



Animal Breeding and Genetics Group
College of Agricultural & Environmental Sciences
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Efficient implementation of random regression models for dairy cattle genomic evaluations

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Introduction

- Random regression models (RRM) are used in many countries for longitudinal traits
- RRM with ssGBLUP are used worldwide for dairy cattle genetic evaluations

Challenges

- Solver convergence
- Approximating reliabilities
- Using external information



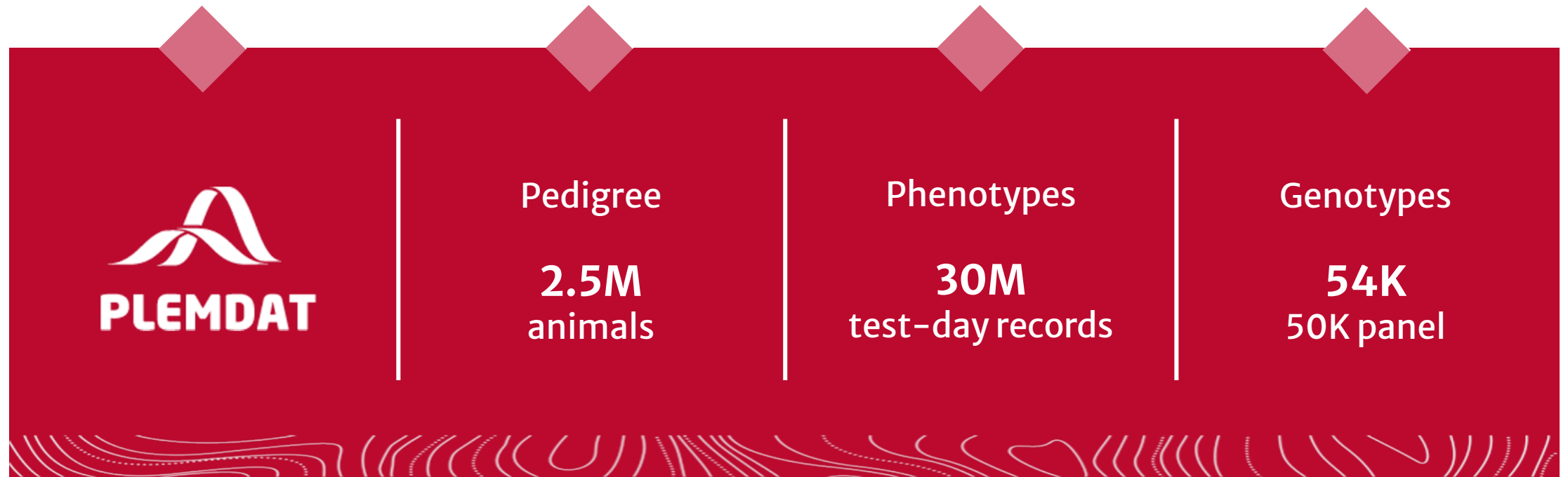
Objective

Improve the efficiency of implementing RRM with ssGBLUP for Czech national dairy evaluations using the BLUPF90 software suite and test a method to approximate reliabilities with genomic information



Data

Dairy data from Czechia for milk yield across three lactations



Model

$$y_{ijklm} = htd_{ik} + \sum_{m=0}^{nr} \phi_{ijlm} u_{ijm} + \sum_{m=0}^{nr} \phi_{ijlm} pe_{ijm} + e_{ijklm}$$

- Czech three lactation model for milk production with 4th order Legendre polynomials
- Effects:
 - Herd-year-season
 - Fixed regression for groups including:
Age in first lactation , Calving interval , Days open × Season
 - Additive and permanent environmental effect



Model

To improve the convergence of the model:

- 1 Use of a general mean
- 2 Redefinition of genetic groups
- 3 Random genetic groups
- 4 Algorithm for proven and young (APY)

