{EBV}} \]

  • calculate accuracy of added value due to DGV:

  \[ r_a = \sqrt{1 - \frac{1}{EDC_G + 1}} \]

$^{2}$Effective Daughter Contribution
Steps in bivariate blending bbGBLUP

• **Step 1**: get reliabilities from AM-BLUP ⇒ $r_{EBV}^2$

• **Step 2**: reliability increase due to genotypes
  - EDC$^2$ for all genotyped animals:
    - bull EDC based on non-genotyped daughters
    - cow EDC is $\frac{\sigma_e^2 r_o^2}{\sigma_u^2 (1 - r_o^2)}$ where $r_o^2 =$ individual Interbull reliability

  - get reliabilities from GBLUP ⇒ $r_{DGV}^2$
    - use EDC from as weight in GBLUP

  - calculate relative increase in evaluation accuracy due to GBLUP for genotyped animals:
    \[
    \text{EDC}_G = \frac{r_{DGV}^2}{1 - r_{DGV}^2} - \frac{r_{EBV}^2}{1 - r_{EBV}^2}
    \]

  - calculate accuracy of added value due to DGV:
    \[
    r_a = \sqrt{1 - \frac{1}{\text{EDC}_G + 1}}
    \]

$^2$Effective Daughter Contribution
Steps in bivariate blending bbGBLUP

• **Step 1**: get reliabilities from AM-BLUP ⇒ $r^2_{EBV}$

• **Step 2**: **reliability increase** due to genotypes
  - $EDC^2$ for all genotyped animals:
    - bull $EDC$ based on non-genotyped daughters
    - cow $EDC$ is $\frac{\sigma^2_e r^2_o}{\sigma^2_g(1-r^2_o)}$ where $r^2_o$ = individual Interbull reliability
  - get reliabilities from GBLUP ⇒ $r^2_{DGV}$
    - use $EDC$ from as weight in GBLUP
  - calculate **relative increase in evaluation accuracy** due to GBLUP for genotyped animals:
    $$EDC_G = \frac{r^2_{DGV}}{1 - r^2_{DGV}} - \frac{r^2_{EBV}}{1 - r^2_{EBV}}$$

• calculate accuracy of added value due to DGV:
  $$r_a = \sqrt{1 - \frac{1}{EDC_G + 1}}$$

$^{2}$Effective Daughter Contribution
Steps in bivariate blending bbGBLUP

• **Step 1**: get reliabilities from AM-BLUP ⇒ $r_{EBV}^2$

• **Step 2**: **reliability increase** due to genotypes
  
  • EDC$^2$ for all genotyped animals:
    
    - bull EDC based on non-genotyped daughters
    - cow EDC is $\frac{\sigma_e^2 r_o^2}{\sigma_u^2 (1 - r_o^2)}$ where $r_o^2 =$ individual Interbull reliability
  
  • get reliabilities from GBLUP ⇒ $r_{DGV}^2$
    
    - use EDC from as weight in GBLUP
  
  • calculate **relative increase in evaluation accuracy** due to GBLUP for genotyped animals:
    
    $EDC_G = \frac{r_{DGV}^2}{1 - r_{DGV}^2} - \frac{r_{EBV}^2}{1 - r_{EBV}^2}$
  
  • calculate accuracy of added value due to DGV:
    
    $r_a = \sqrt{1 - \frac{1}{EDC_G + 1}}$

---

$^2$Effective Daughter Contribution
bbGBLUP continued

• **Step 3:**
  • bivariate blending model by **random regression** AM-BLUP:

\[ y = Xb + K_1 u_1 + K_2 u_2 + e \]

Solutions in \( u_1 \) have GEBV.

