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GEORGIA**

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Genetics Group*

# Approximation of reliabilities for random-regression single-step GBLUP models

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# Introduction

- Random regression models (RRM) are used in many countries for longitudinal traits
- (G)EBV and its reliability are a function of random regression coefficients
  - Weighted average over three lactations of cumulative 305 days milk yield
- Genomics can be incorporated with single-step genomic best linear unbiased predictor
- Reliabilities must be approximated but no method exist when genomics is added
- **Objective:**
  - **Develop an efficient and accurate method to approximate reliabilities in single-step RRM**



# Random regression models

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

- Record for  $i^{th}$  lactation,  $j^{th}$  cow,  $k^{th}$  contemporary group,  $l^{th}$  test day,  $m^{th}$  polynomial coefficient
- Selection is made for  $EBV_j = \mathbf{k}' \hat{\mathbf{u}}_j$
- Our method approximates the reliability of  $EBV_j$



# Approximation without genomics

- Accumulate reliability of different sources:
  - Own phenotype
  - Parents
  - Progeny
- Accumulation in blocks:
  - Traits
  - Correlated effects
- Read the pedigree twice
- Fast and robust

## **Derivation and Calculation of Approximate Reliabilities and Daughter Yield-Deviations of a Random Regression Test-Day Model for Genetic Evaluation of Dairy Cattle**

**Z. Liu, F. Reinhardt, A. Bünger, and R. Reents**  
VIT, Heideweg 1, D-27283 Verden, Germany

## **Approximating prediction error covariances among additive genetic effects within animals in multiple-trait and random regression models**

BY B. TIER and K. MEYER



# Approximation of accuracies in ssGBLUP

- Combine different sources in terms of ERC
- Convert pedigree reliabilities into ERC
- Use ERC as weights in GBLUP
- Obtain GBLUP reliabilities
- Combine reliabilities in terms of ERC and remove double-counting