PCG algorithm

64M equations

14K core animals

42 assigned UPG



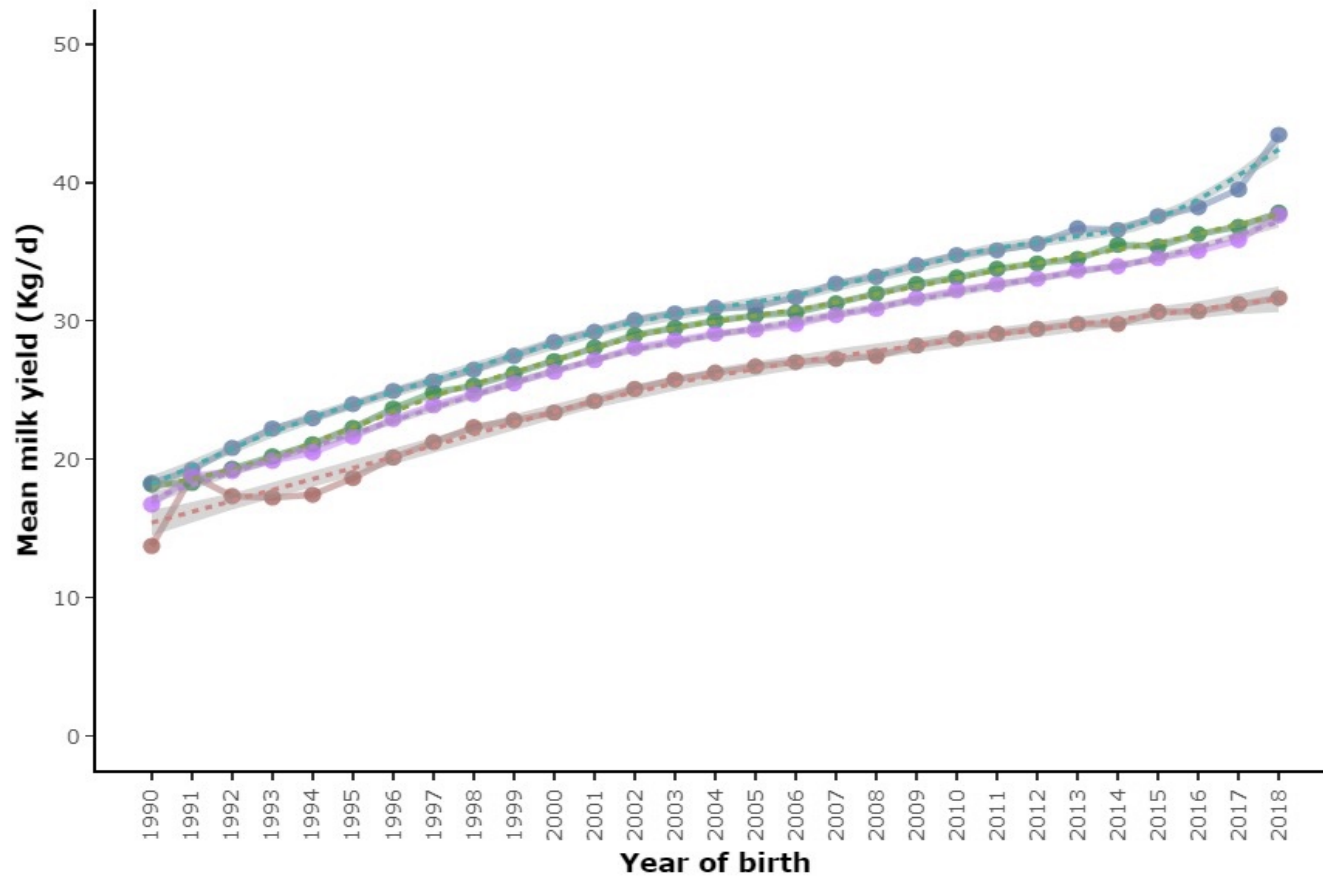
Approximation of reliabilities

Reliabilities of 305-day GEBV (Bermann *et al.*, 2024)



- Weighted average: Cumulative 305d GEBV without genomic information
- ssGBLUP model: Reliability in terms of ERC

