Accuracies of multi-breed genomic evaluation using joint estimation of SNP effects

Y. Steyn, D.A.L. Lourenco, B. Fragomeni & I. Misztal
Introduction

- Multi-breed evaluations a common challenge
- Shared SNP model/effects
- Joint G-matrix simple
- At a cost
- Too many breeds
- Jersey & Holstein
Objective

Investigate the accuracy of multi-breed evaluations (up to 5 breeds) by using different SNP densities and shared SNP effects
Materials and Methods

Simulation using QMSim16 (Sargolzaei & Shenkel, 2009)

- 5 Breeds
- Heritability = 0.30
- 18 chromosomes
- Specified chromosome length & markers per chromosome
- 400 potential QTL (gamma shape 0.4)
- Mutation rate = $2.5 \times 10^{-5}$
- 40K SNPs
10 000 animals

1000 generations
Random

4 000 animals

Breed A
40 males
400 females
Litter size = 6

Breed B
100 males
800 females
Litter size = 5

Breed C
100 males
600 females
Litter size = 6

Breed D
80 males
720 females
Litter size = 5

Breed E
40 males
480 females
Litter size = 7

40 generations
Random

10 generations
Selection

24 400
Genotyped: 5 342

40 900
Genotyped: 5 517

36 700
Genotyped: 5 434

36 800
Genotyped: 5 320

34 120
Genotyped: 5 290
Materials and Methods

- Single-step GBLUP
- Validation on last generation
- \( \text{Acc} = \text{cor}(\text{GEBV, TBV}) \)
Validation
Accuracy using phenotypes of Breed A- 40K
Accuracy using phenotypes of Breed B- 40K
Accuracy using phenotypes of AB - 40K
Accuracy using phenotypes of ABC - 40K

The bar chart illustrates the accuracy using phenotypes of ABC - 40K. The accuracy values are represented for different categories labeled A, B, C, D, and E. The chart compares two phenotypes: AB and ABC.
Accuracy using phenotypes of ABCD - 40K

- AB
- ABC
- ABCD
Accuracy using phenotypes of ABCDE-40K

Average loss: 0.004
Accuracy

\[ Me = 4NeL \]

Independent chromosome segments

Chromosome length (Morgan) 18

Effective population size

\[ \frac{1}{2}\Delta F \]

Generally corresponds to Eigenvalues explaining 98% variation

Average = 41

Daetwyler et al. (2010)

Pocrnic et al. 2017
## Eigenvalues

<table>
<thead>
<tr>
<th>Animal</th>
<th>Ne</th>
<th>Eigen</th>
</tr>
</thead>
<tbody>
<tr>
<td>Angus</td>
<td>113</td>
<td>10.6K</td>
</tr>
<tr>
<td>Holstein</td>
<td>149</td>
<td>14K</td>
</tr>
<tr>
<td>Pig</td>
<td>48</td>
<td>4.1K</td>
</tr>
<tr>
<td>Study</td>
<td>41</td>
<td>1.8K</td>
</tr>
</tbody>
</table>
Accuracy using phenotypes of ABCDE - 10K

Average loss: 0.03
Accuracy using phenotypes of ABCDE- 5K

Average loss: 0.07
Breed A GEBV accuracy

Correlation between GEBV and TBV

- **40K**
- **10K**
- **5K**

---

**Single**

2-breed

3-breed

4-breed

5-breed
Conclusion

• The accuracy of prediction decreases with the inclusion of more breeds in the same evaluation
• Extent of loss depends on SNP density
• Future:
  - Limit the loss
  - Other species
  - Crossbreeds
  - Real data
Thank you