



STØTTET AF
mælkeafgiftsfonden



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

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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
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Estimation of reliability for single-step model

- Nordic genomic evaluations: DGV¹ 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)

¹Direct genomic value

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

Inverse of the coefficient matrix of the MME:

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

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

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

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_{EBV}^2
- **Step 2: reliability increase** due to genotypes
 - EDC for all genotyped animals:
 - bull EDC based on non-genotyped daughters
 - cow EDC is $\frac{\sigma_a^2 r_a^2}{\sigma_a^2(1-r_a^2)}$ where r_a^2 = individual Interbull reliability
 - get reliabilities from GBLUP: r_{DGV}^2
 - use EDC from step 2. 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:

$$r_a = \sqrt{1 - \frac{1}{EDC_G + 1}}$$

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bbGBLUP continued

- **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 $\mathbf{K}$ 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: $\text{Var}(\mathbf{u}_i) = \sigma_u^2 \mathbf{A}, i = 1, 2$ where σ_u^2 is from AM-BLUP.

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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 $h^2 = 0.50$
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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
- Pedigree for all above animals were traced but limited to 2 generations → **73579** animals in AM-BLUP
 - From which 67648 cows with records

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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**

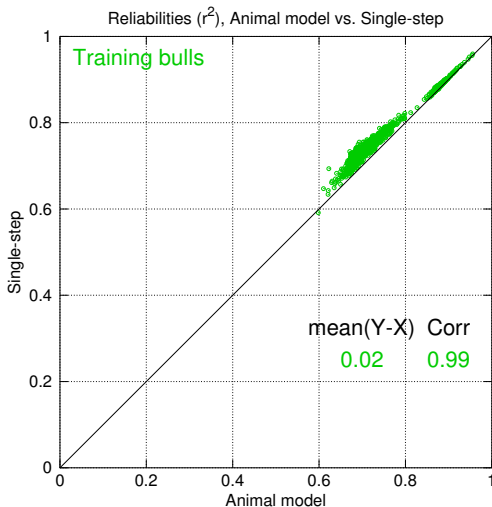
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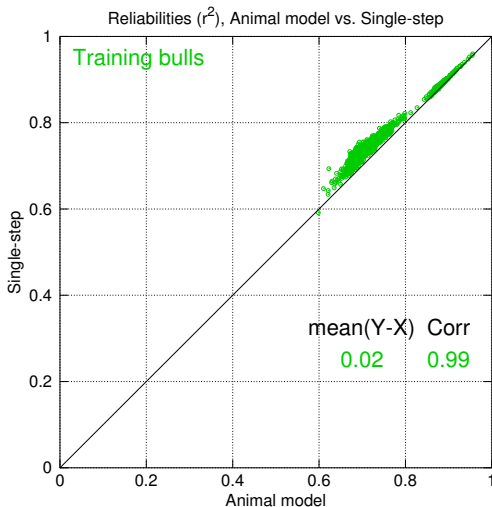
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Results: Animal model vs. Single-step



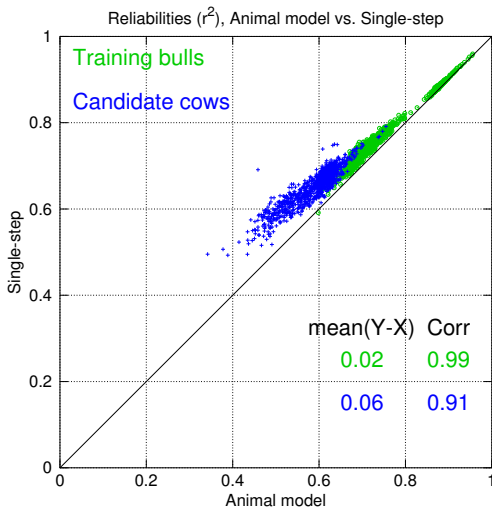
- **X-axis:** reliability of **Animal model** for each animal
- **Y-axis:** reliability of **Single-step** for each animal
- Dots on **diagonal**: no difference in reliabilities.
- **Training bulls**: about the same reliabilities.
- **Candidate cows**: Single-step reliabilities are higher.
- **Candidate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

