Genomic information and inbreeding

AABSC
Inbreeding - revision

• Mating of relatives

• Consequences
  – Many are bad, but not all.....

• Management – restricting mating of relatives
  – Optimal contribution selection

• How does Genomics change this?
  – If performing truncation selection....
  – If performing optimal contribution selection...
Truncation selection

- TBLUP or Pedigree BLUP

\[ V_s = \frac{1}{4} \text{sire} + \frac{1}{4} \text{dam} + \frac{1}{2} \text{MS} \]

- Genomic breeding value (GBLUP)

- Variation in BV among selection candidates
What information is used in BVs

- \( \text{Va} = \frac{1}{4} \text{sire} + \frac{1}{4} \text{dam} + \frac{1}{2} \text{MS} \)

Table 2 - The proportion of variation in breeding value explained by between family (Sire and Dam) and within family (MS) information.

<table>
<thead>
<tr>
<th></th>
<th>LIC</th>
<th>ADHIS</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>BV Sire</td>
<td>Dam</td>
</tr>
<tr>
<td>PA EBV</td>
<td>0.56</td>
<td>0.44</td>
</tr>
<tr>
<td>GEBV</td>
<td>0.43</td>
<td>0.26</td>
</tr>
<tr>
<td>PT</td>
<td>0.21</td>
<td>0.31</td>
</tr>
</tbody>
</table>
Correlation of breeding values and co-selection of relatives

<table>
<thead>
<tr>
<th>Breeding value type</th>
<th>Half sib correlation</th>
<th>Full Sib correlation</th>
<th>Accuracy</th>
</tr>
</thead>
<tbody>
<tr>
<td>PA EBV</td>
<td>0.55</td>
<td>1.0</td>
<td>0.45</td>
</tr>
<tr>
<td>GEBV</td>
<td>0.50</td>
<td>0.85</td>
<td>0.57</td>
</tr>
<tr>
<td>TBV</td>
<td>0.26</td>
<td>0.53</td>
<td>1.0</td>
</tr>
</tbody>
</table>

**Full Sibs**
- share the same Parent average BV (½ sire ½ dam)
- no longer the case with genomics

**Half Sibs**
- Share different PA breeding values
- Small advantage of using G to restrict inbreeding
Sonesson et al 2013

(A) truncation selection - TBLUP

Higher

(B) truncation selection - GBLUP

Lower

----- Selecting 100 sires and 100 dams from 3000 cand. ---- After 10 generations
Truncation selection on breeding values estimated using TBLUP or GBLUP

<table>
<thead>
<tr>
<th>Breeding value estimation</th>
<th>ΔG (se)</th>
<th>ΔF&lt;sub&gt;ped&lt;/sub&gt; (se)</th>
<th>ΔF&lt;sub&gt;IBD&lt;/sub&gt; (se)</th>
</tr>
</thead>
<tbody>
<tr>
<td>TBLUP</td>
<td>2.49 (0.035)</td>
<td>0.0156 (0.0001)</td>
<td>0.0235 (0.0009)</td>
</tr>
<tr>
<td>GBLUP</td>
<td>2.77 (0.026)</td>
<td>0.0053 (0.0002)</td>
<td>0.0209 (0.0005)</td>
</tr>
</tbody>
</table>
Genomics and Optimal contributions

• Measures of genetic merit ($\tilde{g}$)
  – Pedigree vs genomic
    
    *Pedigree based BLUP --- Genomic BLUP*

• Measures of inbreeding
  – Pedigree vs genomic (A or G)
    
    *NRM (Pedigree) --- GRM (genomic)*

\[
\text{Max} = c_t' \tilde{g}_t - \lambda c_t' A_t c_t
\]
Measuring inbreeding

• Pedigree
  – The probability that animals share alleles IBD.

