Nordic collaboration
Some of the work in 2010
Across breed GEBVs (simulations by Guosheng Su)

Original populat. → POP1 → POP1 base → POP1 Gen. 1-4 → POP1 Gen. 5

Original populat. → POP2 → POP2 base → POP2 Gen. 1-4 → POP2 Gen. 5

50 sires, 50 dams per gen.
## Across breed GEBVs (simulations by Guosheng Su)

<table>
<thead>
<tr>
<th>Reference</th>
<th>Pop 1</th>
<th>Pop 2</th>
<th>Pop1 + Pop 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>Test</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Test</td>
<td>Pop 1</td>
<td>Pop1</td>
<td>Pop1</td>
</tr>
<tr>
<td>Test</td>
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</tr>
<tr>
<td>Test</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>10 generations</td>
<td>0.70</td>
<td>0.44</td>
<td>0.77</td>
</tr>
<tr>
<td>20 generations</td>
<td>0.67</td>
<td>0.32</td>
<td>0.74</td>
</tr>
<tr>
<td>50 generations</td>
<td>0.69</td>
<td>0.13</td>
<td>0.75</td>
</tr>
</tbody>
</table>
Across FAY/SRB/RDM GEBVs

- Higher accuracy due to larger reference
- Lower accuracy due to opposite phase
- Haplotype structure (within and between red breeds)
- Genomic model with haplotype effects
- IBD based models
Across Red/Jersey/HF GEBVs

> Potential Red/Jersey/Holstein reference of 21000 bulls
More SNPs (600K)

- Imputation by double genotyping some bulls
- Which and how many bulls to genotype with 600 K
- Biggest advantage for across breeds evaluations
Genomic multitrait models (Udder health)

- Genomic model directly on index - can we do better?

- Estimate SNP effects on component traits (multitrait)

- Value of indicator traits?

- Estimate SNP effects on clinical mastitis and blend with index?

- Comparison of multitrait methods (Bayesian vs. GBLUP)
Summary – another busy year

- Joint HF analyses (DSF / DEU / FR / NL)
- Blended GEBV
  - Method developments
  - Routine evaluations / Interbull
- Multi breed analyses
  - FAY/SRB/RDM
  - Red/Jersey/HF
- Dense SNP chips (600 K)
- Multi trait analyses
  - Method comparison
  - Udder health
Summary – another busy year

› What is the best cross validation method?
   › Compare different studies
   › Choose best method for future comparisons

› Breeding plans

› Genomic test day model (method development)

› QTL mapping