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

Matti Taskinen[1]
Esa A. Mäntysaari[1]   Martin H. Lidauer[1]   Timo Knürr[1]
Jukka Pösö[2]   Guosheng Su[3]   Gert P. Aamand[4]
Ismo Strandén[1]

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

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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 **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)

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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:

$$\mathbf{C}^{-1} = \left[\begin{array}{cc} \mathbf{C}^{b,b} & \mathbf{C}^{b,u} \\ \mathbf{C}^{u,b} & \mathbf{C}^{u,u} \end{array} \right] = \left[\begin{array}{cc} \mathbf{X'R^{-1}X} & \mathbf{X'R^{-1}Z} \\ \mathbf{Z'R^{-1}X} & \mathbf{Z'R^{-1}Z} + \mathbf{V}_u^{-1} \end{array} \right]^{-1}$$

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

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

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 $\Rightarrow$ $\boxed{r^2_{EBV}}$

- **Step 2**: **reliability increase** due to genotypes

  - EDC^2 for all genotyped animals:
    - bull EDC based on non-genotyped daughters
    - cow EDC is $\frac{r^2_G \hat{\sigma}^2_a}{\sigma^2_e (1 - r^2_G)}$ where r^2_G = individual Interbull reliability

  - get reliabilities from GBLUP $\Rightarrow$ $\boxed{r^2_{DGV}}$
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  - 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:

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[2]Effective Daughter Contribution

bbGBLUP continued

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

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

  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

$$\begin{bmatrix} k_1 & k_2 \end{bmatrix} = \begin{bmatrix} 1 & 0 \end{bmatrix}, \quad \text{weights same as in AM-BLUP}$$

  - genomic estimate DGV from GBLUP:

$$\begin{bmatrix} k_1 & k_2 \end{bmatrix} = \begin{bmatrix} \sqrt{r_g^2} & \sqrt{1-r_g^2} \end{bmatrix} \quad \text{weights very large (1000)}$$

- 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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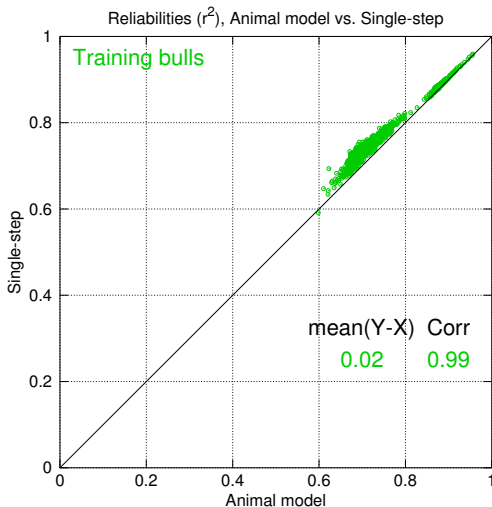 - From which 67648 cows with records
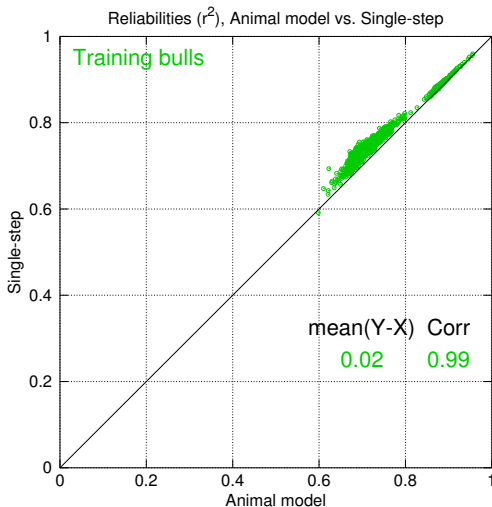
Summary of Setup

