STØTTET AF mælkeafgiftsfonden

Link til European Agricultural Fund for Rural Development

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

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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

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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 revisited 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)

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[1] Direct genomic value

Model reliability: $\mathbf{y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$

Inverse of the coefficient matrix of the MME:

$$\mathbf{C}^{-1} = \begin{bmatrix} \mathbf{C}^{b,b} & \mathbf{C}^{b,u} \\ \mathbf{C}^{u,b} & \mathbf{C}^{u,u} \end{bmatrix} = \begin{bmatrix} \mathbf{X}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{X}'\mathbf{R}^{-1}\mathbf{Z} \\ \mathbf{Z}'\mathbf{R}^{-1}\mathbf{X} & \mathbf{Z}'\mathbf{R}^{-1}\mathbf{Z} + \mathbf{V}_u^{-1} \end{bmatrix}^{-1}$$

AM-BLUP: $\mathbf{V}_u^{-1} = \frac{1}{\sigma_u^2}\mathbf{A}^{-1}$

ssGBLUP: $\mathbf{V}_u^{-1} = \frac{1}{\sigma_u^2}\left[\mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}^{-1} - (\mathbf{A}_{22})^{-1} \end{bmatrix}\right]$

where

- $\mathbf{A}$= pedigree based relationship matrix
- $\mathbf{G}$= genomic relationship matrix
- $\mathbf{A}_{22}$= pedigree based relationships of genotyped animals

Reliability for animal *i*:

$$r_i^2 = 1 - \frac{\{\mathbf{C}^{u,u}\}_i}{\sigma_u^2}$$

where $\{\mathbf{C}^{u,u}\}_i$ is diagonal element corresponding animal *i*.

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Steps in bivariate blending bbGBLUP

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

$$\mathrm{EDC}_G = \frac{r^2_{DGV}}{1-r^2_{DGV}} - \frac{r^2_{EBV}}{1-r^2_{EBV}}$$

  - calculate accuracy of added value due to DGV:

$$r_a = \sqrt{1 - \frac{1}{\mathrm{EDC}_G + 1}}$$

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

    $$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{K}_1\mathbf{u}_1 + \mathbf{K}_2\mathbf{u}_2 + \mathbf{e}$$

    Solutions in $\mathbf{u}_1$ 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: $\mathrm{Var}(\mathbf{u}_i) = \sigma_u^2\mathbf{A}, i = 1,2$ where σ_u^2 is from AM-BLUP.

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- 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

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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

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- Three **methods**:
  - Animal model
  - Single-step
  - Bivariate blending
- Five **animal groups** examined:
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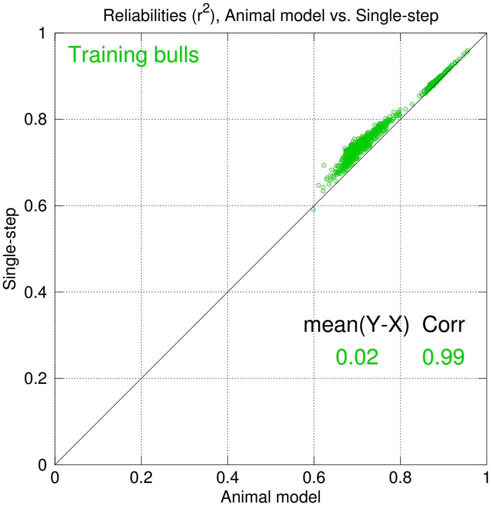
Results: Animal model vs. Single-step



- **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.
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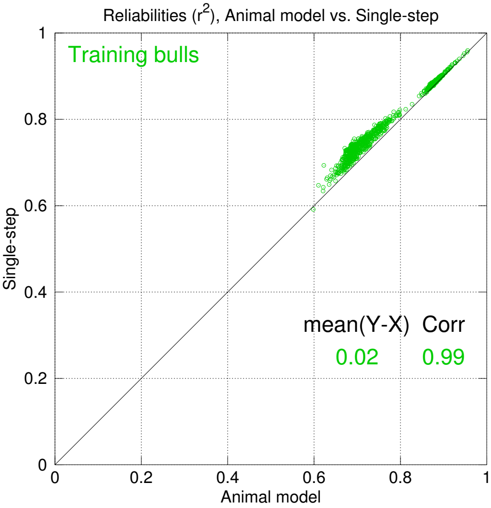