## **Approximating Genomic Reliabilities for National Genomic Evaluation**

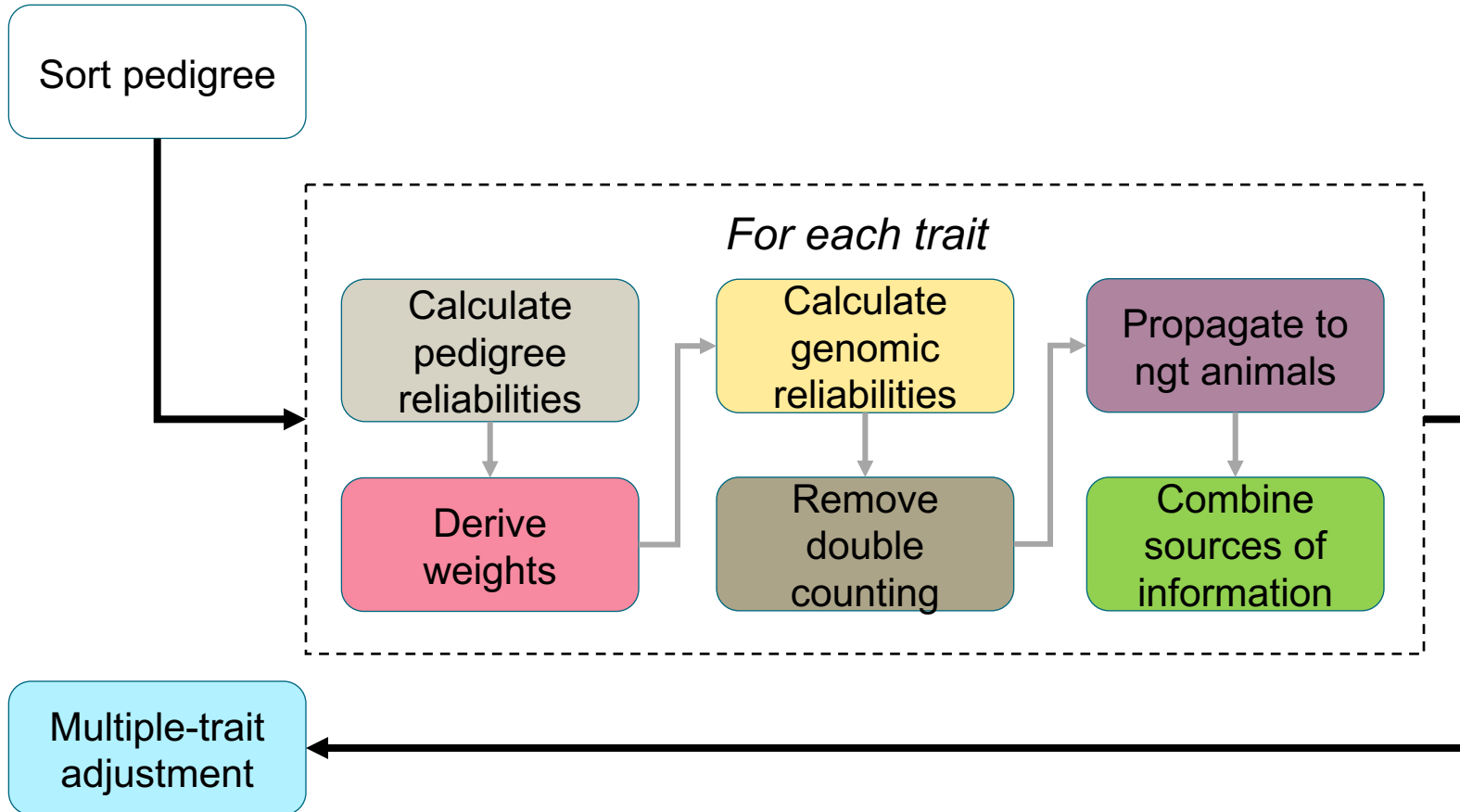
*Z. Liu<sup>1</sup>, P. M. VanRaden<sup>2</sup>, M.H. Lidauer<sup>3</sup>, M. P. Calus<sup>4</sup>, H. Benhajali<sup>5</sup>, H. Jorjani<sup>5</sup>  
and V. Ducrocq<sup>6</sup>*

## **Efficient approximation of reliabilities for single-step genomic best linear unbiased predictor models with the Algorithm for Proven and Young**