Phenotypic trend



31.65 Kg

Lactation 1

37.85 Kg

Lactation 2

43.44 Kg

Lactation 3

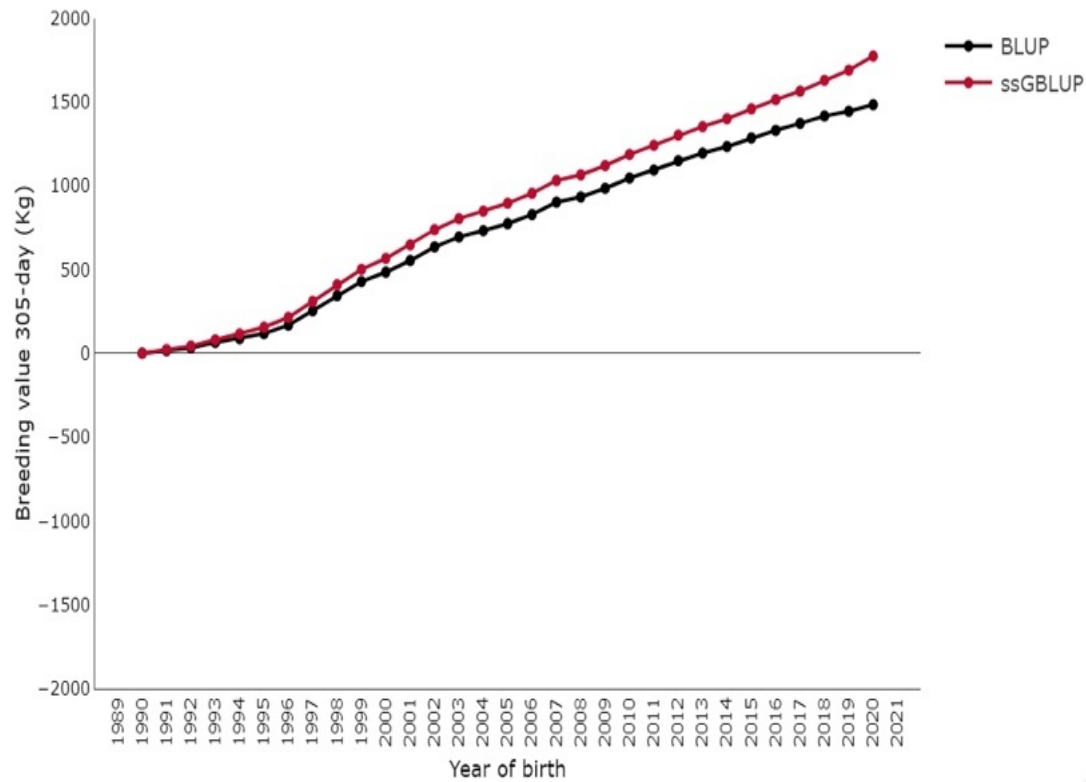
37.64 Kg

Average

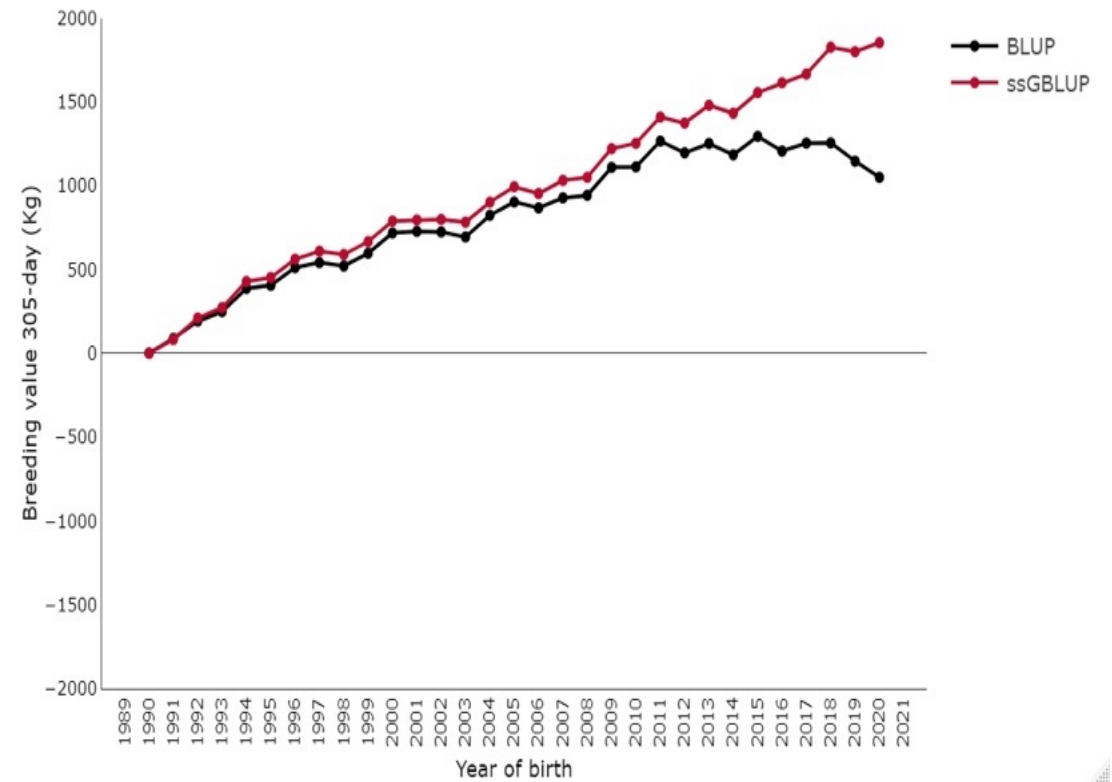


Genetic trends

Cows with phenotypes

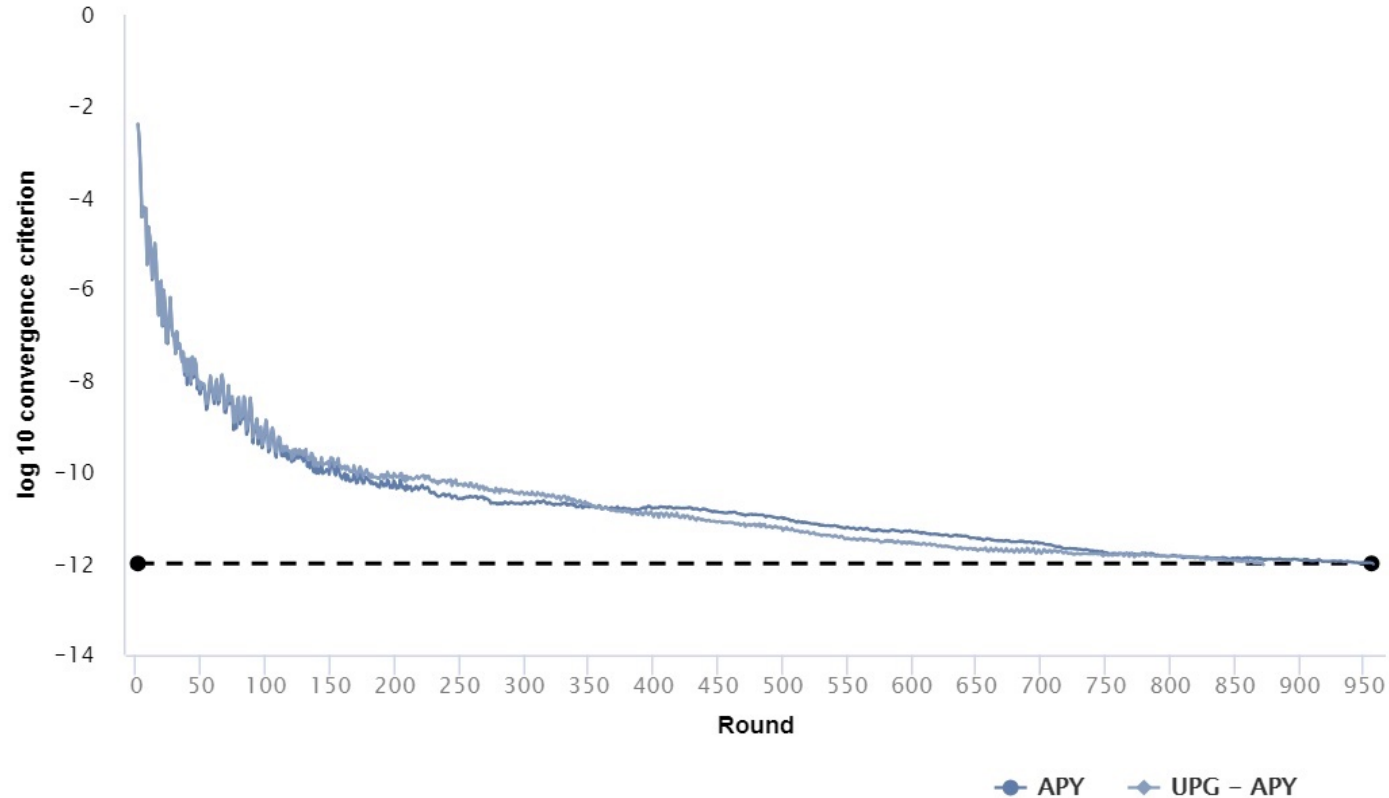


Genotyped bulls



Convergence

All models converged successfully after implementing the strategies