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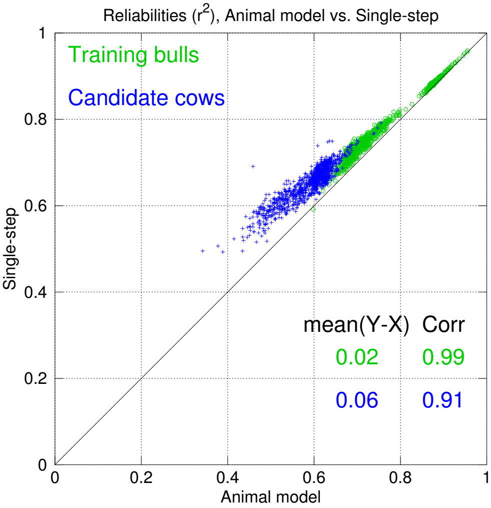

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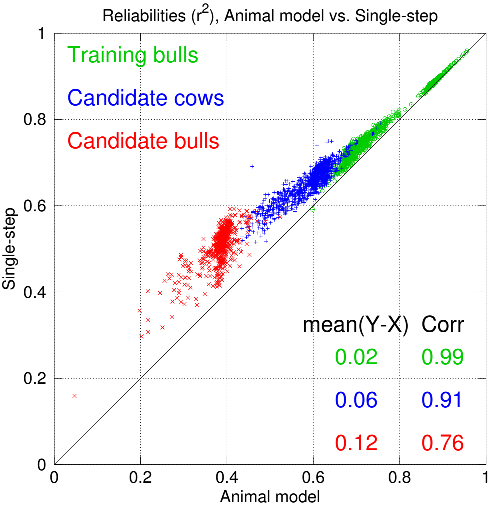

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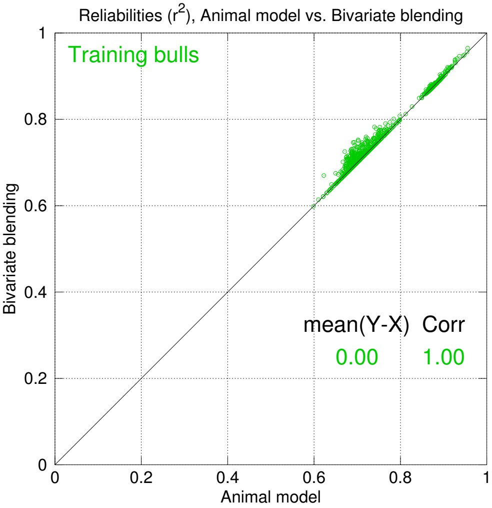
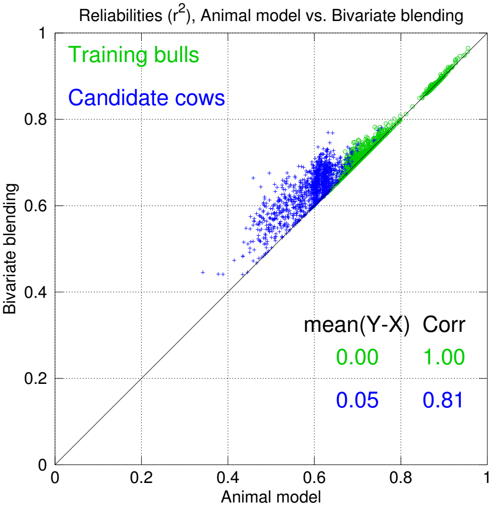


- Now: **Y-axis** has reliabilities of **Bivariate blending**
- Bivariate blending reliabilities are also **higher** than Animal model