• Values in design matrices \( K \) and weights depend on type of the observation. When observation is:
  • same DRP as in AM-BLUP
    \[
    \begin{bmatrix}
    k_1 \\
    k_2
    \end{bmatrix} = \begin{bmatrix}
    1 \\
    0
    \end{bmatrix}, \text{ weights same as in AM-BLUP}
    \]
  • genomic estimate DGV from GBLUP:
    \[
    \begin{bmatrix}
    k_1 \\
    k_2
    \end{bmatrix} = \begin{bmatrix}
    \sqrt{r_a^2} \\
    \sqrt{1 - r_a^2}
    \end{bmatrix}, \text{ weights very large (1000)}
    \]

• Variances: \( \text{Var}(u_i) = \sigma^2 u A, i = 1, 2 \) where \( \sigma^2 u \) is from AM-BLUP.
bbGBLUP continued

- **Step 3:**
  - bivariate blending model by *random regression* AM-BLUP:
    
    \[
    y = Xb + K_1 u_1 + K_2 u_2 + e
    \]

    Solutions in \( u_1 \) have GEBV.
  - Values in design matrices \( K \) and weights depend on type of the observation. When observation is:
    - same DRP as in AM-BLUP
      \[
      \begin{bmatrix}
      k_1 \\
      k_2
      \end{bmatrix} = \begin{bmatrix} 1 & 0 \end{bmatrix}, \quad \text{weights same as in AM-BLUP}
      \]
    - genomic estimate DGV from GBLUP:
      \[
      \begin{bmatrix}
      k_1 \\
      k_2
      \end{bmatrix} = \begin{bmatrix} \sqrt{r_a^2} & \sqrt{1 - r_a^2} \end{bmatrix}, \quad \text{weights very large (1000)}
      \]
  - Variances: \( \text{Var}(u_i) = \sigma_u^2 A, i = 1, 2 \) where \( \sigma_u^2 \) is from AM-BLUP.
bbGBLUP continued

• **Step 3:**
  - bivariate blending model by *random regression* AM-BLUP:
    \[
    y = Xb + K_1 u_1 + K_2 u_2 + e
    \]

    Solutions in \( u_1 \) have GEBV.

  - Values in design matrices \( K \) and weights depend on type of the observation. When observation is:
    - same DRP as in AM-BLUP
      \[
      [ k_1 \quad k_2 ] = [ 1 \quad 0 ], \quad \text{weights same as in AM-BLUP}
      \]
    - genomic estimate DGV from GBLUP:
      \[
      [ k_1 \quad k_2 ] = \left[ \frac{\sqrt{r_a^2}}{\sqrt{1 - r_a^2}} \right], \quad \text{weights very large (1000)}
      \]

  - Variances: \( \text{Var} (u_i) = \sigma_u^2 A, i = 1, 2 \) where \( \sigma_u^2 \) is from AM-BLUP.
bbGBLUP continued

• **Step 3:**
  • bivariate blending model by **random regression** AM-BLUP:
    \[ y = Xb + K_1 u_1 + K_2 u_2 + e \]

  Solutions in \( u_1 \) have GEBV.

  • Values in design matrices \( K \) and weights depend on type of the observation. When observation is:
    • same DRP as in AM-BLUP
      \[
      \begin{bmatrix}
      k_1 \\
      k_2 
      \end{bmatrix} =
      \begin{bmatrix}
      1 \\
      0 
      \end{bmatrix}, \quad \text{weights same as in AM-BLUP}
      \]
    • genomic estimate DGV from GBLUP:
      \[
      \begin{bmatrix}
      k_1 \\
      k_2 
      \end{bmatrix} =
      \begin{bmatrix}
      \sqrt{r_a^2} \\
      \sqrt{1 - r_a^2} 
      \end{bmatrix}, \quad \text{weights very large (1000)}
      \]

  • Variances: \( \text{Var}(u_i) = \sigma_U^2 A, i = 1, 2 \) where \( \sigma_U^2 \) is from AM-BLUP.
bbGBLUP continued

- **Step 3:**
  - bivariate blending model by *random regression* AM-BLUP:
    \[ y = Xb + K_1 u_1 + K_2 u_2 + e \]
  
  Solutions in \( u_1 \) have GEBV.

