The G_REL INTERBULL WG

Formed in 2014

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(Bevin Harris 2014-2016)

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Interbull technical workshop – August 25-26, 2018 – Dubrovnik, Croatia
Currently:

- Genomic reliabilities are not comparable between countries
  - Different methods used
  - Lack of standard calculation procedure

- Consistency across evaluation?
  - Between conventional and genomic evaluations
  - Consistency across time: candidates → getting own phenotypes, → entering reference population
Similar situation in the past with conventional EDC

In 2011:

Interbull developed standardized procedures for calculating conventional EDC
(https://wiki.interbull.org/public/CoP_AppendixIV)

An Interbull standard method for approximating Genomic reliabilities?
Mission

To develop standard procedures for approximating GREL for national genomic evaluation

- Comparable GREL between countries
- Consistent with conventional reliabilities
- Feasible for any number of genotyped animals
- Applicable to single-step genomic models
- Efficient for frequent genomic evaluation
- Consistent with the genomic validation $R^2$
The method in short

Based on a SNP BLUP model
without a residual polygenic effect (at this stage)

(Liu et al., 2017, Interbull Bulletin: 51:75-85.)

Six steps

SNP Rel → DGV Rel → Adjust to realized Rel → Genomic EDC gain (G-A 22 )

propagation of genomic information to non-genotyped relatives

Final reliabilities enhanced with genomic information

Snp_blup_rel
(Mäntysaari & Strandén 2016)

optional

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The method:

- Was presented at the Interbull open meeting in Tallin, 2017
  [http://www.interbull.org/static/web/09_00_Liu.pdf](http://www.interbull.org/static/web/09_00_Liu.pdf)


- An additional document providing recommendation on how to avoid double counting of performance data contribution of cows, in case of a mixed reference population
Still things to be done

- Effect of allele frequency of SNP markers
  - Base population, current population, 0.5 for all

- How to get quick and frequent estimates of GREL
  - REL SNP most time-consuming
  - NGS: need for weekly genomic evaluations

- Verification and validation in different national evaluations systems
  - Purpose of today’s session
Today

- Snp_blup_rel - A tool to calculate reliabilities of individual genomic evaluations. *Esa A Mäntysaari, Martin Lidauer and Ismo Strandén*

- Experiences with the Interbull genomic reliability method applied to a mixed reference population. *Zengting Liu, H. Alkhoder and F. Reinhardt*


- Reliabilities for genomic evaluation: Test of the SNPBLUP software with Spanish Holsteins data. *N. Charfeddine*

- Experiences with the implementation of the Interbull genomic reliability protocol. *H. Eding, J. Vanderplas, G de Jong*

- Using the snp-blup-rel software for prediction reliability of DGV in Poland. *Tomasz Suchocki, M. Mielczarek, A. Zarnecki, and J. Szyda*

- Approximating genomic reliabilities for genotyped Walloon Holstein cattle using the SNP-BLUP software. First experiences. *S. N. Darbaghshahi, S. Vanderick, R. Reis Mota, Nicolas Gengler.*
All documents cited in this presentation can be downloaded from www.interbull.org

If you need help

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snp_blup_rel is developed and owned by Natural Resources Institute Finland (Luke). With the permission of Luke, the evaluation centers of the Interbull members can use snp_blup_rel program to estimate reliabilities for the snp BLUP genomic evaluations. You are not allowed to distribute the program to third parties. For other than above specified use, please contact Luke.

All our colleagues who helped testing snp_blup_rel or the new Interbull Grel method, in particular today’s speakers

Thanks to all of you for attending the GREL session