



# Report of the Genomic Reliability Calculation working group

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On behalf of all members of the WG



THE GLOBAL STANDARD  
FOR LIVESTOCK DATA





# Interbull Working Group GREL

- Members of the Working Group
  - Paul VanRaden (USDA)
  - Jeremie Vandenplas (Univ. Wageningen, NLD), Herwin Eding (CRV, NLD)
  - Ismo Strandén and Martin Lidauer (Luke, Finland)
  - Katrine Haugaard (Interbull center)
  - Zengting Liu (vit, DEU) as chair of the working group



## Activity since the Technical Workshop in Rome

- Zoom meeting on 26 July, 2023
  - Ismo Strandén, Katrine Haugaard, and Zengting Liu
  - How to improve the speed and reduce RAM usage of *snp\_blup\_rel* for extremely large reference population like DEU HOL
- Zoom meeting on 02 August, 2023
  - Paul VanRaden, Jeremie Vandenplas, Katrine Haugaard, and Zengting Liu
  - Jeremie informed us of his work on GREL development
  - Report on an application using German test-day and conformation data
- Katrine distributed two minutes to all members on 04 Aug 2023

## The Interbull genomic reliability method

- Interbull Genomic Reliability Working Group developed the method (Liu et al. 2017)
  - Goal: Make national genomic reliabilities **comparable** across countries
- Applicable for the single-step model
- Genomic reliability changes fully correlated with the changes in GEBV variance



## Features of the Interbull genomic reliability method (1)

- Main features of the Interbull genomic reliability method (Liu et al. 2017, Interbull Bulletin 51)
  - Genotype data treated as an additional source of information contributing to total reliability
  - Keep using **traditional reliability methods for conventional part** of single-step model
    - a random regression test-day model for milk production and somatic cell scores
    - a maternal-effect animal model for calving traits
    - a multi-parity, multi-trait animal model for fertility traits
  - Include [young animals](#) and all genotyped animals



## Features of the Interbull genomic reliability method (2)

- Main features of the Interbull genomic reliability method
  - Consider genomic relationship among **ALL** genotyped animals
  - DGV reliabilities of young candidates depend on relationship to reference animals
  - **No longer approximating DGV reliabilities** for young candidates (Liu et al. 2010, Wiggans & VanRaden, 2010)
  
  - By applying the SNP BLUP model via the efficient Software **snp\_blup\_rel** (Strandén et al., LUKE, Finland)
  - Allow to run multiple 'single traits' simultaneously
  - High efficiency of the software for extremely large data set with > 1 million genotyped animals



## Features of the Interbull genomic reliability method (3)

- Main features of the Interbull genomic reliability method
  - High theoretical DGV reliability level with extremely large reference population
  - Build-in step for genomic reliability validation
  - **Adjusting genomic reliabilities** based on Interbull GEBV test (VanRaden & O'Connell, 2018)
    - $$\text{Exp(GREL\_change)} = \text{Var}(\text{GEBV}_{\text{later}} - \text{GEBV}_{\text{early}}) / \text{genetic variance}$$

$$= [ \text{Var}(\text{GEBV}_{\text{later}}) - \text{Var}(\text{GEBV}_{\text{early}}) ] / \text{genetic variance}$$
  - Avoiding too high GREL in case of extremely large reference population



## Test scenarios of selecting equidistant SNP markers (April 2021 data)

TEST SCENARIOS Equally-spaced SNP markers selected	No. SNP markers	Total run time (minutes)	Peak RAM (Gb)	Comments
All SNP markers selected (RELall)	45,613	215	88	
Every 2 SNP markers (RELevery2)	22,807	96	42	executed on the same server
Every 3 SNP markers (RELevery3)	15,205	71	28	
Every 4 SNP markers (RELevery4)	11,404	60	21	
Every 5 SNP markers (RELevery5)	9,123	55	18	
Every 10 SNP markers (RELevery10)	4,562	47	10	