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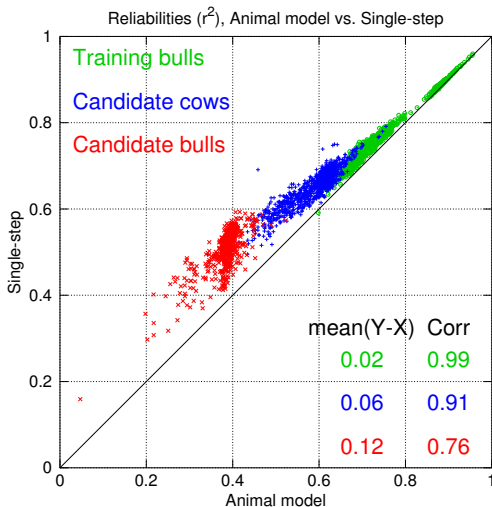
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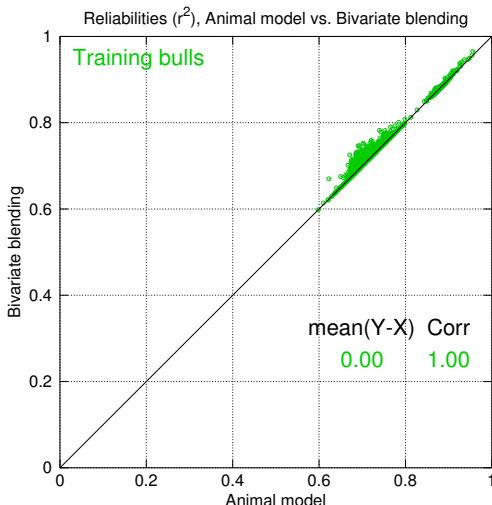
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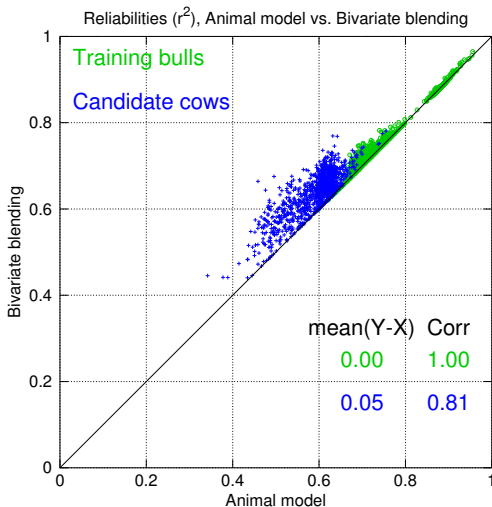
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Results: Animal model vs. Bivariate blending



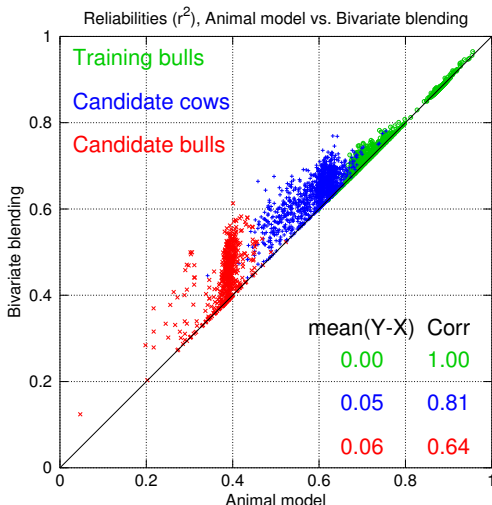
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- Bivariate blending reliabilities are also **higher** than Animal model

Results: Animal model vs. Bivariate blending



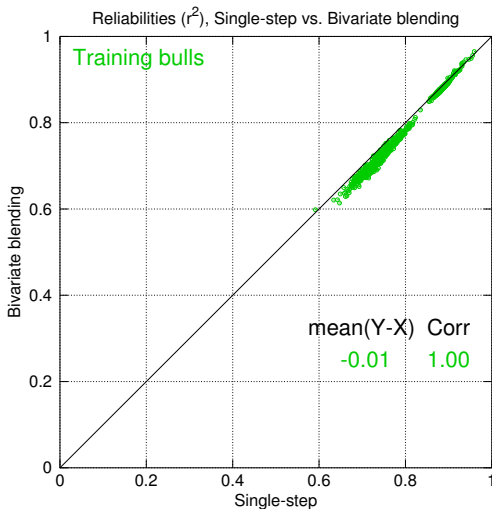
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Results: Animal model vs. Bivariate blending



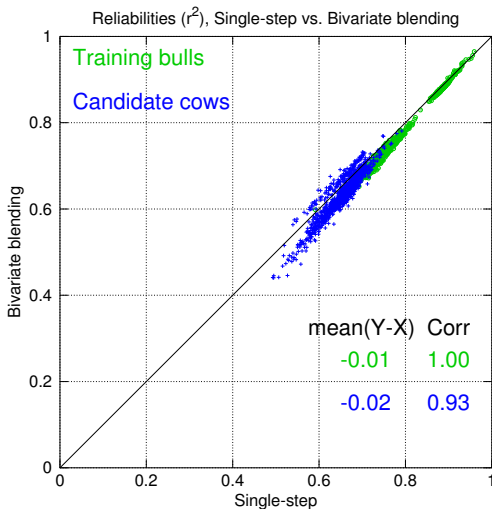
- Now: **Y-axis** has reliabilities of **Bivariate blending**
- Bivariate blending reliabilities are also **higher** than Animal model

Results: Single-step vs. Bivariate blending



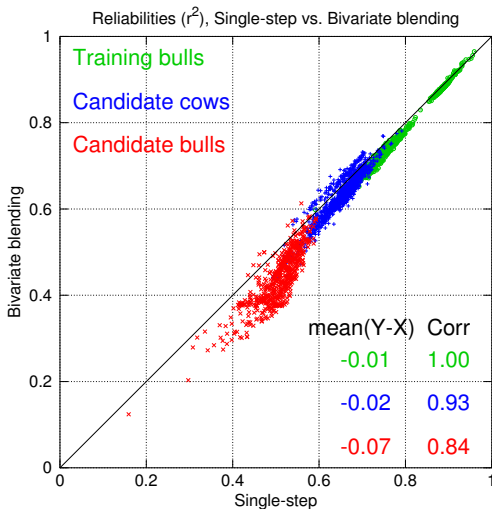
- Now: comparing **Single-step** (X-axis) and **Bivariate blending** (Y-axis)
- Bivariate blending reliabilities are **lower** than Single-step

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)
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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

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