- **Values in design matrices** \( K \) and weights depend on type of the observation. When observation is:
  - same DRP as in AM-BLUP
    \[ \begin{bmatrix} k_1 \\ k_2 \end{bmatrix} = \begin{bmatrix} 1 \\ 0 \end{bmatrix}, \text{ weights same as in AM-BLUP} \]
  - genomic estimate DGV from GBLUP:
    \[ \begin{bmatrix} k_1 \\ k_2 \end{bmatrix} = \begin{bmatrix} \sqrt{r_a^2} \\ \sqrt{1 - r_a^2} \end{bmatrix}, \text{ weights very large (1000)} \]

- **Variances:** \( \text{Var}(u_i) = \sigma^2_u A, i = 1, 2 \) where \( \sigma^2_u \) is from AM-BLUP.
Data

- Study data was extracted from the **production trait evaluation** of Nordic Red dairy cattle
- For simplicity **deregressed proofs** (DRP) were assumed
- NOTE: actual phenotypic data (DRP) were not used! Only the EDCs and pedigree
- We assumed $h^2 = 0.50$
- **Genotype information**: after edits, 38194 SNPs from BovineSNP50
Data

• Study data was extracted from the production trait evaluation of Nordic Red dairy cattle

• For simplicity deregressed proofs (DRP) were assumed
• NOTE: actual phenotypic data (DRP) were not used! Only the EDCs and pedigree

• We assumed $h^2 = 0.50$

• Genotype information: after edits, 38194 SNPs from BovineSNP50
Study data was extracted from the production trait evaluation of Nordic Red dairy cattle.

For simplicity, deregressed proofs (DRP) were assumed.

NOTE: actual phenotypic data (DRP) were not used! Only the EDCs and pedigree.

We assumed $h^2 = 0.50$

Genotype information: after edits, 38194 SNPs from BovineSNP50.
Data

- Study data was extracted from the **production trait evaluation** of Nordic Red dairy cattle
- For simplicity **deregressed proofs** (DRP) were assumed
- NOTE: actual phenotypic data (DRP) were not used! Only the EDCs and pedigree
- We assumed $h^2 = 0.50$
- **Genotype information**: after edits, 38194 SNPs from BovineSNP50
Numbers

- **Genotyped animals:**
  - **Training** animals: genotyped bulls born 2001-2005
  - **Candidates**: genotyped animals born 2006-

- Number of training bulls (genotyped): 1055

- Daughters (w. records) to the training bulls were searched
  - “Best” 522 bulls: 40 daughters
  - “Average” 533 bulls: 10 daughters
  - Total number of daughters for these bulls 26060

- Number of candidate animals (genotyped): 1830
  - 607 candidate bulls
  - 1223 candidate cows w. records

- Pedigree for all above animals were traced but limited to 2 generations → **73579** animals in AM-BLUP
  - From which 67648 cows with records
Numbers

• Genotyped animals:
  • **Training** animals: genotyped bulls born 2001-2005
  • **Candidates**: genotyped animals born 2006-

• Number of **training bulls** (genotyped): **1055**
  • Daughters (w. records) to the training bulls were searched
    • “Best” 522 bulls: 40 daughters
    • “Average” 533 bulls: 10 daughters
    • Total number of daughters for these bulls 26060

• Number of candidate animals (genotyped): **1830**
  • 607 candidate bulls
  • 1223 candidate cows w. records

• Pedigree for all above animals were traced but limited to 2 generations → **73579** animals in AM-BLUP
  • From which 67648 cows with records
Numbers

- Genotyped animals:
  - Training animals: genotyped bulls born 2001-2005
  - Candidates: genotyped animals born 2006-

- Number of training bulls (genotyped): 1055

- Daughters (w. records) to the training bulls were searched
  - “Best” 522 bulls: 40 daughters
  - “Average” 533 bulls: 10 daughters
  - Total number of daughters for these bulls 26060

- Number of candidate animals (genotyped): 1830
  - 607 candidate bulls
  - 1223 candidate cows w. records