Total # genotyped animals: 947,637

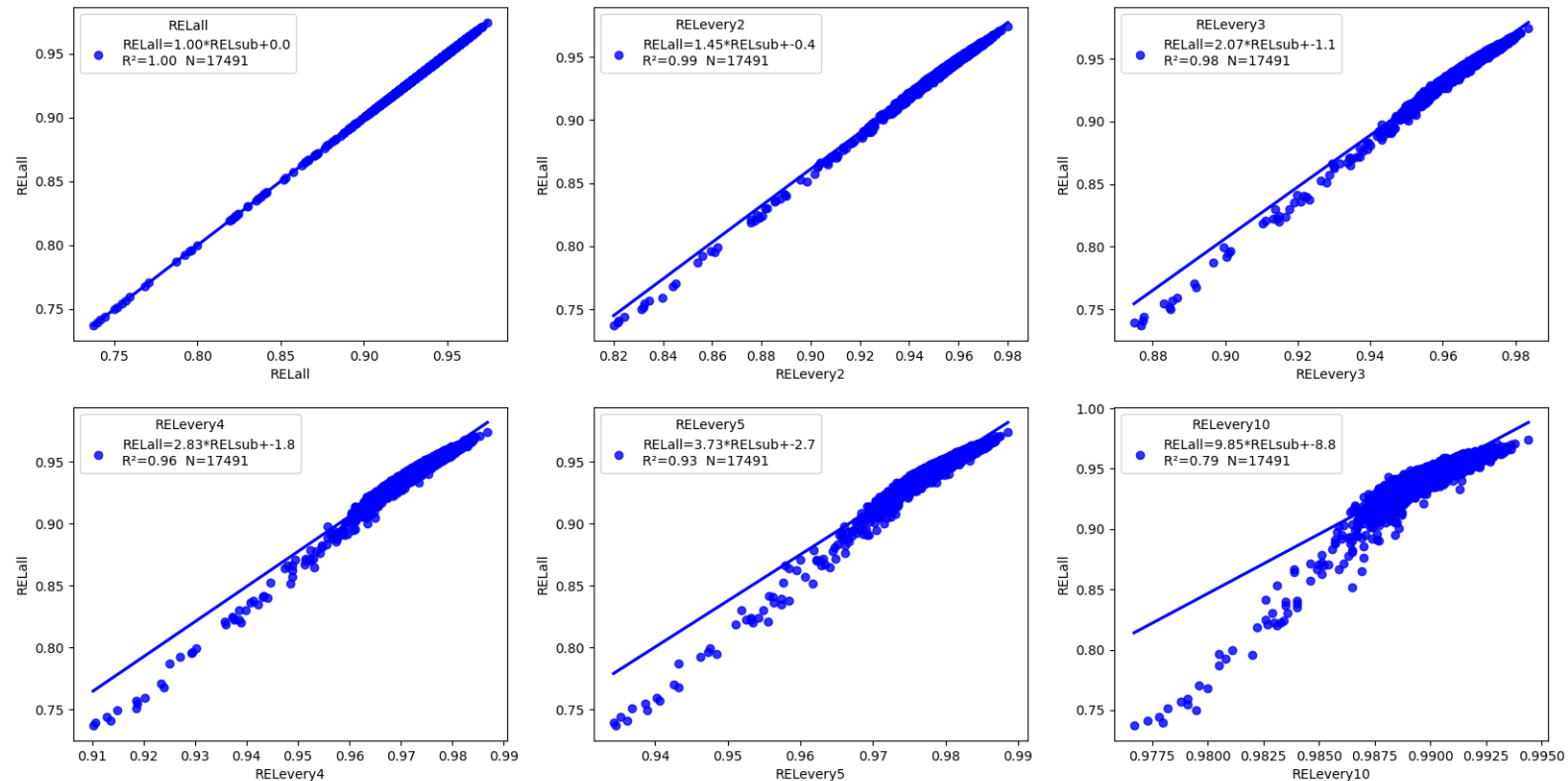
10 cores used





# Regression of SNP reliabilities of the base scenario

$REL_{all} = b_0 + b_1 * RE_{Leveryx}$  for genotyped animals born after 2020 (April 2021 evaluation)



embryos excluded



## Summary and conclusions

- Comparable national genomic reliabilities by implementing the Interbull method
  - For a new model implementation or a major model update:
    - Calculate exact DGV reliabilities via the `snp_blup_rel` provided by Luke
    - Adjust genomic reliability level using GEBV test results
  - For routine single-step evaluation with computing resources limitation
    - A constant genomic EDC gain is a good alternative for faster calculation
    - Another option is to reduce the number of SNP markers to 15,000



## Summary and conclusions (II)

- R&D projects by the Interbull genomic reliability method working group
  - Consider the residual polygenic effect in DGV reliability calculation
  - Multi-trait models at every step of the reliability calculation



Thank you for your attention!

Thanks to the members of  
Interbull GREL working group!



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