Can MACE and ssGBLUP cohabitate without double-counting?

Jeremie Vandenplas
06/02/2017
Aim

Investigation of possible double-counting within MACE if the MACE input comes from national ssGBLUP integrating MACE information
MACE requires DRP and EDC

⇒ Deregression of national EBV
Current situation + genomic evaluation

- Genomic (pre-)selection
- MACE: no (obvious?) double-counting

Pribyl et al., 2012; Vandenplas et al., 2014; VanRaden et al., 2009
What happens with national ssGBLUP?

- Double-counting of (pedigree-)genomic information
  - Importance of the **deregression** of national GEBV
Avoiding double-counting of genomic info

Solutions?

1. MACE

- **EDC without pedigree-genomic information**
- **Deregression of GEBV** by mimicking a ssGBLUP
  - \( H^{-1} \) for all (genotyped) bulls
  - **EDC** = Amount of information coming from
    - own records
    - relatives (national daughters)
  
⇒ no pedigree-genomic information
EDC without pedigree-genomic info

Different estimation approaches

a. Current approach
   1. Estimation of REL based on own performance
   2. Combination of sources of information

b. Solving \[ \text{diag} \left( (\text{EDC} + \mathbf{H}^{-1} \lambda)^{-1} \right) = \text{PEV} \]

EDC to be estimated
Pedigree-genomic relationship matrix between (genotyped) bulls
Prediction error variances from national ssGBLUP

Fikse and Banos, 2001; Vandenplas et al., 2017
Slovenian ssGBLUP integrating IG GEBV

Internally used bulls

Internally unused bulls

Both avoided

Both avoided

Relatives - Not avoided

Relatives - Not avoided

Double-counting (mostly) avoided

Overestimation due to double-counting of pedigree-genomic information

InterGenomics REL

InterGenomics REL

Vandenplas et al., 2017
Avoiding double-counting of genomic info

Solutions?

1. MACE
   - EDC without pedigree-genomic information
   - Deregression of GEBV by mimicking a ssGBLUP

2. MACE $\Rightarrow$ GMACE
   - EDC with genomic information
   - Deregression of GEBV by mimicking a BLUP
     - $A^{-1}$ for all (genotyped) bulls

VanRaden and Sullivan, 2010
Double-counting: pedigree-genomic info

- **Impact of double-counting** (e.g., Fikse and Banos, 2001; Vandenplas et al., 2014; Calus et al., 2016)
  - **EBV**: low
  - **REL**: overestimation
    - Especially for animals with low REL (cows, young bulls)

- **Solutions exist**
  - Must be tested (in the context of ssGBLUP)
What happens with ssGBLUP+MACE?

1. National data → National ssGBLUP → GEBV
2. National data → National ssGBLUP → GEBV → MACE → MACE EBV
3. National data → National ssGBLUP → GEBV → MACE
What happens with ssGBLUP+MACE?

- Double-counting of own national information “solved”
What happens with ssGBLUP+MACE?

- Double-counting of own national information "solved"
- Double-counting of "foreign" information at MACE level
Double-counting: foreign information

- Double-counting at MACE level
  - BUT specific to each national evaluation!

- DRP + EDC from national ssGBLUP+MACE
  - Free of pedigree-genomic information
  - Includes
    - National information
    - Foreign information provided by other ssGBLUP+MACE
Avoiding double-counting of foreign info

1. Residual covariances (~GMACE)?

2. Deregression of foreign information
   ➔ Subtraction of foreign information from the total amount of information used in ssGBLUP+MACE

3. Others?
External info = EBV+REL from joint evaluation (national + foreign data)

- Amount of internal information: ~46%

<table>
<thead>
<tr>
<th>Correlation</th>
<th>External</th>
<th>Internal</th>
</tr>
</thead>
<tbody>
<tr>
<td>Joint - Internal</td>
<td>0.57 (0.13)</td>
<td>0.93 (0.02)</td>
</tr>
<tr>
<td>Joint – (Internal + ext. info)</td>
<td>0.96 (0.02)</td>
<td>0.98 (0.00)</td>
</tr>
<tr>
<td>Joint - (Internal + ext. info. – int. info)</td>
<td>&gt;0.99 (0.00)</td>
<td>&gt;0.99 (0.00)</td>
</tr>
</tbody>
</table>

⇒ Double-counting avoided
Walloon evaluation + MACE info

- MACE includes Walloon information ➔ double-counting
- Ref.: MACE EBV

<table>
<thead>
<tr>
<th>Milk yield</th>
<th>Corr.</th>
<th>Regr. coef.</th>
<th>REL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Walloon</td>
<td>0.89</td>
<td>0.87</td>
<td>0.74 (0.22)</td>
</tr>
<tr>
<td>Walloon+MACE</td>
<td>0.99</td>
<td>0.98</td>
<td>0.91 (0.05)</td>
</tr>
<tr>
<td>Walloon+MACE - Walloon</td>
<td>0.99</td>
<td>&gt;0.99</td>
<td>0.90 (0.06)</td>
</tr>
</tbody>
</table>

- Low impact
- To be evaluated per national evaluation, type of animals,...

Vandenplas et al., 2014
ssGMACE?

MACE using a pedigree-genomic relationship matrix?
Conclusions

- Double-counting can be avoided (theoretically?)
  - Pedigree-genomic information
  - Foreign information

- Solutions exist!
  - Must be tested
  - In practice, many approximations at several stages

- Impact of double-counting may differ among countries
Questions?