Heterogeneous Variance Adjustment in Across-Country Genetic Evaluation with Country-Specific Heritabilities

M.H. Lidauer[1], E.A. Mäntysaari[1], J. Pösö[2], J.-Å. Eriksson[3], U.S. Nielsen[4], G.P. Aamand[5]

[1]MTT Agrifood Research Finland, [2]Faba Service, Finland, [3]Swedish Dairy Association, [4]The Danish Agricultural Advisory, [5]NAV Nordic Cattle Genetic Evaluation

MTT faba svenskmjölk SWEDISH DAIRY ASSOCIATION DANSK·KVÆG Nordisk Avlsværdivurdering

Motivation

- Across-country genetic evaluation
  1. Single trait approach
  2. Multiple trait approach but $r_{g\ \text{across countries}} = \text{unity}$
  3. Multiple trait approach with $r_{g\ \text{across countries}} < \text{unity}$
- Approaches 1 and 2 yield one set of breeding values

→ how to ensure a homogeneous genetic variance across countries?

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- Nordic random regression TDM for Red Cattle
  - Multiple trait approach but $r_{g \text{ across countries}} = 1.0$
  - Finnish Ayrshire, Red Danish Cattle, Swedish Red Breed
  - Different variance components for each country (breed)

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Estimated heritabilities compiled for 305-d yields

Trait	Milk			Protein			Fat		
Lactation	1	2	3	1	2	3	1	2	3
Finnish Ayrshire	**0.38**	**0.33**	**0.31**	**0.33**	**0.32**	**0.31**	**0.35**	**0.34**	**0.33**
Red Danish Cattle	**0.42**	**0.35**	**0.34**	**0.38**	**0.35**	**0.35**	**0.39**	**0.35**	**0.34**
Swedish Red Breed	**0.44**	**0.33**	**0.34**	**0.43**	**0.34**	**0.35**	**0.43**	**0.34**	**0.37**

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Aim

- Estimation of genetic variances using Mendelian sampling deviations
- Calibration of the heterogeneous variance adjustment method to ensure homogeneous genetic variance across countries

Estimation of genetic variance from Mendelian sampling deviations

- $\hat{\sigma}^2_{a_t}$ estimated from a group of animals (Sullivan, 1999):

$$\hat{\sigma}^2_{a_t} = \frac{1}{n_t} \sum_{k=1}^{n_t} d_k \left[\hat{m}^2_{kt} + PEV(\hat{m}_{kt}) \right]$$

  - n_t number of animals
  - d_k is 2, 4/3, or 1 depending on known parents
  - $\hat{m}_{kt} = EBV_{kt} - ½\left(EBV_{st} + EBV_{dt}\right)$ Mendelian sampling deviation for animal *k* and trait *t*
  - $PEV(\hat{m}_{kt})$ prediction error variance for animal *k* and trait *t*

Estimation of genetic variance from Mendelian sampling deviations

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- Considering formulation:

$$PEV = \sigma_a^2 - \left[Var(\hat{u})/Var(u)\right]\sigma_a^2$$

- $\hat{\sigma}_{a_t}^2$ can be estimated for a sufficiently large animal group:

$$\hat{\sigma}_{a_t}^{2[q]} = \frac{1}{n_t}\sum_{k=1}^{n_t} d_k \hat{m}_{kt}^{2[q]} \left[\sum_{k=1}^{n_t} d_k \tilde{m}_{kt}^2 \Big/ \sum_{k=1}^{n_t} d_k \hat{\tilde{m}}_{kt}^2 \right]$$

  - $\hat{m}_{kt}$ Mendelian sampling deviation from the real data
  - $\tilde{m}_{kt}$ true Mendelian sampling deviation of the simulated data
  - $\hat{\tilde{m}}_{kt}$ estimated Mendelian sampling deviation from the simulated data