Matias Bermann,<sup>1</sup>  Daniela Lourenco, and Ignacy Misztal<sup>1</sup> 

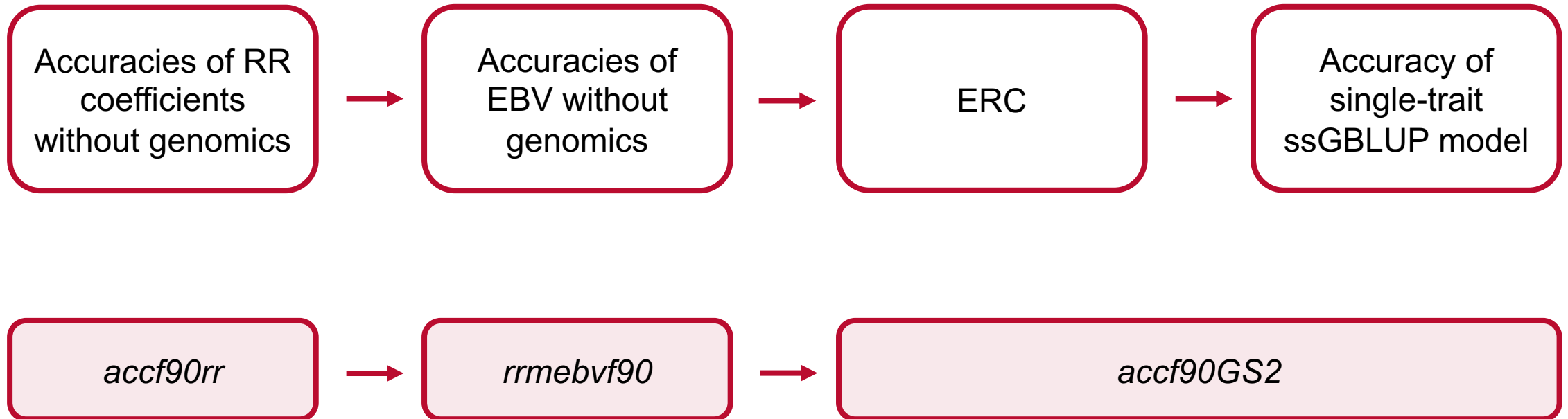


# ACCF90GS2 flowchart



- Maximum number of generation
- Recursive quicksort
- Harris & Johnson (1998)
- Supplied by user
- Back-solve pedigree reliabilities with a root-finding technique
- Block sparse inversion
- Back-solve pedigree reliabilities and set to zero contributions from ngt animals
- Back-solve genomic reliabilities and use them as weights
- Effective daughter/records contribution
- Strabel & Misztal (2001)

# Approximation of accuracies with genomics



# Datasets

- Czech three lactation model for milk production
- Selection on average over the three lactations of 305 days cumulative milk production
- 4<sup>th</sup> order Legendre polynomials
- Effects:
  - General mean
  - Herd-year-season
  - Fixed regression for groups including:
    - Age in first lactation
    - Calving interval
    - Days open
    - Season
  - Additive effect
  - Permanent environmental effect





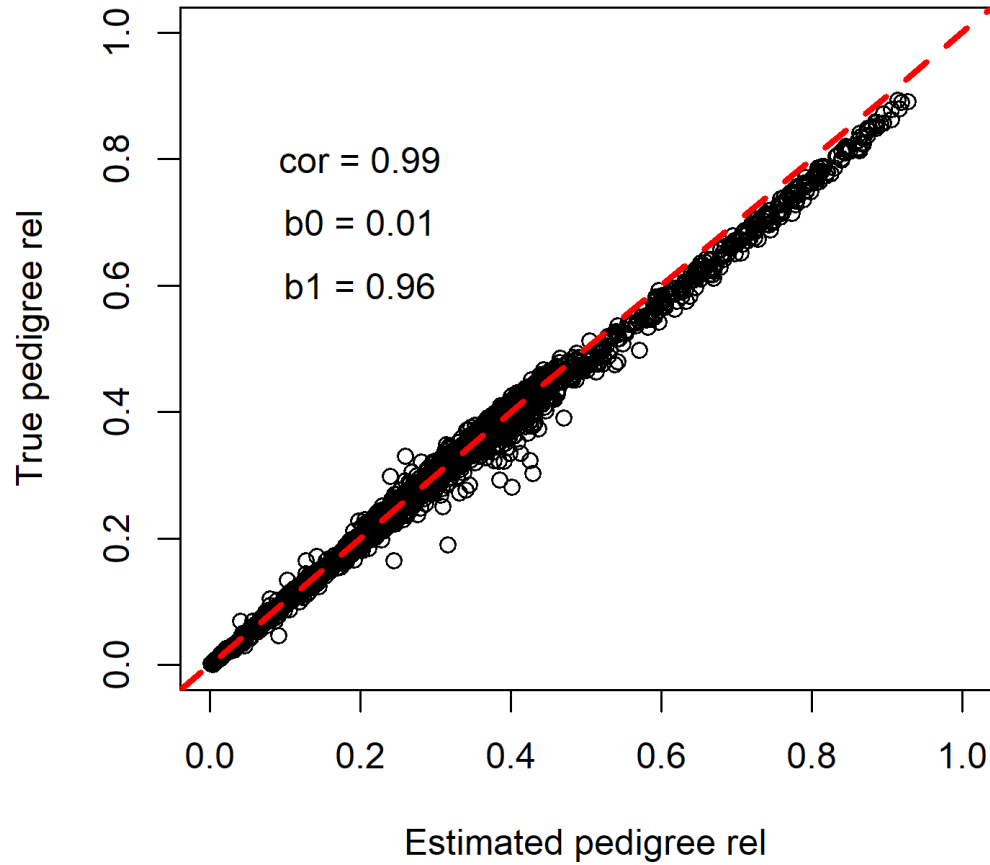
# Datasets

- Small dataset:
  - 111,494 test-day records
  - 44,582 animals in the pedigree
  - 2,892 genotyped animals
- Large dataset:
  - 30,366,184 test-day records
  - 2,512,681 animals in the pedigree
  - 54,221 genotyped animals