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  - Animal model
  - Single-step
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- Five **animal groups** examined:
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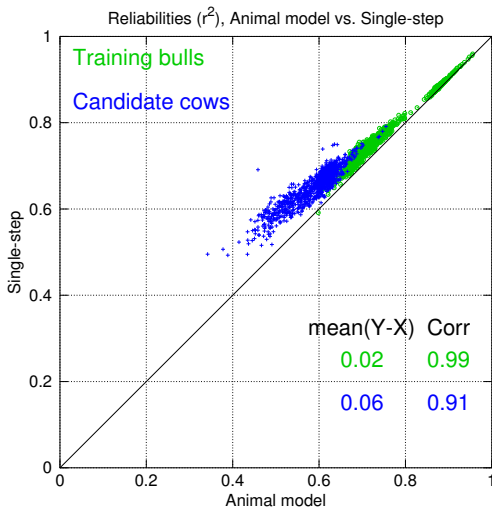
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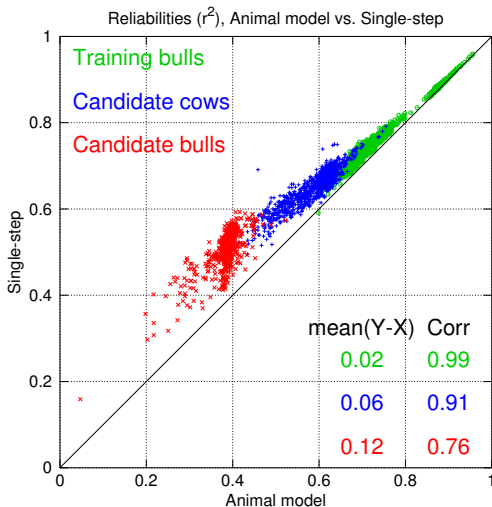
Training bulls

mean(Y-X): 0.02 Corr: 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.
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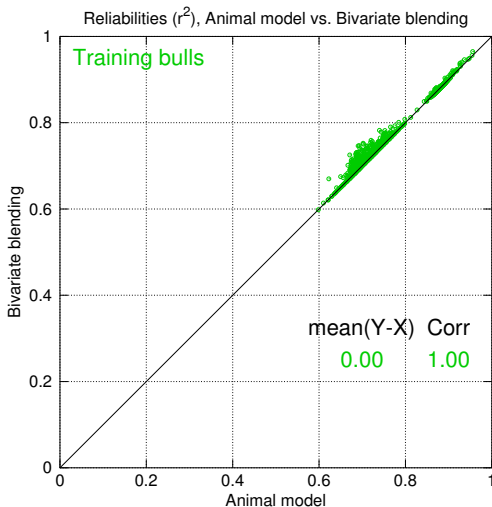

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Results: Animal model vs. Single-step

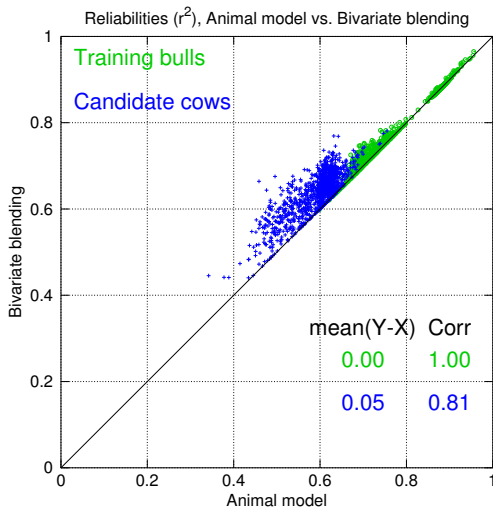Reliabilities (r^2), Animal model vs. Single-step

- **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.