ssGBLUP with APY

1.88 days

~~UPG-ssGBLUP~~
1208 rounds

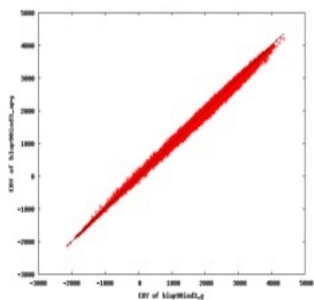
2.07 days

~~UPG-APYBLUP~~
1246 rounds

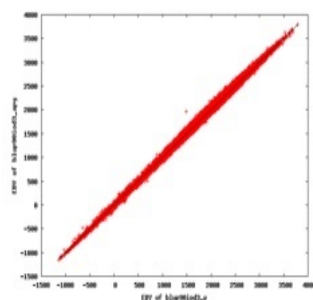
Convergence

Computing time with APY was 4.76 h, ten-fold faster than without it

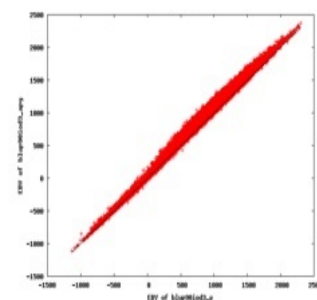
Correlation between GEBV with and without APY was 0.99