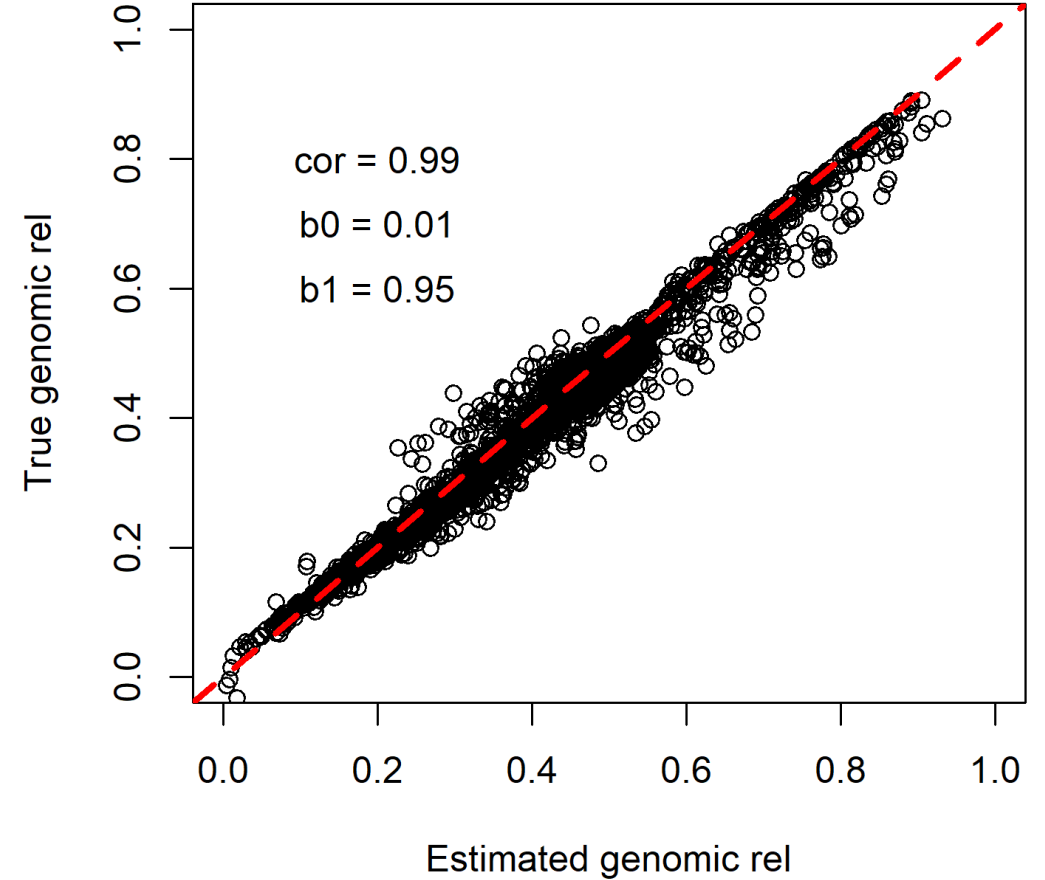


# Small dataset

Pedigree reliabilities

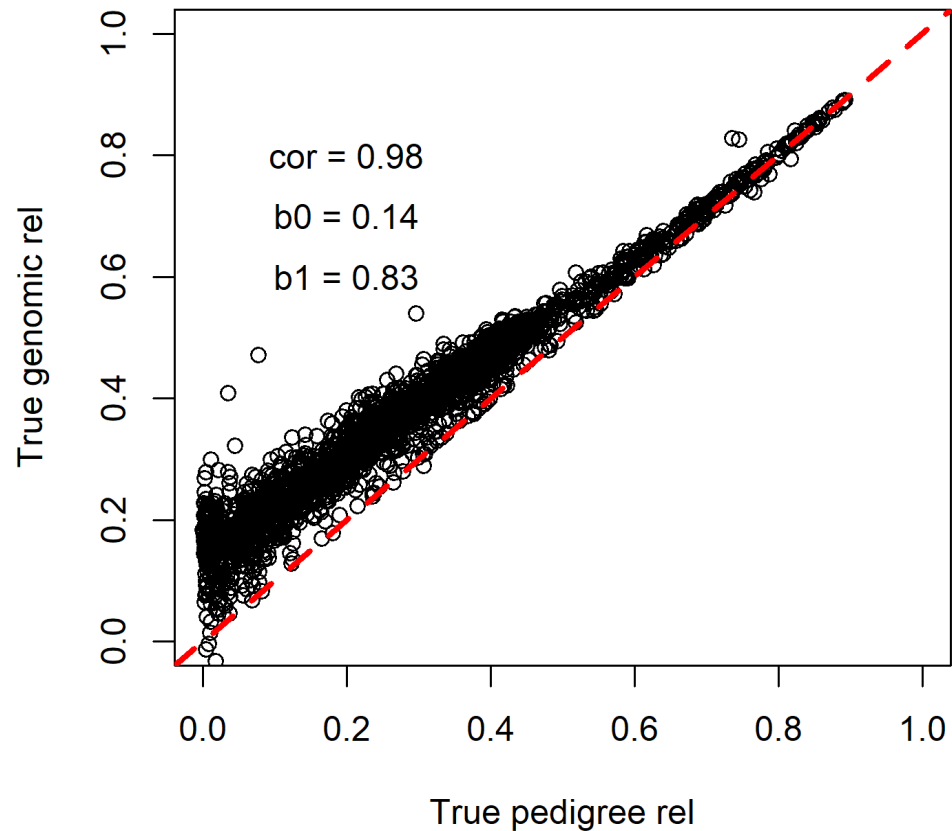


Genomic reliabilities