Full model sampling to obtain $\tilde{m}_{ktr}$ and $\hat{\tilde{m}}_{ktr}$

- Nordic Red Cattle yield evaluation data
  - 68 million test-day records on milk, protein and fat
  - 4.3 million animals

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- Multiplicative reduced rank random regression TDM:

$$\mathbf{y}_{ti}\lambda_{ti} = \mathbf{X}_{ti}\mathbf{b}_t + \mathbf{T}_{ti}\mathbf{h}_t + \mathbf{Z}_{ti}\mathbf{a} + \mathbf{U}_{ti}\mathbf{p} + \mathbf{V}_{ti}\mathbf{w} + \mathbf{e}_{ti}$$

$\mathbf{y}_{ti}$	observations of trait *t* in stratum *i*
λ_{ti}	multiplicative adjustment factor for stratum *i*
$\mathbf{b}_t, \mathbf{h}_t$	vector of fixed effects for trait *t*
$\mathbf{a}, \mathbf{p}, \mathbf{w}$	add. genetic and non-add. genetic animal effects
$\mathbf{e}_{ti}$	random residuals

Full model sampling to obtain $\tilde{m}_{ktr}$ and $\hat{\tilde{m}}_{ktr}$

- Following García-Cortés et al. (1992)
  - $\tilde{\mathbf{b}}_t = \mathbf{0}, \tilde{\mathbf{h}}_t = \mathbf{0}$
  - $\tilde{\mathbf{a}} = (\mathbf{L} \otimes \mathbf{T}_{\mathrm{a}})\mathbf{x}_{\mathrm{n_a t_a}}$
  - $\tilde{\mathbf{p}} = (\mathbf{I}_{\mathrm{n_p}} \otimes \mathbf{T}_{\mathrm{p}})\mathbf{x}_{\mathrm{n_p t_p}}$, $\tilde{\mathbf{w}} = (\mathbf{I}_{\mathrm{n_w}} \otimes \mathbf{T}_{\mathrm{w}})\mathbf{x}_{\mathrm{n_w t_w}}$
  - $\tilde{\mathbf{e}}_{\mathrm{j}} = \mathbf{P}_{\mathrm{j}} \mathbf{T}_{\mathrm{r}} \mathbf{x}_{\mathrm{t_r}}$

    where $\mathbf{L}, \mathbf{T}_{\mathrm{a}}, \mathbf{T}_{\mathrm{p}}, \mathbf{T}_{\mathrm{w}}, \mathbf{T}_{\mathrm{r}}$ are Cholesky decompositions of A and of the corresponding VCV matrices,
    and $\mathbf{x}_{\mathrm{n}} \sim N(\mathbf{0}, \mathbf{I}_{\mathrm{n}})$ are random samples from stand.N.D.
  - $\tilde{\lambda}_{ti} = 1$

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    and $\mathbf{x}_{\mathrm{n}} \sim N(\mathbf{0}, \mathbf{I}_{\mathrm{n}})$ are random samples from stand.N.D.
  - $\tilde{\lambda}_{ti} = 1$
- … yields: $\tilde{\mathbf{y}}_{ti}\tilde{\lambda}_{ti} = \mathbf{X}_{ti}\tilde{\mathbf{b}}_t + \mathbf{T}_{ti}\tilde{\mathbf{h}}_t + \mathbf{Z}_{ti}\tilde{\mathbf{a}} + \mathbf{U}_{ti}\tilde{\mathbf{p}} + \mathbf{V}_{ti}\tilde{\mathbf{w}} + \tilde{\mathbf{e}}_{ti}$

Heterogeneity of genetic variance across countries

- Estimation of genetic variances
  - Applied to evaluation model which accounts for heterogeneous variance within traits only
  - For each cow birth year group