- Pedigree for all above animals were traced but limited to 2 generations → 73579 animals in AM-BLUP
  - From which 67648 cows with records
Numbers

• Genotyped animals:
  • Training animals: genotyped bulls born 2001-2005
  • Candidates: genotyped animals born 2006-

• Number of training bulls (genotyped): 1055

• Daughters (w. records) to the training bulls were searched
  • “Best” 522 bulls: 40 daughters
  • “Average” 533 bulls: 10 daughters
  • Total number of daughters for these bulls 26060

• Number of candidate animals (genotyped): 1830
  • 607 candidate bulls
  • 1223 candidate cows w. records

• Pedigree for all above animals were traced but limited to 2 generations → 73579 animals in AM-BLUP
  • From which 67648 cows with records
**Numbers**

- **Genotyped animals:**
  - *Training* animals: genotyped bulls born 2001-2005
  - *Candidates*: genotyped animals born 2006-

- Number of *training bulls* (genotyped): 1055

- Daughters (w. records) to the training bulls were searched
  - “Best” 522 bulls: 40 daughters
  - “Average” 533 bulls: 10 daughters
  - Total number of daughters for these bulls 26060

- Number of candidate animals (genotyped): 1830
  - 607 candidate bulls
  - 1223 candidate cows w. records

- Pedigree for all above animals were traced but limited to 2 generations → **73579** animals in AM-BLUP
  - From which 67648 cows with records
Summary of Setup

• Three **methods**:  
  • Animal model  
  • Single-step  
  • Bivariate blending

• Five **animal groups** examined:  
  • Genotyped:  
    • Training bulls  
    • Candidate bulls  
    • Candidate cows  
  • Non-genotyped: (not interested, skipped)  
    • bulls  
    • cows

• Comparing **reliabilities**
Summary of Setup

• Three **methods**:  
  • Animal model  
  • Single-step  
  • Bivariate blending

• Five **animal groups** examined:  
  • Genotyped:  
    • Training bulls  
    • Candidate bulls  
    • Candidate cows  
  • Non-genotyped: (not interested, skipped)  
    • bulls  
    • cows

• Comparing **reliabilities**
Summary of Setup

• Three **methods**:  
  - Animal model  
  - Single-step  
  - Bivariate blending

• Five **animal groups** examined:  
  - Genotyped:  
    - Training bulls  
    - Candidate bulls  
    - Candidate cows  
  - Non-genotyped: (not interested, skipped)  
    - bulls  
    - cows

• Comparing **reliabilities**
Results: Animal model vs. Single-step

- **X-axis:** reliability of Animal model for each animal
- **Y-axis:** reliability of Single-step for each animal
- Dots on diagonal: no difference in reliabilities.
- Training bulls: about the same reliabilities.
- Candidate cows: Single-step reliabilities are higher.
- Candidate bulls:
  - Single-step reliabilities are clearly higher.
  - Cows have observations ⇒ reliabilities higher.

Training bulls

 mean(Y-X) Corr

0.02 0.99

X-axis: reliability of Animal model for each animal
Y-axis: reliability of Single-step for each animal
Dots on diagonal: no difference in reliabilities.
Training bulls: about the same reliabilities.
Candidate cows: Single-step reliabilities are higher.
Candidate bulls:
  - Single-step reliabilities are clearly higher.
  - Cows have observations ⇒ reliabilities higher.
Results: Animal model vs. Single-step

- **X-axis**: reliability of Animal model for each animal
- **Y-axis**: reliability of Single-step for each animal
- Dots on diagonal: no difference in reliabilities.
- Training bulls: about the same reliabilities.
- Candidate cows: Single-step reliabilities are higher.
- Candidate bulls:
  - Single-step reliabilities are clearly higher.
  - Cows have observations ⇒ reliabilities higher.
Results: Animal model vs. Single-step