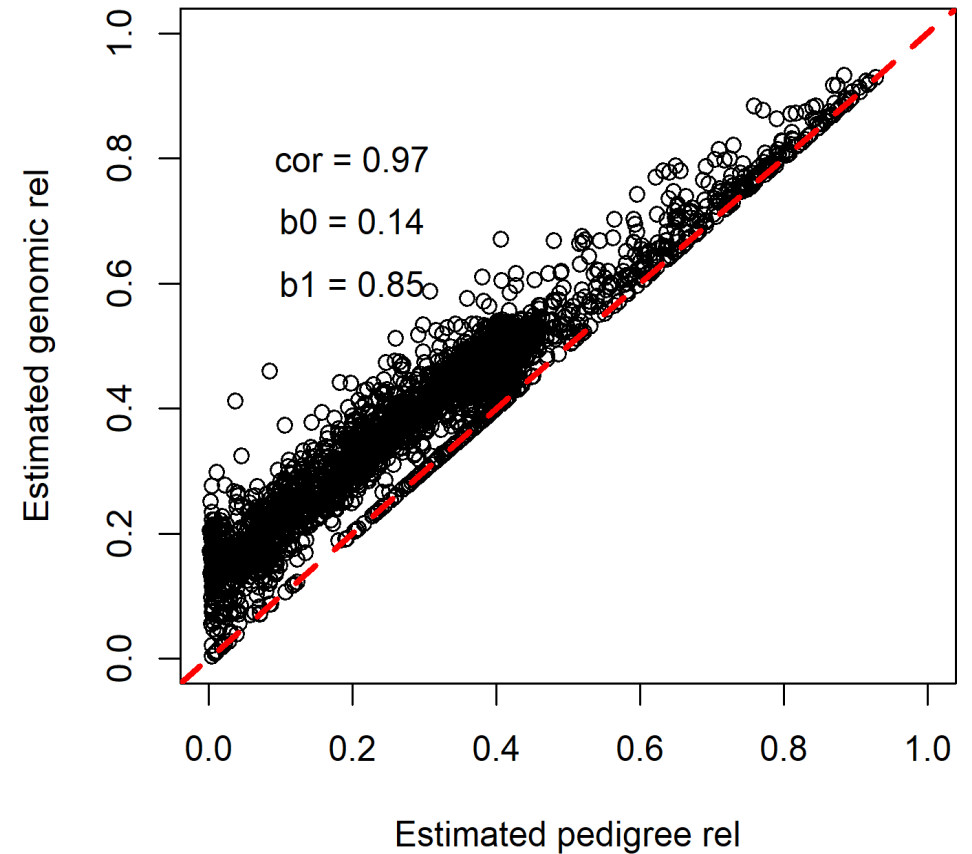


# Small dataset

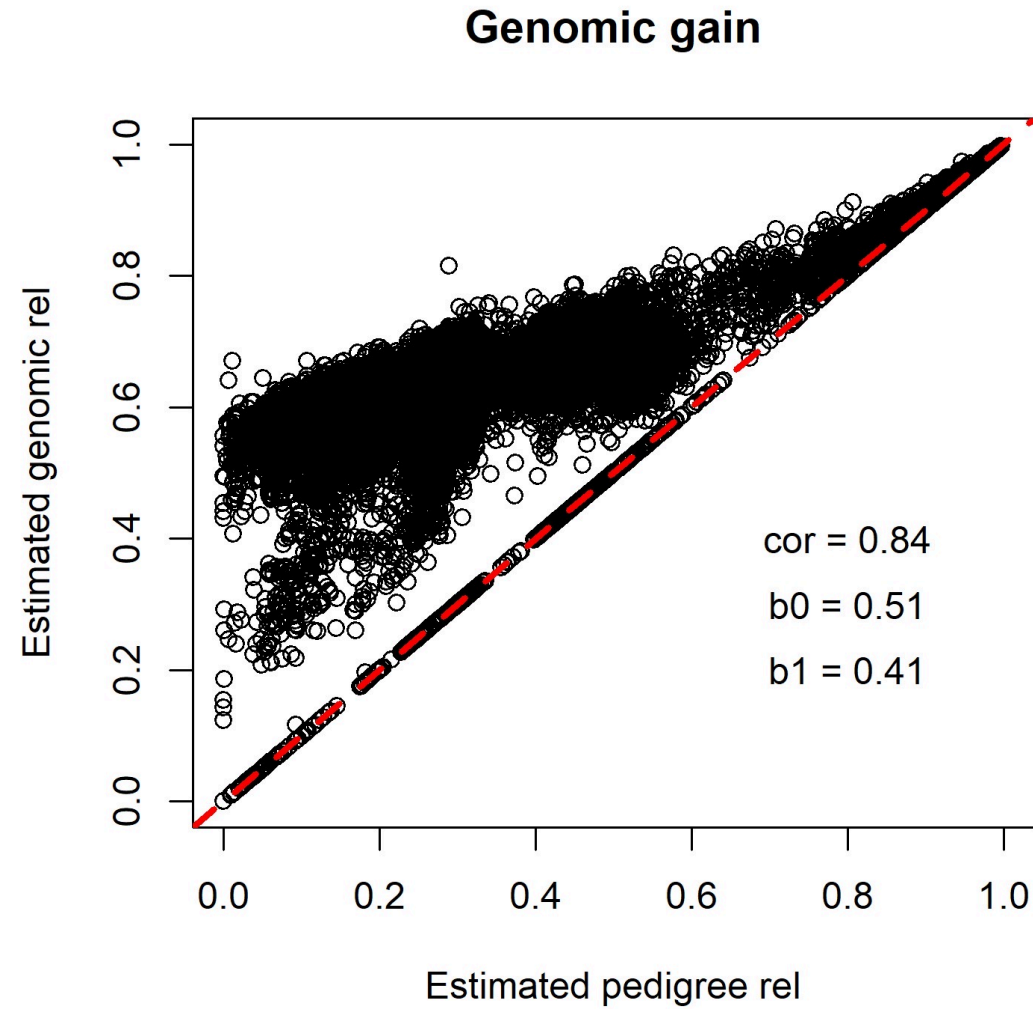
Genomic gain



Genomic gain



# Large dataset



# Challenges

- Models with different traits: fat, protein, SCS
- Timepoint vs. cumulative EBV
- External information: Interbull

