

# **Approximate Reliabilities for genomic evaluation: Application of the Interbull proposal to Spanish Holsteins data**

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# Introduction

- Nov'2012: Genomic evaluation with Random boosting (*Jiménez-Montero et al. 2012*).
- June 2014: GBLUP with polygenic effect (*Charfeddine et al. 2013*).
- Interbull working group (*2017 Liu et al.*): Proposal for approximate genomic reliability for national genomic evaluations.
- Interbull request to test proposal.

# Genomic Evaluation in Spain

2-Step Procedure: Executed one a month

- **Model:** GBLUP with Polygenic effect (28 traits)
- **Inputs:** DRPs, Pedigree and genomic information
- **Reliability:** Two values of reliability are currently used

- $REL_{LHS}$  used for weighting DGV in blending process

$$b_{DGV} = \frac{Rel_{DGV}}{(1 - Rel_{DGV})} / \left[ \frac{Rel_{DGV}}{1 - Rel_{DGV}} + \frac{Rel_{EBV}}{1 - Rel_{EBV}} \right]$$

- $REL_{CV}$  used to calculate  $REL_{GEBV} = REL_{EBV} + REL_{gain}$

## Computing resources

### Intel Xenon Server :

- ✓ 2 Processors E5-2630v4 2.20 GHz (10 cores)
- ✓ 256 GB RAM
- ✓ 3 TB disc
- ✓ OS Windows Server 64 bit.

### Software :

- ✓ GBLUP\_rel program (Ismo Stranden and Esa Mäntysaari, Luke, FINLAND) (Version 0.23) Nov'2017

# Test application to Spanish Data

## Genotypes & phenotypes: June 2018 evaluation

### Data:

- Reference population: EuroGenomics Holstein reference bulls 35,405 (3,184 ESP)
- 42,619 females & candidates
- Total: 78,024 genotyped animals & 42,981 SNP markers

## Computing performance

### Cumulative time and use of RAM memory

Using all animals	SNP_BLUP_Rel	GBLUP_rel with Polygenic effect
Time-Reading genotypes	15'02"	30'43"
Time-Inverting MME- 1 <sup>st</sup> step	31'02"	2h12'02"
Time-Calculating R <sup>2</sup> - 2 <sup>sd</sup> Step	38'09"	2h22'01"
Total time	51'37"	3h00'09"
Peak RAM	47.9 GB	95.6 GB

Computing separately Reference bulls and candidates	SNP_BLUP_Rel
Time-Reading genotypes	2'12"
Time- Inverting MME and calculating R <sup>2</sup> and BV for reference animals 1 <sup>st</sup> step	1h08'09"
Time- Reading MME inverse and Calculating R <sup>2</sup> and BV for candidates 2 <sup>sd</sup> Step	42'14"
Total time	1h50'23"
Peak RAM	33.6 GB

# Cross Validation Study

- Phenotypes from April 2018 Mace Evaluation
- Genotypes from June 2018 evaluation
  - **28,752** EuroGenomics reference bulls born before 2009
  - **538** Spanish bulls born between 2009-2012 as testing bulls
- Traits: 4 traits are selected:
  - **Milk ( $h^2=0.28$ )**
  - **Udder Depth ( $h^2=0.30$ )**
  - **Locomotion ( $h^2=0.12$ )**
  - **Days open ( $h^2=0.043$ )**

# Validation results

Traits	h <sup>2</sup>	N <sub>bulls</sub> ≥ 20 EDC	SNP BLUP	GBLUP with Polygenic effect
			Reliability <sub>cv</sub>	Reliability <sub>cv</sub>
Milk	0.280	533	0.72	0.72
Udder Depth	0.300	527	0.63	0.64
Locomotion	0.120	533	0.33	0.27
Days Open	0.043	361	0.58	0.58

Polygenic=50%

Cross Validation Reliability is practically equal, except for Locomotion



## Reliability averages calculated by matrix inversion for candidates

	% Polygenic effect	SNPBLUP	SNPBLUP considering polygenic effect (Liu et al. 2017)	GBLUP with Polygenic effect
Milk	15	0.90	0.76	0.72
Udder Depth	5	0.91	0.86	0.79
Locomotion	50	0.68	0.34	0.40
Days Open	5	0.86	0.82	0.71

$$Rel_{DGV} = (1 - k) * r_{IMP}^2 * Rel_{SNP}$$

*k*: proportion of residual polygenic variance

## Adjusting to realized reliability of DGV

GEBV validation test :  $DRP = b_0 + b_1 * GEBV + e$  (Mäntysaari et al. 2010)

$$EDC_{DGV}^{Real} = f * EDC_{DGV}$$

Traits	h <sup>2</sup>	f_factor	EDC <sub>DGV</sub>	EDC <sub>DGV</sub> <sup>Real</sup>
Milk	0.280	1.00	43.7	43.7
Udder Depth	0.300	0.55	83.3	45.5
Locomotion	0.120	0.17	20.4	16.7
Days Open	0.043	0.65	343.5	224.6

## Genomic EDC gain

$$EDC_{gain} = EDC_{DGV}^{Real} - EDC_{A22} \text{ (Liu et al. 2017)}$$

Rel<sub>Pedigree Index</sub>

Traits	EDC <sub>DGV</sub> <sup>Real</sup>	EDC <sub>A22</sub>	EDC <sub>gain</sub>
Milk	43.7	6.2	37.5
Udder Depth	45.5	6.1	39.4
Locomotion	16.7	14.6	2.1
Days Open	224.6	40.6	183.9

# Final Reliability

$$EDC_{final} = EDC_{gain} + EDC_{EBV} \text{ (Liu et al. 2017)}$$

$$Rel_{final} = \frac{EDC_{final}}{EDC_{final} + \lambda}$$

**Final Reliability calculated for candidates compared with current reliability**

Traits	Rel <sub>final</sub>	Rel <sub>GEBV</sub>
Milk	0.77	0.73
Udder Depth	0.78	0.72
Locomotion	0.34	0.43
Days Open	0.71	0.65

Current Reliability Value

## Conclusions

- SNP\_BLUP\_REL software is clearly faster and less RAM demanding.
- Cross validation reliabilities are virtually similar except for Locomotion.
- Expected reliabilities calculated for candidates by the new method are slightly higher than reliability calculated currently in our evaluation, except for Locomotion.

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