- X-axis: reliability of Animal model for each animal
- Y-axis: reliability of Single-step for each animal
- Dots on diagonal: no difference in reliabilities.
- Training bulls: about the same reliabilities.
- Candidate cows: Single-step reliabilities are higher.
- Candidate bulls:
  - Single-step reliabilities are clearly higher.
  - Cows have observations ⇒ reliabilities higher.
Results: Animal model vs. Single-step

- **X-axis**: reliability of Animal model for each animal
- **Y-axis**: reliability of Single-step for each animal
- Dots on **diagonal**: no difference in reliabilities.
- Training bulls: about the same reliabilities.
- Candidate cows: Single-step reliabilities are higher.
- Candidate bulls:
  - Single-step reliabilities are clearly higher.
  - Cows have observations ⇒ reliabilities higher.
Results: Animal model vs. Bivariate blending

- Now: **Y-axis** has reliabilities of **Bivariate blending**
- Bivariate blending reliabilities are also higher than Animal model
Results: Animal model vs. Bivariate blending

- Now: Y-axis has reliabilities of Bivariate blending
- Bivariate blending reliabilities are also higher than Animal model
Results: Animal model vs. Bivariate blending

- Now: Y-axis has reliabilities of Bivariate blending
- Bivariate blending reliabilities are also higher than Animal model
Results: Single-step vs. Bivariate blending

- Now: comparing **Single-step** (X-axis) and **Bivariate blending** (Y-axis)

- Bivariate blending reliabilities are **lower** than Single-step
Results: Single-step vs. Bivariate blending

- Now: comparing **Single-step** (X-axis) and **Bivariate blending** (Y-axis)

- Bivariate blending reliabilities are **lower** than Single-step
Results: Single-step vs. Bivariate blending

- Now: comparing Single-step (X-axis) and Bivariate blending (Y-axis)

- Bivariate blending reliabilities are lower than Single-step
Conclusions

• Bivariate blending was computationally **lighter** than Single-step in reliability calculation due to better **sparsity** — and can use standard software used for AM-BLUP

• Genomic reliabilities in single-step GBLUP **increased** — due to genomic information
  • also in bivariate blending

• In general bivariate blending reliability estimates were **lower** than single-step

• Bivariate blending **avoided double counting** of relationship information ⇒ uses less information
Conclusions

• Bivariate blending was computationally **lighter** than Single-step in reliability calculation due to better **sparsity** — and can use standard software used for AM-BLUP

• Genomic reliabilities in single-step GBLUP **increased** — due to genomic information
  • also in bivariate blending

• In general bivariate blending reliability estimates were **lower** than single-step

• Bivariate blending **avoided double counting** of relationship information ⇒ uses less information
Conclusions

• Bivariate blending was computationally **lighter** than Single-step in reliability calculation due to better **sparsity** — and can use standard software used for AM-BLUP

• Genomic reliabilities in single-step GBLUP **increased** — due to genomic information
  • also in bivariate blending

• In general bivariate blending reliability estimates were **lower** than single-step

• Bivariate blending **avoided double counting** of relationship information ⇒ uses less information
Conclusions

• Bivariate blending was computationally lighter than Single-step in reliability calculation due to better sparsity — and can use standard software used for AM-BLUP

• Genomic reliabilities in single-step GBLUP increased — due to genomic information
  • also in bivariate blending

• In general bivariate blending reliability estimates were lower than single-step

• Bivariate blending avoided double counting of relationship information ⇒ uses less information
Conclusions

• Bivariate blending was computationally lighter than Single-step in reliability calculation due to better sparsity — and can use standard software used for AM-BLUP

• Genomic reliabilities in single-step GBLUP increased — due to genomic information
  • also in bivariate blending

• In general bivariate blending reliability estimates were lower than single-step

• Bivariate blending avoided double counting of relationship information ⇒ uses less information
Acknowledgements

- Nordic genomic selection project (VikingGenetics, Aarhus University, NAV, FABA, Svensk Mjölk (Växa Sverige)) provided the genotypes
- NAV and FABA provided the data