• Genomics
  – GRM (IBS) or what is shared.
  – others
Genomic Inbreeding estimates

• Estimates of the number of homozygotes
  – Sharing of markers (IBS)
  – Long runs of homozygotes (more IBD)

• Genomic relationships (IBS)
  – Various methods
  – Choice of allele frequencies
Example GRM

• \( Z = M - 2(\pi - 0.5) \)
• \( ZZ'/2 * \text{sum } \pi(qi) \) (more weighting to rare alleles)

• Choice of allele frequencies
  – Forni 2012
  – Sets base population
  – Although this is relative and is more important when combining data (Single step)
management

• Optimal contribution

• Pedigree or genomic
  – Pedigree – expected based on IBD prob.
  – Genomic observed (although an estimate)
<table>
<thead>
<tr>
<th>Ntest</th>
<th>$\Delta F_d$</th>
<th>$\Delta G$ (se)</th>
<th>$\Delta F_{ped}$ (se)</th>
<th>$\Delta F_{IBD}$ (se)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>$\Delta F_A$ constraint – GBLUP</td>
<td>$\Delta F_G$ constraint – GBLUP</td>
<td>$\Delta F_A$ constraint – TBLUP</td>
<td>$\Delta F_G$ constraint – TBLUP</td>
</tr>
<tr>
<td>3000</td>
<td>0.005</td>
<td>3.08 (0.035)</td>
<td>0.0050 (0.0001)</td>
<td>0.0211 (0.0004)</td>
</tr>
<tr>
<td>6000</td>
<td>0.005</td>
<td>3.10 (0.035)</td>
<td>0.0048 (0.0001)</td>
<td>0.0226 (0.0004)</td>
</tr>
<tr>
<td>6000</td>
<td>0.010</td>
<td>3.31 (0.037)</td>
<td>0.0098 (0.0003)</td>
<td>0.0422 (0.0008)</td>
</tr>
<tr>
<td>3000</td>
<td>0.005</td>
<td>1.91 (0.026)</td>
<td>0.0041 (0.0001)</td>
<td>0.0051 (0.0001)</td>
</tr>
<tr>
<td>6000</td>
<td>0.005</td>
<td>1.95 (0.024)</td>
<td>0.0039 (0.0001)</td>
<td>0.0053 (0.0001)</td>
</tr>
<tr>
<td>6000</td>
<td>0.010</td>
<td>2.41 (0.028)</td>
<td>0.0071 (0.0002)</td>
<td>0.0102 (0.0002)</td>
</tr>
<tr>
<td>3000</td>
<td>0.005</td>
<td>2.26 (0.003)</td>
<td>0.0050 (0.0001)</td>
<td>0.0068 (0.0001)</td>
</tr>
<tr>
<td>6000</td>
<td>0.005</td>
<td>2.50 (0.003)</td>
<td>0.0049 (0.0001)</td>
<td>0.0074 (0.0001)</td>
</tr>
<tr>
<td>6000</td>
<td>0.010</td>
<td>2.63 (0.003)</td>
<td>0.0102 (0.0002)</td>
<td>0.0151 (0.0003)</td>
</tr>
<tr>
<td>3000</td>
<td>0.005</td>
<td>1.41 (0.041)</td>
<td>0.0193 (0.0004)</td>
<td>0.0121 (0.0002)</td>
</tr>
<tr>
<td>6000</td>
<td>0.005</td>
<td>1.44 (0.039)</td>
<td>0.0185 (0.0004)</td>
<td>0.0122 (0.0002)</td>
</tr>
<tr>
<td>6000</td>
<td>0.010</td>
<td>1.48 (0.046)</td>
<td>0.0300 (0.0008)</td>
<td>0.0183 (0.0003)</td>
</tr>
</tbody>
</table>

Genetic gain ($\Delta G$), rate of inbreeding based on pedigree ($\Delta F_{ped}$) and on genomic IBD ($\Delta F_{IBD}$) relationship matrices at generation G10 when the constraint on relationship was either pedigree-based ($\Delta F_A$) or marker-based ($\Delta F_G$) with TBLUP or GBLUP breeding value estimates.

$^a$Ntest = number of test sibs; $\Delta F_A$ = desired rates of inbreeding; number of selection candidates = 3000.
Entire frontier

![Graph showing Merit (TBV) vs Genomic co-ancestry for GEBV and PA EBV.](image-url)
Half sibs

The graph shows the relationship between Merit (TBV) and genomic co-ancestry for half sibs, with two lines representing genomic and pedigree methods.
Full sibs
Genomic information helps to manage inbreeding

• In two ways:
  • 1. Using genomic relationships helps to restrict genomic inbreeding.
  • 2. GEBV’s utilize more Mendelian sampling variance.