Direct Use of MACE EBV in the Walloon Single-Step Bayesian Genomic Evaluation System

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Genomic Selection 101

- Common perception
  - Very simple
  - Easy to explain
- But
  - Is this correct?

Reality obviously much more complex!
Reference Population

**Phenotypes:**
- limited availability
- can not be used directly
- rely on external sources (MACE EBV* for dairy)

**Genotypes:**
- limited availability
- often not on same animals as phenotypes

**Methods need to be adapted**

* Estimated breeding values (EBV) obtained from INTERBULL Multiple Across Country Evaluation (MACE) procedure based on EBV provided by partner countries

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**Multi-Step Methods**

**Estimated Breeding Values** (including MACE EBV)

**Phenotypes**

**Pseudo-phenotypes** (deregressed proofs)

**Genotypes**

**Prediction equation**

**Direct Genomic Values (DGV)**

**Pedigree**

**Genomically Enhanced Breeding Values (GEBV)**

* If polygenic effect included

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**Single-Step Methods**

**Phenotypes**

**Pedigree**

**Genotypes**

**Single-Step Genomic Evaluation (ssGBLUP)**
- replacing pedigree information in mixed models by combined pedigree and genomic information

**Genomically Enhanced Breeding Values (GEBV)**
Innovations Needed!

- Considering simultaneously
  - Genotypes
  - Pedigree
  - Phenotypes
  - but all local and foreign information simultaneously
- Avoiding
  - Deregression
  - Multiple considerations of contributions
- Maximum flexibility
  - Allowing to add and to subtract contributions from different information sources (e.g., local, MACE)
  - Avoiding double counting (e.g., local information already contributing to MACE EBV)

Bayesian Integration

- Creating system equivalent to mixed model equations
  - Integration of external information
  - Avoids deregression
- Adaptation to include multiple sources of information
  - E.g., adding MACE EBV, subtract local EBV included in MACE EBV

Context of Single-Step Genomic Prediction

- Replacing pedigree information in mixed models by combined pedigree and genomic
- Can therefore be applied to Bayesian models

Single-Step Bayesian Method

Estimated Breeding Values (including MACE EBV) → Phenotypes → Pedigree → Genotypes

Single-Step Bayesian Genomic Evaluation (ssBAYES) (reconstructing mixed model equations also using combined pedigree and genomic information) → Genomically Enhanced Breeding Values (GEBV)

Proof of Concept

Walloon Genomic Evaluation System

- Small population (southern part of Belgium)
- Few genotypes
- Phenotypes use of MACE EBV + local EBV
  ⇒ ssBAYES: optimal use of available data (including MACE EBV)

Local test-run ⇒ GMACE test-run

- 02/2013: passed the GEBV tests for yields + most type traits
- Results using data for 06/2013:
  - 16,234 animals
  - 12,046 Walloon EBV added
  - 1981 MACE EBV added (601 bulls sent, EBV subtracted)
  - 1909 cows and bulls with genotypes
## Proof of Concept – Results for Milk Yield

### Increase in average reliabilities REL (SD) through the incorporation of MACE EBV into the Walloon genomic evaluation system

<table>
<thead>
<tr>
<th>REL&lt; 0.50</th>
<th>0.50-0.74</th>
<th>≥ 0.75</th>
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<tbody>
<tr>
<td>N</td>
<td>629</td>
<td>163</td>
</tr>
<tr>
<td>EBV&lt;sub&gt;W&lt;/sub&gt;</td>
<td>0.24 (0.12)</td>
<td>0.63 (0.07)</td>
</tr>
<tr>
<td>GEBV&lt;sub&gt;W&lt;/sub&gt;</td>
<td>0.43 (0.10)</td>
<td>0.69 (0.06)</td>
</tr>
<tr>
<td>GEBV&lt;sub&gt;W+M&lt;/sub&gt;</td>
<td>0.82 (0.04)</td>
<td>0.88 (0.02)</td>
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### ssBAYES

- allowed optimal use of MACE EBV
- all sires (also REL< 0.50) becoming publishable

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## Proof of Concept – Results for Milk Yield

### Recovery of large amounts of foreign phenotypic information (expressed as daughter equivalents) through the incorporation of MACE EBV into the Walloon genomic evaluation system

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<tr>
<td>EBV&lt;sub&gt;W&lt;/sub&gt;</td>
<td>3.5</td>
<td>17.5</td>
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<tr>
<td>GEBV&lt;sub&gt;W&lt;/sub&gt;</td>
<td>7.8</td>
<td>22.6</td>
</tr>
<tr>
<td>GEBV&lt;sub&gt;W+M&lt;/sub&gt;</td>
<td>45.9</td>
<td>73.0</td>
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### ssBAYES

- recovered on average at least 38 daughter equivalence from MACE

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Conclusions

Single-Step Bayesian Genomic Evaluation (ssBAYES)
- Bayesian approach integrates well MACE results into ssGBLUP
  - Recovers indirectly large amount of phenotypic information
- Improved genomic prediction strategy in dairy cattle
  - Especially for small population
- Optimal approach in many situations:
  - Deregression should (needs to) be avoided
  - Limited local, but extensive external phenotypic information
  - Optimal combination of different sources needed
  - Easy to deal with double counting (allows to + or – information)

Conclusions

Extension to Other Settings and Species
- Developed for dairy cattle (for a small population)
- Multi-trait version under development
  - Adding to local (novel) trait external EBV for other, correlated, trait(s)
- Approach could also be of interest for (some examples)
  - Beef: integration of external EBV (EPD) into limited genotyped populations
  - Swine: use of field data EBV in genomic evaluations using station data
- Bayesian priors on every type of effect
  - “Fixed” and random effects: genetic (e.g., additive, non-additive, SNPs), non genetic

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Maximum flexibility
(cf origin of Bayesian method for beef evaluations)

If interested in collaborations
Do not hesitate to contact us!
Acknowledgements

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