Approximating genomic reliabilities for genotyped Walloon Holstein cattle using the SNP-BLUP software - First experiences

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Walloon Genomic System

Current Walloon Holstein genomic evaluation system:
Single-step genomic “Bayesian” procedure (ssGBayes)
- Blending genomic, local and MACE information using EBV and REL
- Subtract Walloon information contributing to MACE
Larger Project

- Current Walloon Holstein genomic evaluation system: Single-step genomic “Bayesian” procedure (ssGBayes)
  - Blending genomic, local and MACE information using EBV and REL
  - Subtract Walloon information contributing to MACE

- However needed:
  - “Continuous” generation of GEBV ← flow of genotypes
  - Generating also associated GREL → SNP-BLUP software

- Context of this presentation
Objectives

- Reported here:
  - First experiences with INTERBULL method
  - For genotyped Walloon Holstein cattle and improve its efficiency

- Comparison facilitated because routine GREL in our evaluation based on $\text{diag}(\mathbf{C}^{-1})$
How was the method used?

Step 1: Reliabilities of SNP genotypes using the SNP_BLUP software using ~9000 genotyped animals ($R_i^{SNP}$)

Step 2: Reliabilities of DGV

\[ R_i^{DGV} = R_i^{SNP} \]
How was the method used?

Step 3: Adjusting the theoretical reliabilities

\[ EDC_{i}^{DGV} = \lambda \ Ri^{DGV} / (1 - Ri^{DGV}) \]

\[ EDC_{real-i}^{DGV} = f \times EDC_{i}^{DGV} \]

\[ \lambda = \frac{4 - h^2}{h^2} \]

\[ f = 1 \]

\[ f = \text{regression expected} - \text{observed} \]
How was the method used and tested?

- **Step 4**: Calculating the genomic EDC gain

\[ EDC_i^{\text{Gain}} = EDC_{\text{real-}i}^{DGV} - EDC_i^{A22} \]

- **Step 5**: Final reliabilities enhanced with genomic information

\[ EDC_i^{\text{Final}} = EDC_i^{\text{CONV}} + EDC_i^{\text{Gain}} \]

\[ R_i^{\text{Final}} = \frac{EDC_i^{\text{Final}}}{EDC_i^{\text{Final}} + \lambda} \]

**EDC**:
- \( EDC_i^{\text{CONV}} \): EDC based on conventional EBV (updated with MACE) (6600 animal)
- \( EDC_i^{W-MACE} \): EDC based on MACE value (2411 animal)

- **EDC** based on conventional and local parent average

How was the method used and tested?

INTERBULL Workshop 2018 Dubrovnik
How was the method tested?

<table>
<thead>
<tr>
<th>Information</th>
<th>Cor(R_REL, IB_REL)</th>
<th>Mean_R_REL</th>
<th>Mean_IB_REL</th>
</tr>
</thead>
<tbody>
<tr>
<td>MACE</td>
<td>0.99</td>
<td>0.828</td>
<td>0.827</td>
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<tr>
<td>Sire and/or maternal grand sire with MACE</td>
<td>0.76</td>
<td>0.630</td>
<td>0.626</td>
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<tr>
<td>Total</td>
<td>0.96</td>
<td>0.684</td>
<td>0.680</td>
</tr>
</tbody>
</table>

Animals with own MACE value

Animals with conventional REL but needing MACE updates
Conclusions

- First results – promising
- Depend clearly on group of animals
- To emulate our system where MACE information flows in ⇒ update of conventional REL also needed
- Currently our published conventional EBV and REL are also updated (other method) ⇒ to be continued

⇒ SNP-REL method entering well current efforts