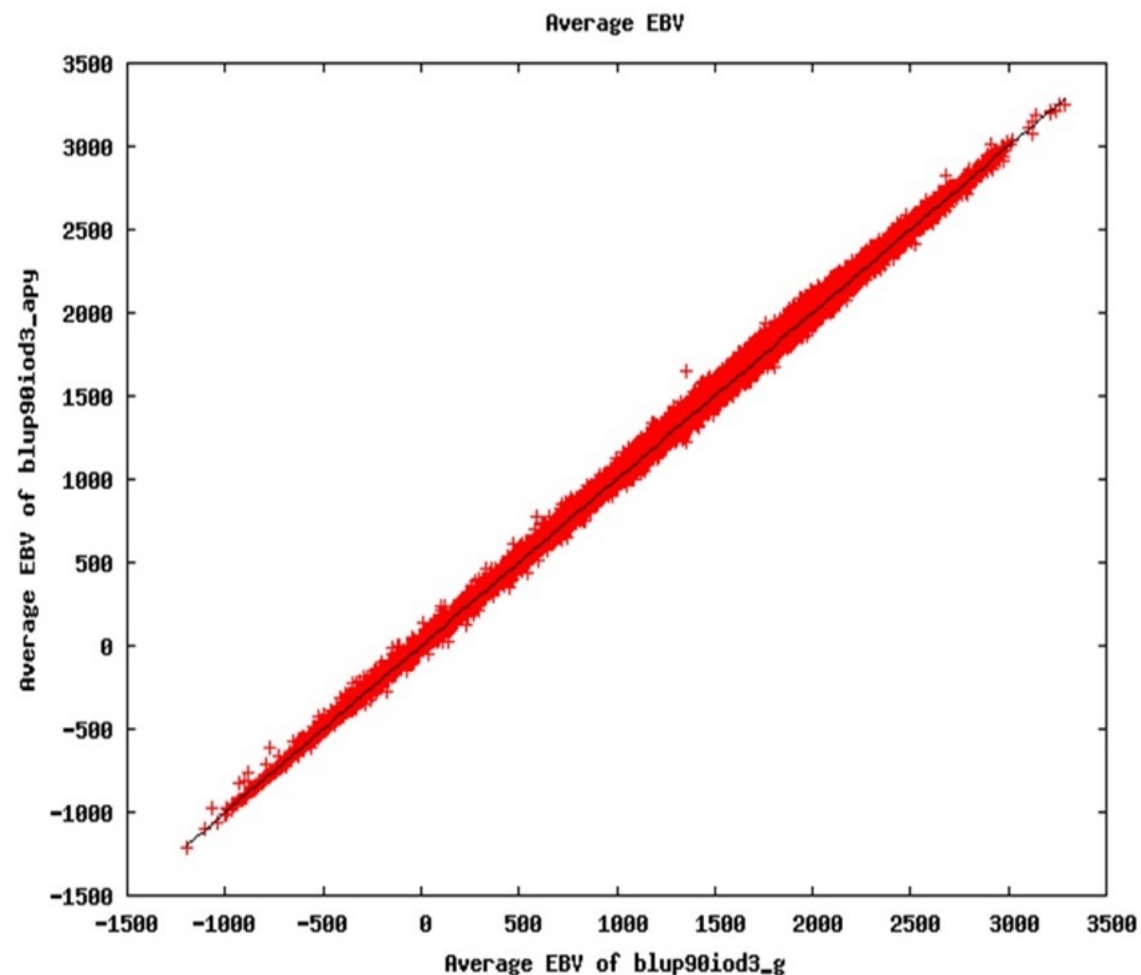
1st lactation



2nd lactation



3rd lactation



Cross validation

1 Data

- Whole data: Phenotypes of cows born up to 2023
- Partial data: Phenotypes of cows born up to 2018

2 Linear regression method (LR; Legarra & Reverter, 2018)

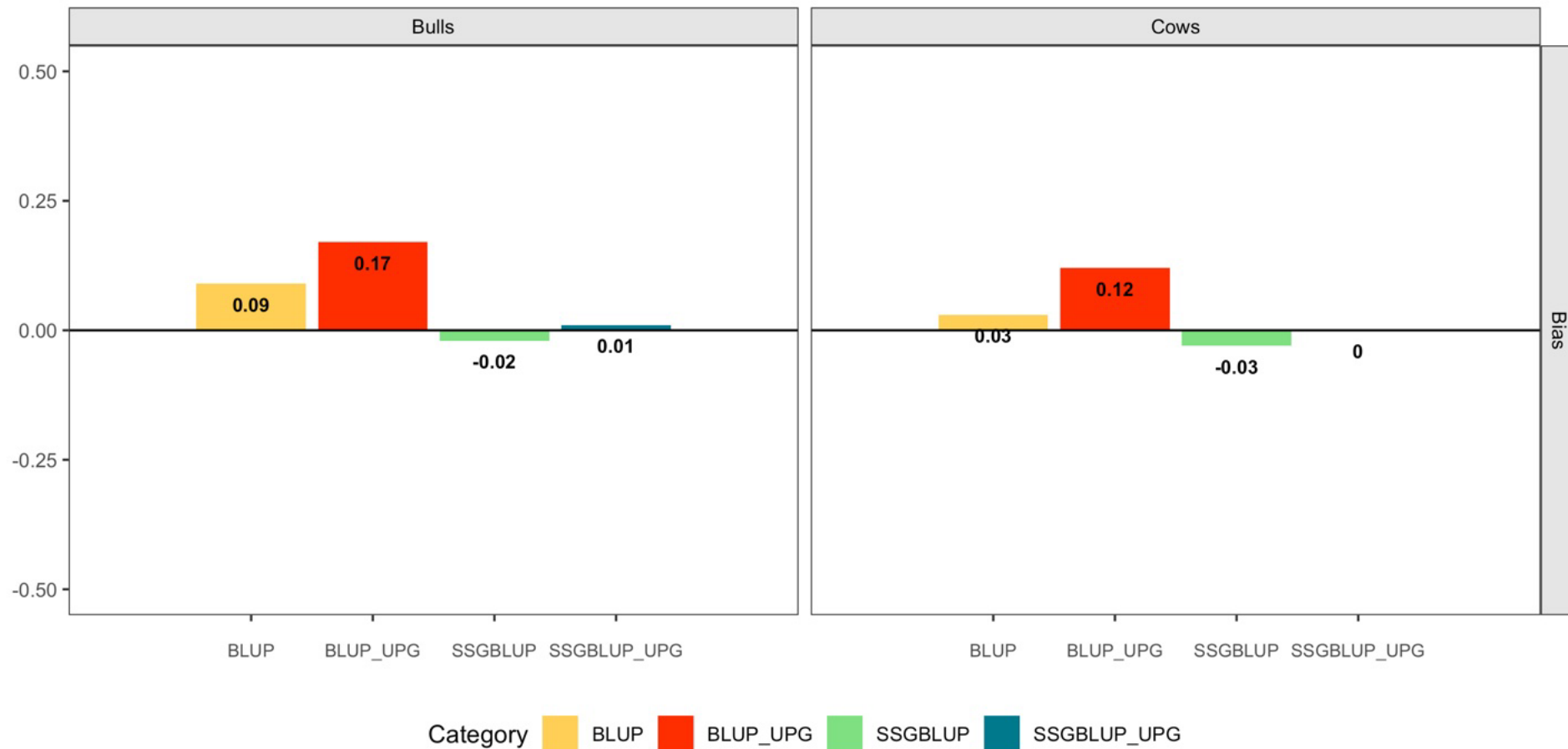
- Females born in 2018–2023 with no phenotypes in the reduced dataset
- Genotyped bulls with no daughters in the reduced and at least 10 in the complete dataset

