Deregressed genomic breeding values from single-step evaluations of test-day traits using all genotype data

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I) Deregression of conventional estimated breeding values

- Pedigree-based EBV deregression by Jairath et al. (1998)
  - More accurate than EBV deregression “one animal at time” (Calus et al. 2016)

- Interbull uses deregressed national bull EBV as ‘pseudo-records’ for MACE evaluation

- Many countries use deregressed EBV (DRP) for the current 2-step genomic evaluation

- A reversibility test for validating deregressed EBV (vit, 2020)
  - Validation of deregressed bull MACE EBV on DEU scale
  - Validation of deregressed cow national EBV for all trait groups
I) Deregression of single-step genomic breeding values

- Why deregressed single-step GEBV?
  - Deregressed bull GEBV as input ‘pseudo-records’ for conventional MACE evaluation
  - Countries no longer need to conduct the old conventional evaluation besides the single-step evaluation
  - Independent and most accurate response variable for GEBV validation
  - Circumvent the difficulty of DYD or YD calculation for complex model, such as random regression model

- Approaches for single-step deregression
  - Single-step GBLUP model (Masuda et al., 2021)
  - Single-step SNP BLUP model (Liu et al., 2021, 2022)
  - Separately for cows with phenotypic records and for bulls with daughters
  - Using all genotype data
  - Using all genomic reference information
## II) Data materials for deregressing single-step cow GEBV

<table>
<thead>
<tr>
<th>April 2023 evaluation</th>
<th>Single-step evaluation</th>
<th>GEBV deregression</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Frequency of</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Genotyped Holstein animals</td>
<td>1,318,780 (1,138,039 females and 180,741 males)</td>
<td></td>
</tr>
<tr>
<td>Animals with phenotype data</td>
<td>13,528,444</td>
<td></td>
</tr>
<tr>
<td>--- phenotypic input data</td>
<td>263,673,267 test-day records</td>
<td>13,528,444 GEBV</td>
</tr>
<tr>
<td>--- record weight</td>
<td>Specific for each record</td>
<td>Effective record contribution</td>
</tr>
<tr>
<td>Genotyped or phenotyped animals</td>
<td>14,402,662</td>
<td></td>
</tr>
<tr>
<td>Animals in pedigree</td>
<td>21,850,276</td>
<td></td>
</tr>
</tbody>
</table>
II) Special issue for deregressing single-step bull GEBV

- Conventional bull EBV deregression by switching phenotyped animals from cows to bulls
  - Bulls having daughters: EBV and EDC
  - Use bull pedigree (bulls and their ancestors)

- With genotyped cows available, genotyped bulls no longer represent the full reference population
  - Add reference cows (genotyped cows with own phenotypic records) to the deregression
  - Avoid double counting of cows’ ERC in the mixed bull and cow reference population

- Animals with GEBV and EDC/ERC for bull GEBV deregression
  - Bulls with daughters and reference cows: 664,548

- Also use all genotype records of 1,318,780 animals, including young candidates
II) Validation of the single-step deregressed GEBV (a reversibility test)

<table>
<thead>
<tr>
<th>Cow GEBV deregression</th>
<th>Original single-step evaluation</th>
<th>Single-step evaluation using deregressed GEBV</th>
</tr>
</thead>
<tbody>
<tr>
<td>Statistical model</td>
<td>Random regression test-day model for 3 correlated lactations</td>
<td>Single trait model with a general mean and GEBV</td>
</tr>
<tr>
<td>Animals with phenotypic data</td>
<td>13,528,444</td>
<td></td>
</tr>
<tr>
<td>Number of phenotypic records</td>
<td>264 million test-day records</td>
<td>13.5 million deregressed GEBV pseudo-records</td>
</tr>
<tr>
<td>Pedigree file</td>
<td>Same pedigree with 22 million animals</td>
<td></td>
</tr>
<tr>
<td>Genotype data</td>
<td>Same data with 1.4 million genotyped animals</td>
<td></td>
</tr>
<tr>
<td>Validation animals with phenotype</td>
<td>Equal GEBV for all animals with own phenotypes?</td>
<td></td>
</tr>
<tr>
<td>Validation genotyped animals</td>
<td>Equal GEBV for all young, genotyped candidates?</td>
<td></td>
</tr>
</tbody>
</table>
II) Deregressing GEBV of single-step evaluation and validation

- Single-step model for test-day traits
  - A multi-lactation random regression test-day model
  - A SNP BLUP model

- Model for deregression: $\text{DRP} = \mu + \text{GEBV} + \text{error}$ with EDC/ERC as weight
  - A single-trait model

- GEBV deregression via MiX99 (Strandén and Mäntysaari, 2010)
  - Version April 2023
  - Separate deregression processes for cows and for bulls

- Single-step evaluations for validating the deregressed GEBV
  - Same model as for GEBV deregression

- Deregression process required a little less computing time and memory usage than the original single-step evaluation
11.8 million Holstein cows with test-day records

genetic standard deviation of milk yield: 640 kg

\[
\frac{\text{std}(\text{GBEV})}{\text{std}(\text{dereg. GEBV})} = 0.48
\]
III) Deregression results: Deregressed GEBV of bulls with daughters

24,016 Holstein bulls with >= 10 herds in Germany

Genetic standard deviation of protein yield: 17.9 kg
III) Validation of cow GEBV deregression: comparison of single-step GEBV from test-day yields and from deregressed GEBV

Trait: 305-day milk yield on a combined lactation basis

12.6 million Black and White Holstein females

(cows with test-day records, female ancestors, genotyped candidates)

std(GEBV using dereg. GEBV)

std(GEBV using test day data)
III) **Validation of bull GEBV deregression**: comparison of single-step GEBV from test-day yields and from deregressed GEBV

Trait: 305-day **protein yield** on a combined lactation basis

10,770 Black and White German Holstein **AI bulls**
IV) Summary and conclusions (1)

- GEBV deregression tested for the single-step evaluation of four test-day traits
  - For cows with test-day records as well as for bulls with daughters

- For bull GEBV deregression, GEBV of all reference cows must be included as input data

- Deregressed GEBV of the cows or bulls
  - Highly or moderately correlated with their GEBV, depending on reliabilities
  - Slightly lower trends than GEBV, especially those with lactations in progress
  - Higher variance than GEBV

- Deregressed GEBV versus deregressed EBV
  - Higher trend of deregressed GEBV
IV) Summary and conclusions (2)

- Perfect validation results showed the GEBV deregression is a reversible process
  - Equal single-step GEBV using the original test-day yields and from the deregressed GEBV
  - For all cows with test-day data and for all bulls with daughters
  - For all genotyped animals, especially young candidates

- Deregressed GEBV desirable 'pseudo-phenotype'
  - Less auto-correlation between early (candidate) GEBV and later deregressed GEBV of validation bulls

- The deregression of single-step GEBV issue solved!
Dr. Ismo Strandén and Dr. Esa Mäntysaari for their help in using MiX99 for this project
Thank you for your attention!