Estimation of Breeding Values for Haploid Chromosomes

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Introduction

Extreme methods used to estimate genomic breeding values:

- **G-BLUP (genomic relationship matrix)**
  - Straightforward implementation (standard software)
  - Effects and variance components estimated \textit{per animal}

- **Models with explicit estimates per SNP locus (e.g. BayesC)**
  - Implementation is less straightforward
  - Effects estimated \textit{per SNP}
  - Variance components are NOT obtained at ‘animal’ level
Can we model effects at an intermediate, biologically more relevant level?

=> Estimate breeding values at chromosome level

- Straightforward implementation
- Effects and variances can easily be translated to ‘animal’ level
- Identical-by-descent information can be used
- Opportunities for mate allocation
Objective

- Estimate genomic breeding values and variances at chromosome level, and compare to established models.
Models

- A: animal model with A matrix
- G: animal model with G (genomic relationship) matrix
- BayesC: SNP based
- CHROM:
  - Phase genotype data
  - Calculate average similarity between all pairs of haploid chromosomes => per chromosome a matrix with similarities
  - Estimate breeding values and variances (ASReml):
    - for each chromosome in a separate model
    - for all chromosomes simultaneously
Analysis

Data:
- 516 cows with genotypes and phenotypes for fat%
- 41,272 mapped SNPs after editing
- 121 mother-daughter pairs
- Many animals have paternal half-sibs

10-fold cross-validation:
- Each animal had its phenotype predicted once
### Results

<table>
<thead>
<tr>
<th>Model</th>
<th>Res. var</th>
<th>Gen. var</th>
<th>$h^2$</th>
<th>se</th>
<th>Phenotype included</th>
<th>Phenotype excluded</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>0.019</td>
<td>0.148</td>
<td>0.886</td>
<td>0.096</td>
<td>0.996</td>
<td>0.425</td>
</tr>
<tr>
<td>G</td>
<td>0.037</td>
<td>0.120</td>
<td>0.764</td>
<td>0.078</td>
<td>0.984</td>
<td>0.463</td>
</tr>
<tr>
<td>CHROM</td>
<td>0.027</td>
<td>0.368</td>
<td>0.933</td>
<td>0.028</td>
<td>0.985</td>
<td>0.597</td>
</tr>
<tr>
<td>BayesC</td>
<td>0.019</td>
<td></td>
<td></td>
<td></td>
<td>0.998</td>
<td>0.781</td>
</tr>
</tbody>
</table>

Accuracy of predicting phenotype
Heritability per chromosome

Estimated heritability

Chromosome number

- 1 chromosome in model
- all chromosomes in model
Differences in variance components

- Variance components BayesC not on animal level

- Differences in variance components is mainly due to differences in base generation
  - CHROM: generation where similarities between chromosomes are 0
  - A: first generation in pedigree
  - G: current generation

=> Chronological order base generations:
- CHROM << A < G
Conclusion

- Estimation of chromosome GEBV is good alternative

- For comparison of variance components, base generations need to be standardized across models

- For a trait with one gene with a large effect, accuracy CHROM is intermediate to G & BayesC
Acknowledgements

- RobustMilk (providing genotypes); www.robustmilk.eu