	mean(Y-X)	Corr
	0.02	0.99
	0.06	0.91
	0.12	0.76

Results: Animal model vs. Bivariate blending

Reliabilities (r^2), Animal model vs. Bivariate blending

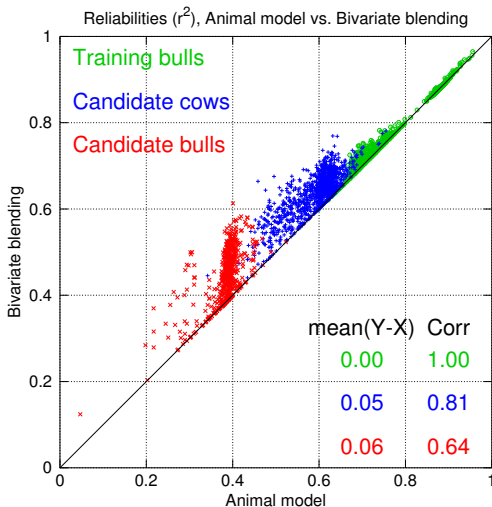Training bulls

mean(Y-X) Corr
0.00 1.00

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

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

Results: Animal model vs. Bivariate blending

Reliabilities (r^2), Animal model vs. Bivariate blending

Training bulls

Candidate cows

Bivariate blending

Animal model

| mean(Y-X)	Corr
0.00	1.00
0.05	0.81

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

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

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Results: Animal model vs. Bivariate blending

Reliabilities (r^2), Animal model vs. Bivariate blending
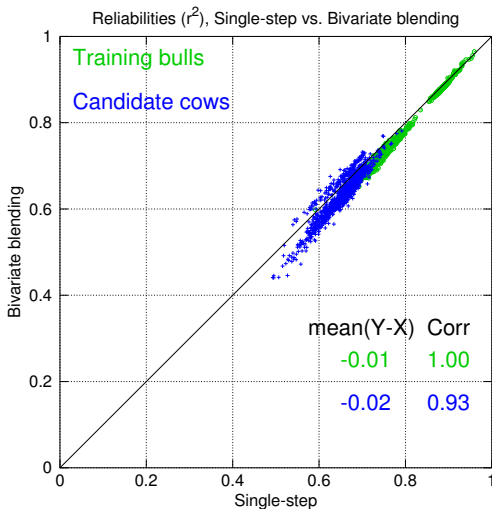
- Now: **Y-axis** has reliabilities of **Bivariate blending**

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Results: Single-step vs. Bivariate blending
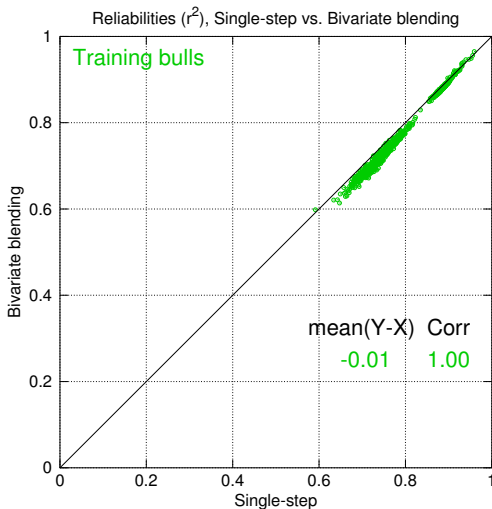
Reliabilities (r^2), Single-step vs. Bivariate blending

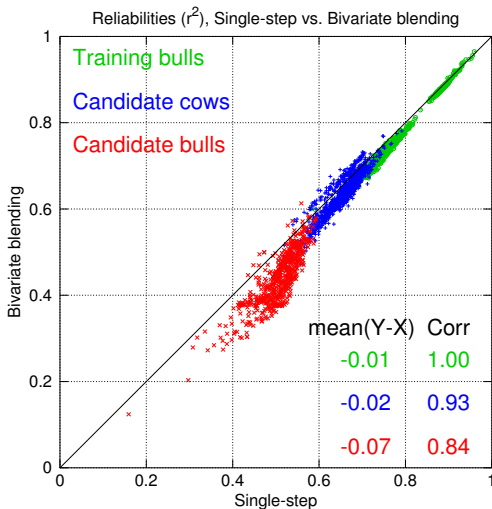Training bulls

mean(Y-X)   Corr
-0.01   1.00

- 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

Reliabilities (r^2), 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

Reliabilities (r^2), 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 $\Rightarrow$ uses less information

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