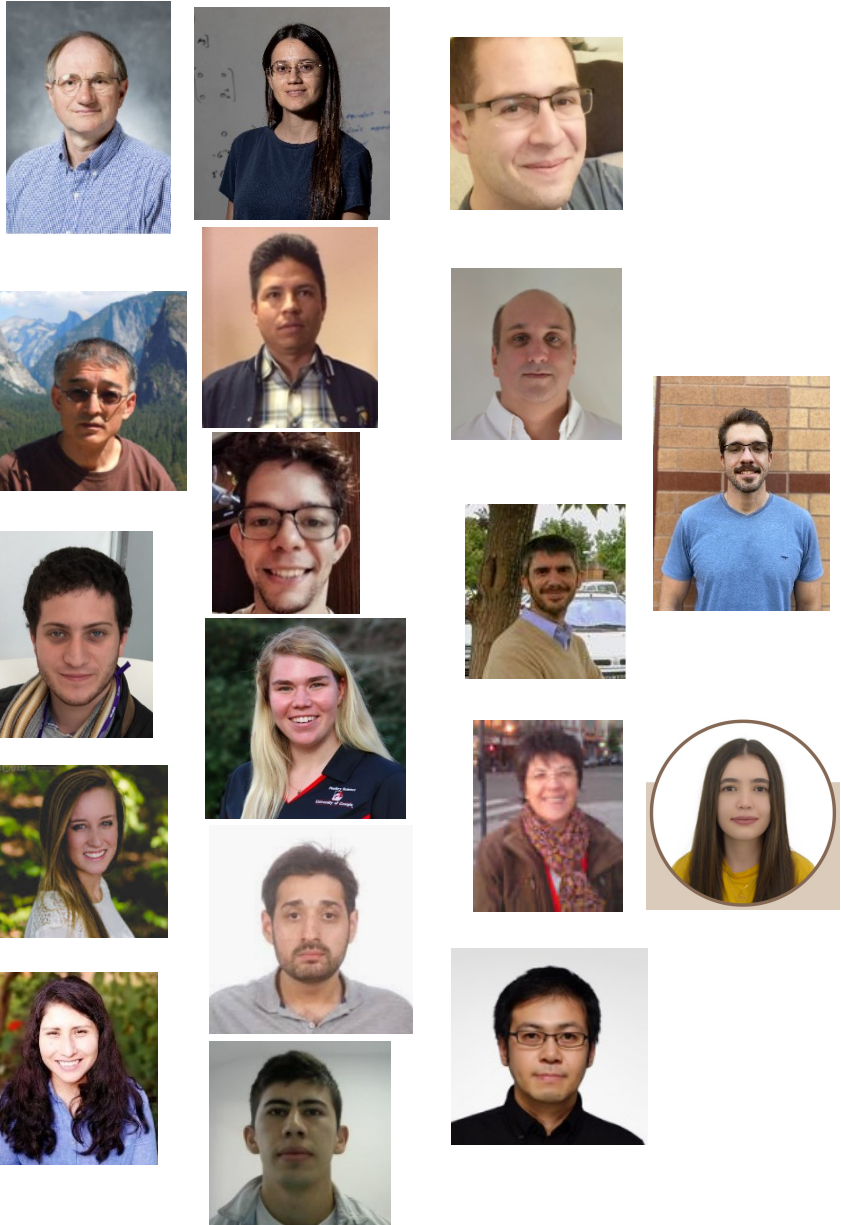


# Conclusions

- Approximation of reliabilities worked well
- Scalable for large datasets
- Reliabilities of each random regressor with genomics are not needed
- Testing the method in different datasets is required



# UGA Team



# *Questions?*

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