3 Estimates

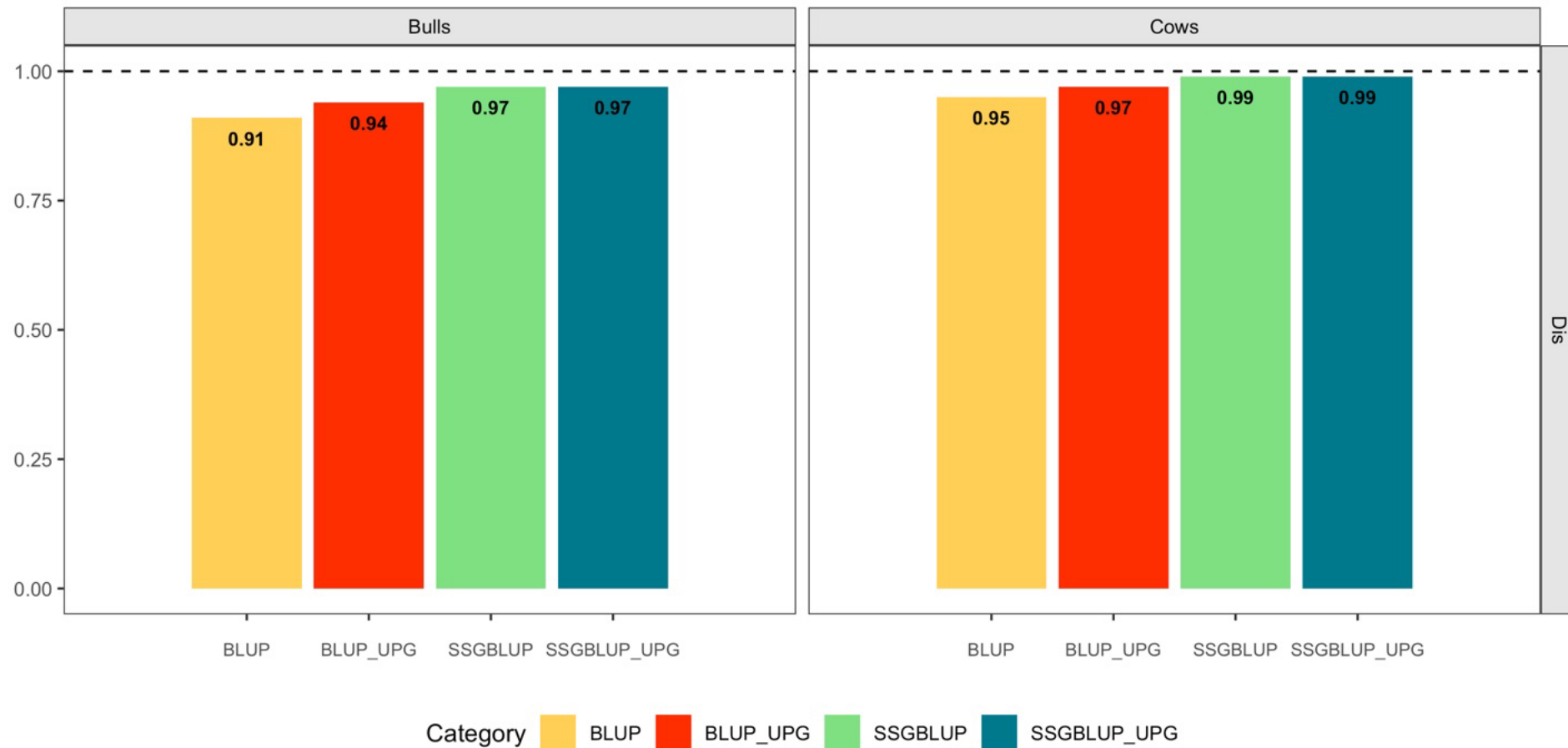
- Bias, dispersion and correlation



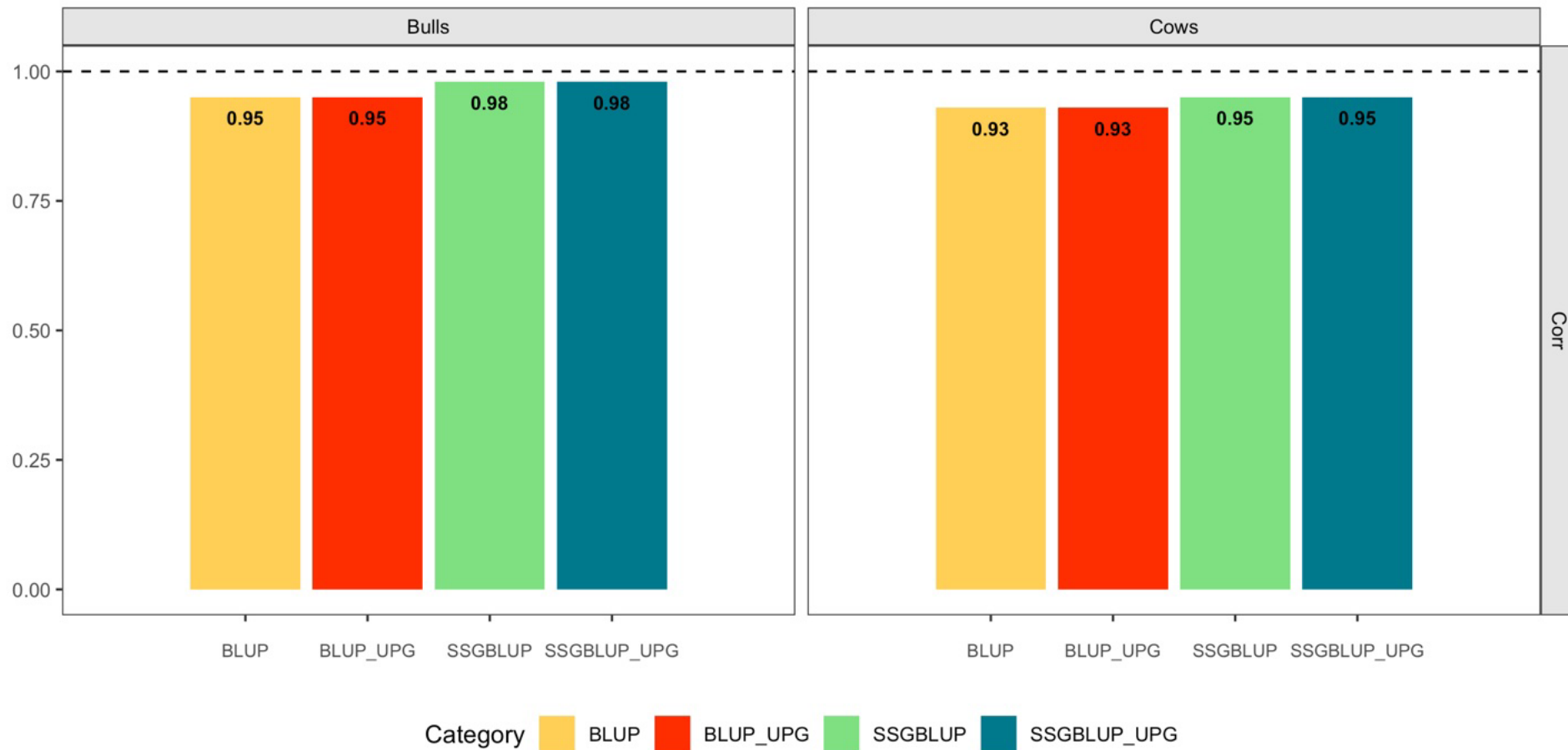
Cross validation



Cross validation



Cross validation



Reliabilities (G)EBV

1

Small dataset

- 11,494 test-day records
- 44,582 animals in the pedigree
- 2,892 genotyped animals



Test method

2

Large dataset

- 30,366,184 test-day records
- 2,512,681 animals in the pedigree
- 54,221 genotyped animals



