Single-step genomic evaluation for fertility in Nordic Red dairy cattle

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Background

- Female fertility genetic evaluations (BLUP) has been done in Nordic countries since 1970’s
- Joint Nordic fertility evaluations have been done since 2005
  - Nordic Cattle Genetic Evaluations NAV
- The model has been upgraded in 2015
  - From sire to animal model
  - From repeatability to multi-trait model for lactations
- Next step: Genomic evaluation

Objective

- Single step genomic model (ssGBLUP) to take into account phenotypic, pedigree and genomic data simultaneously
- Genetic groups may cause problems in the convergence of the genomic model

  → QP-transformation for genomic model

Janne Lehtinen / MTT:n arkisto

Traits

- NAV fertility evaluations are done in two different trait groups
- Model for trait group 1 contains 11 correlated traits
  - Heifer traits:
    - non-return rate (NRR0)
    - length of service period (IFL0)
  - Cow traits for lactations 1-3:
    - non-return rate (NRR1, NRR2, NRR3)
    - interval from calving to first breeding (ICF1, ICF2, ICF3)
    - length of service period (IFL1, IFL2, IFL3)

Data

- RDC data in routine joint Nordic fertility evaluations in 2015
  - Number of animals with observations: 4,057,316
  - Number of animals in the pedigree: 5,257,722
  - Number of genotyped animals: 23,514
- Genetic parameters used in routine joint Nordic fertility evaluations in 2015
  - Low heritabilities (0.015-0.04)
  - High correlations among traits (0.60-0.88 between lactations)

Relationships in genomic evaluation

- In ssGBLUP the inverse of the relationship matrix is

$$\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix}$$

  where
  - **A** is relationships based on the pedigree
  - $\mathbf{A}_{22}$ is relationships based on the pedigree for genotyped animals
  - **G** is relationships based on genomic information and $\mathbf{G}_w = (1 - w)\mathbf{G} + w\mathbf{A}_{22}$, where w is weight for polygenic information (we used 10%)

QP-transformation for genomic model

- Let rows in matrix **Q** describe phantom parent group (PPG) compositions to each animal
- Usually, **A**$^{-1}$ is augmented to include PPG:

$$\mathbf{H}^{-1} = \begin{bmatrix} \mathbf{A}^{-1} + \begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1} \end{bmatrix} & -\mathbf{A}^{-1}\mathbf{Q} \\ -\mathbf{Q}'\mathbf{A}^{-1} & \mathbf{Q}'\mathbf{A}^{-1}\mathbf{Q} \end{bmatrix} = \mathbf{A}^* + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix}$$

- However, contributions to PPG due to genomic relationships can be similarly accounted (Misztal et al., 2013):

$$\mathbf{H}^{-1} = \mathbf{A}^* + \begin{bmatrix} \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1} & \boxed{-(\mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1})\mathbf{Q}_2} \\ \mathbf{0} & \boxed{-\mathbf{Q}_2'(\mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1})} & \boxed{\mathbf{Q}_2'(\mathbf{G}_w^{-1} - \mathbf{A}_{22}^{-1})\mathbf{Q}_2} \end{bmatrix}$$

where $\mathbf{Q}_2$ is a submatrix for genotyped animals.

Analyses

- Three analyses were performed
  1. BLUP
  2. ssGBLUP, where QP-transformation for pedigree based relationship matrix only
  3. ssGBLUP_QP, where QP-transformation both for pedigree and genomic information based relationships
- Models were solved by MiX99, which uses iterative preconditioned conjugate gradient algorithm (PCG)

Comparisons between analyses

- Convergence
- Breeding values (for ICF2 and NRR3 shown as an example):
    1. Genetic trend based on sires' (G)EBV
    2. Annual EBV and GEBV correlations for both sires and females
- Validation

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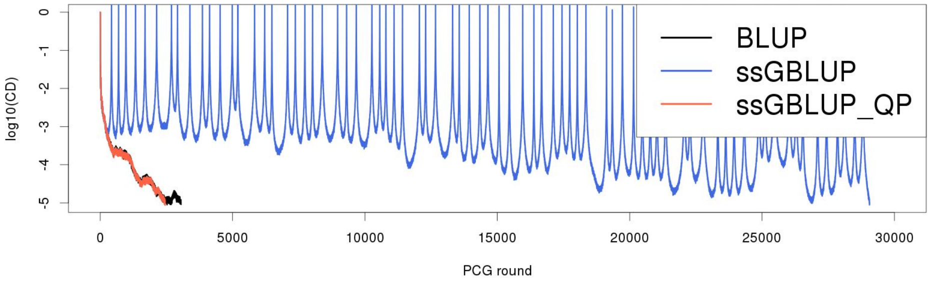
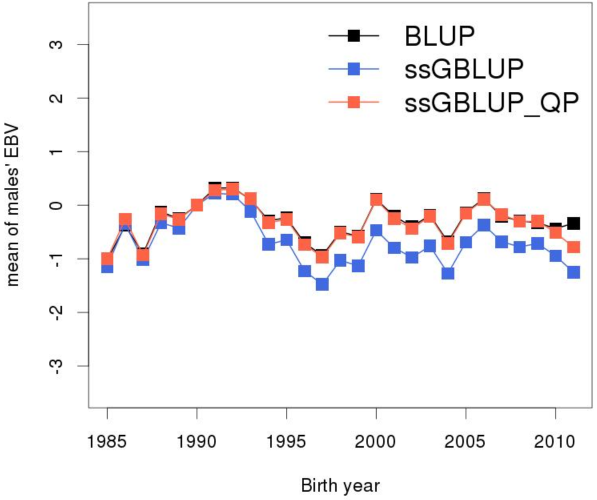
Convergence