Results: Animal model vs. Bivariate blending



- Now: **Y-axis** has reliabilities of **Bivariate blending**
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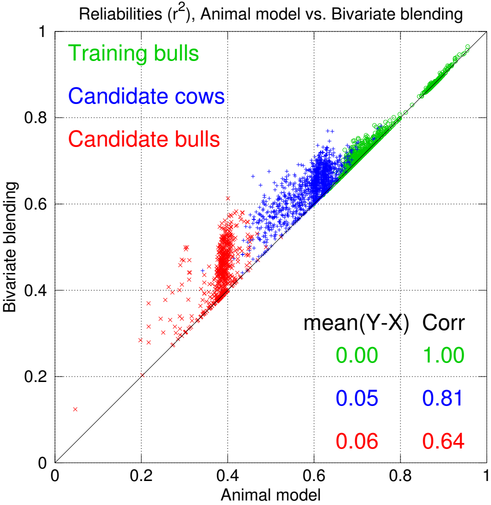

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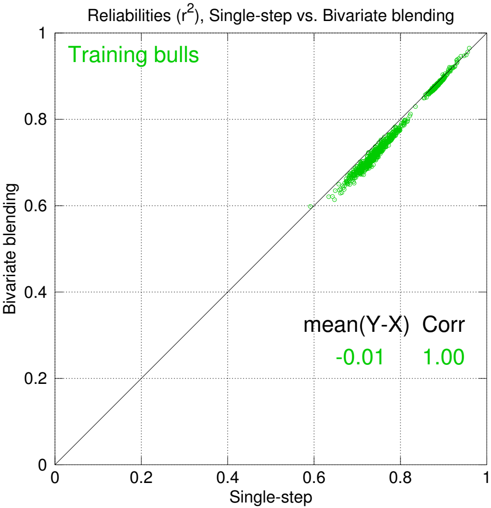
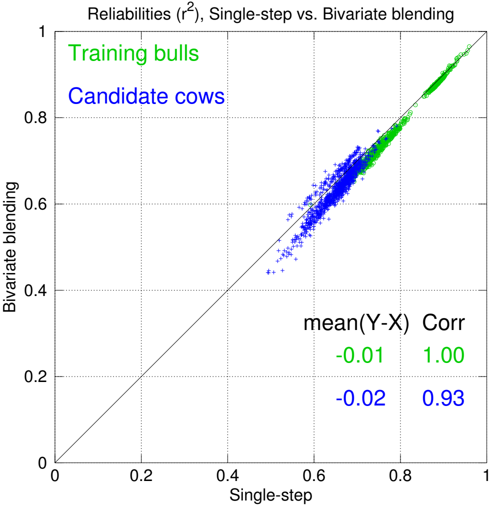
Results: Single-step vs. Bivariate blending



- 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



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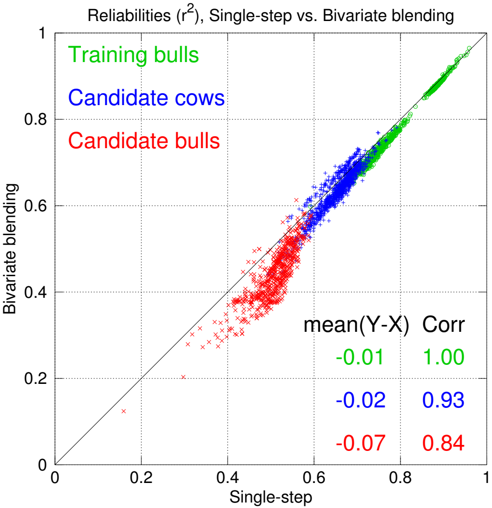

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- Genomic reliabilities in single-step GBLUP **increased** — due to genomic information
  - also in bivariate blending
- In general bivariate blending reliability estimates were **lower** than single-step
- Bivariate blending **avoided double counting** of relationship information ⇒ uses less information

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Acknowledgements

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