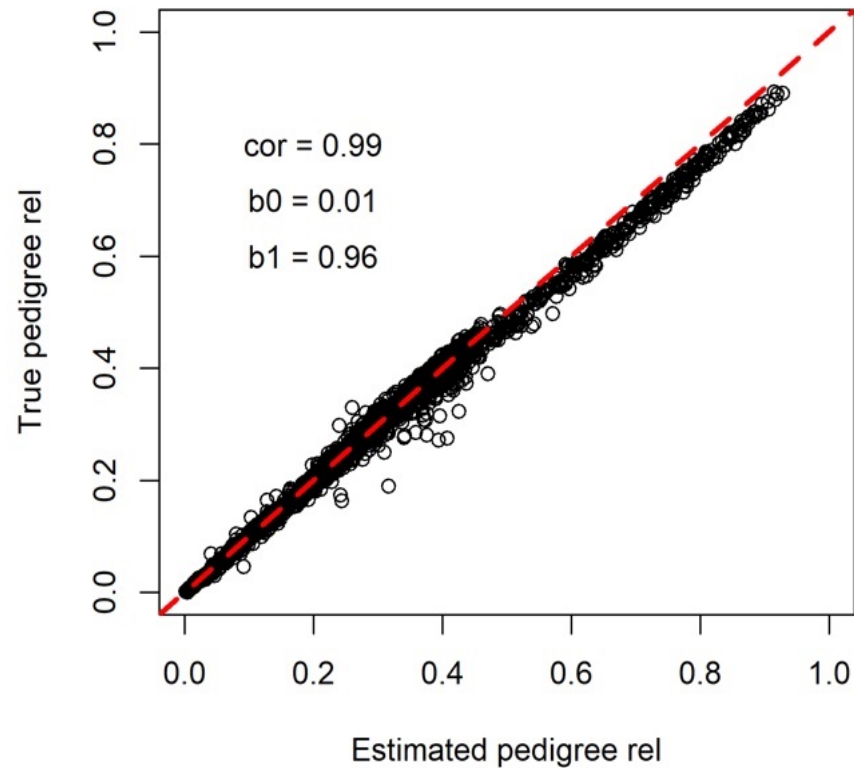
Get estimates



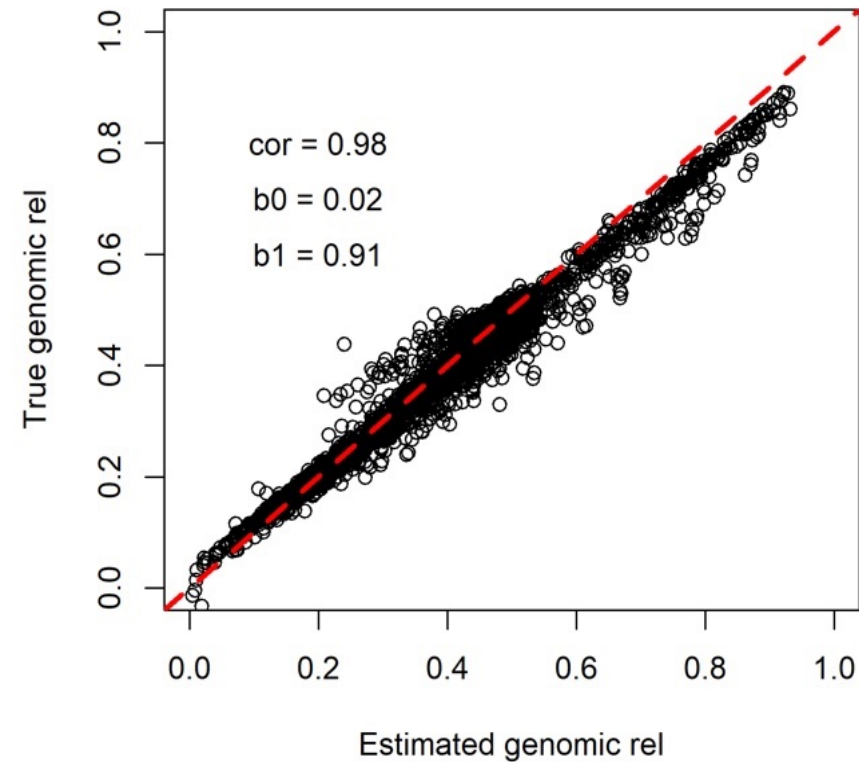
Reliabilities (G)EBV

Approximated reliabilities vs. based on the inverse of the **MME**

Pedigree reliabilities



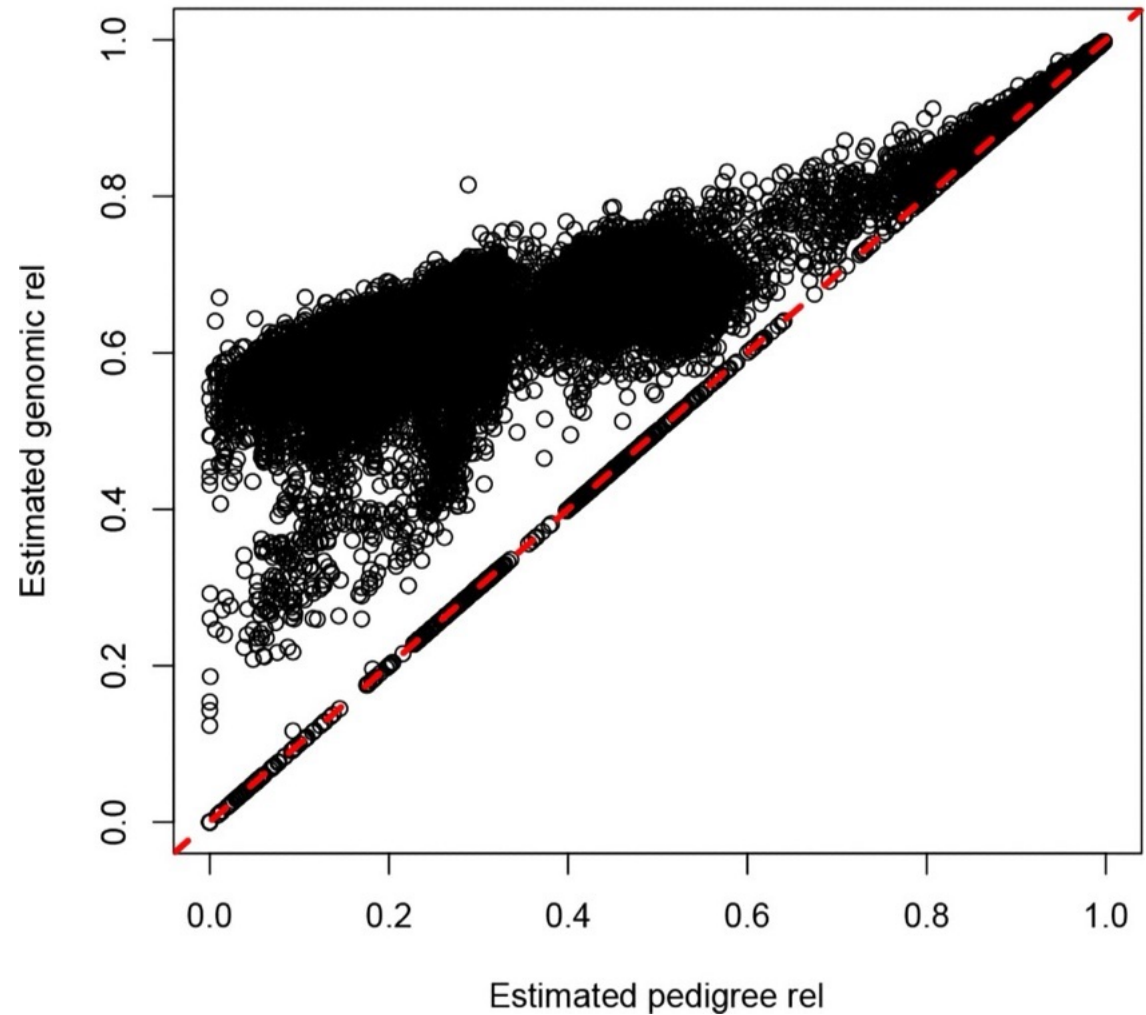
Genomic reliabilities



Reliabilities (G)EBV

For the whole Czech dataset:

The elapsed time to
approximate
reliabilities was less
than **20 minutes**



Conclusions

- 01 The general mean and redefining genetic groups reduced the iterations
- 02 Using APY reduced computing time without reranking
- 03 Approximation of reliabilities worked well
- 04 The proposed modifications make ssGBLUP suitable for Czech dairy evaluation with RRM
- 05 Include external information of Interbull (in progress)



Acknowledgments





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Questions?

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