Model	PCG rounds	Time	Time / round
BLUP	3 052	4 h 40 min	6 s
ssGBLUP	29 063	~ 7 d	20 s
ssGBLUP_QP	2 453	13 h 21 min	20 s

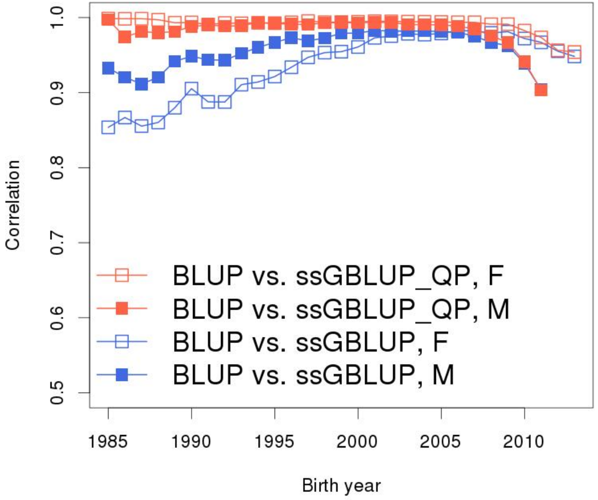


Comparisons for interval from calving to first breeding in second parity (ICF2)

Genetic trend

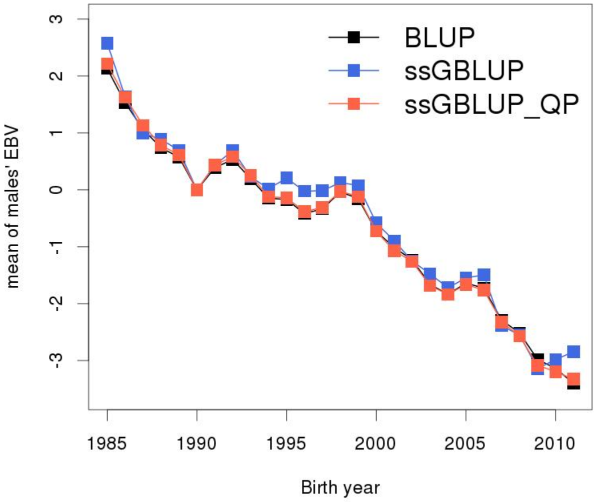


Annual correlations

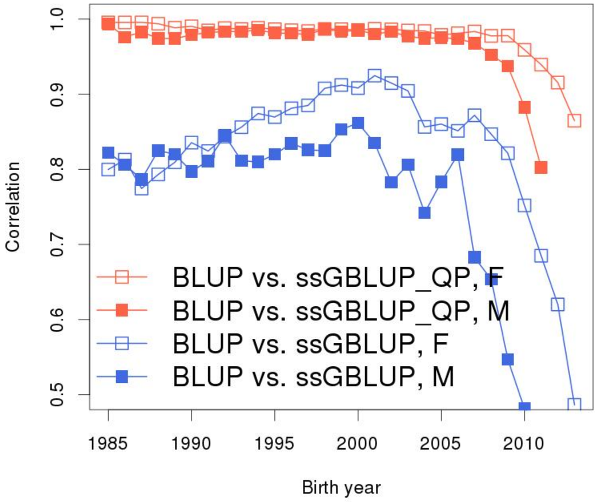


Comparisons for non-return rate in third parity (NRR3)

Genetic trend



Annual correlations



Validation

- Validation reliability (R^2) and regression coefficient (b_1) from the regression of deregressed genetic predictions from the full data on EBV and GEBV from the reduced data
  - Observations from the latest 6 years were removed
- Validation group contained 867 genotyped bulls
  - Sires for which effective record contribution ERC > 10 based on full data and ERC = 0 based on reduced data

Validation reliabilities R^2

Trait	EBV	GEBV	$\Delta_{GEBV-EBV}$
NRR0	0.13	**0.18**	+0.05
IFL0	**0.20**	0.24	+0.04
NRR1	0.11	0.21	+0.10
ICF1	0.17	0.28	+0.11
IFL1	0.15	**0.33**	+0.18
NRR2	**0.08**	0.19	+0.11
ICF2	0.17	0.29	+0.12
IFL2	0.15	0.32	+0.17
NRR3	0.10	0.22	+0.12
ICF3	0.17	0.28	+0.11
IFL3	0.16	**0.33**	+0.17

NRR = Non-return rate
IFL = Length of service period
ICF = Interval from calving to first breeding

0 = Heifer
1-3 = Parity

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Regression coefficients b_1

Trait	EBV	GEBV	$\Delta_{GEBV-EBV}$
NRR0	1.01	**0.74**	-0.27
IFL0	**1.14**	0.82	-0.32
NRR1	0.92	0.78	-0.14
ICF1	1.09	0.91	-0.18
IFL1	1.03	**0.98**	-0.05
NRR2	1.09	0.83	-0.26
ICF2	**0.88**	0.85	-0.03
IFL2	0.95	0.97	+0.02
NRR3	0.98	0.87	-0.11
ICF3	0.97	0.88	-0.09
IFL3	0.98	**0.98**	-0.00

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Conclusions

- Genomic evaluation for fertility in Nordic RDC was feasible.
- Accounting of genetic groups in genotype information via QP-transformation was necessary:
    - Faster convergence
    - More consistent genomic breeding values when compared with traditional breeding values
- Model validation showed that ssGBLUP improved the fertility evaluations, especially for cow traits.

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Thank you!

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