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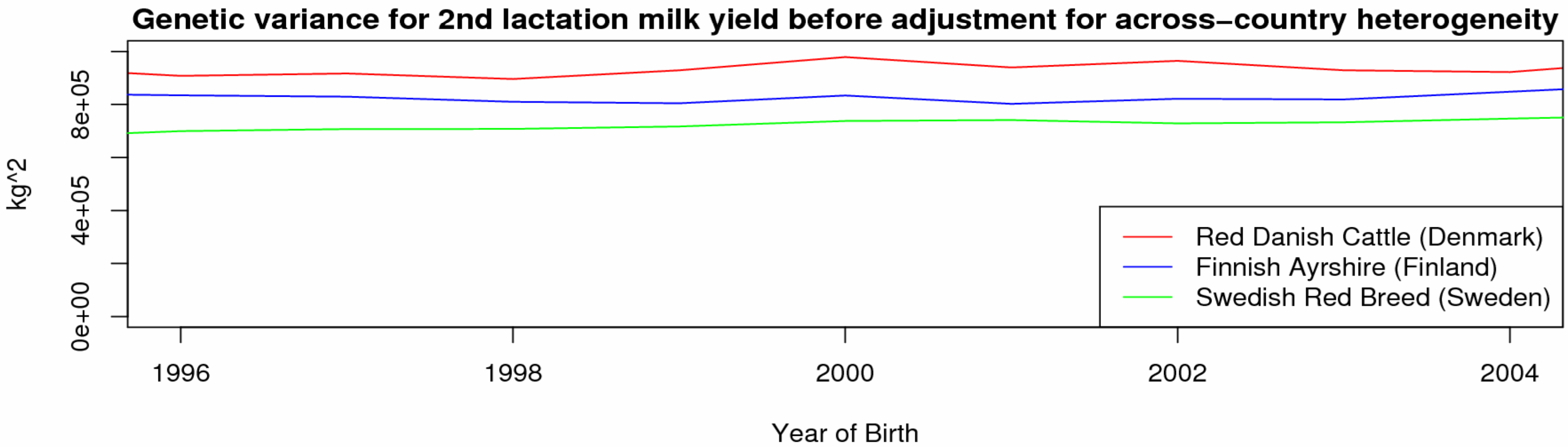

Calibration of heterogeneous variance adjustment method

- Multiplicative mixed model approach (Meuwissen et. al., 1996)
  - Scales all effects in the model in proportionality to the residual variance
  - Converges to a set of solutions, which fulfill:

$$n_{ti}\hat{\sigma}^2_{e_t} = \mathbf{y}^{\mathrm{T}}_{ti}\lambda_{ti}\hat{\mathbf{e}}_{ti}$$

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modified condition

$$n_{ti}\hat{\sigma}^2_{e_t}\alpha_t = \mathbf{y}^{\mathrm{T}}_{ti}\lambda_{ti}\hat{\mathbf{e}}_{ti}$$

where α_t is a calibration factor for trait t

Calibration of heterogeneous variance adjustment method

- Iterative procedure to obtain α_t
  - initialize q=1, $\alpha_t^{[q]} = 1.0$
  - Solve multiplicative random regression TDM
  - Estimate genetic variances $\hat{\sigma}_{a_t}^{2[q]}$
  - Update calibration factors $\alpha_{t.c}^{[q+1]} = \alpha_{t.c}^{[q]} \hat{\sigma}_{a_{t.BASE}}^{2[q]} \Big/ \hat{\sigma}_{a_{t.c}}^{2[q]}$

    where *c* is either Finland or Denmark and *BASE* is Sweden
  - Repeat until differences in genetic SDs < +/- 1%

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  - Repeat until differences in genetic SDs < +/- 1%
- Animal groups for estimation of genetic variances
  - All cows born in 2002 to 2004

Finnish Ayrshire:	**180 573**
Red Danish Cattle:	**50 067**
Swedish Red Breed:	**159 961**

Results

- One data sample was sufficient for sampling the mean prediction error variances for the three cow groups
- Calibration factors converged after six calibration cycles

  Range of calibration factors: 0.75 … 1.38

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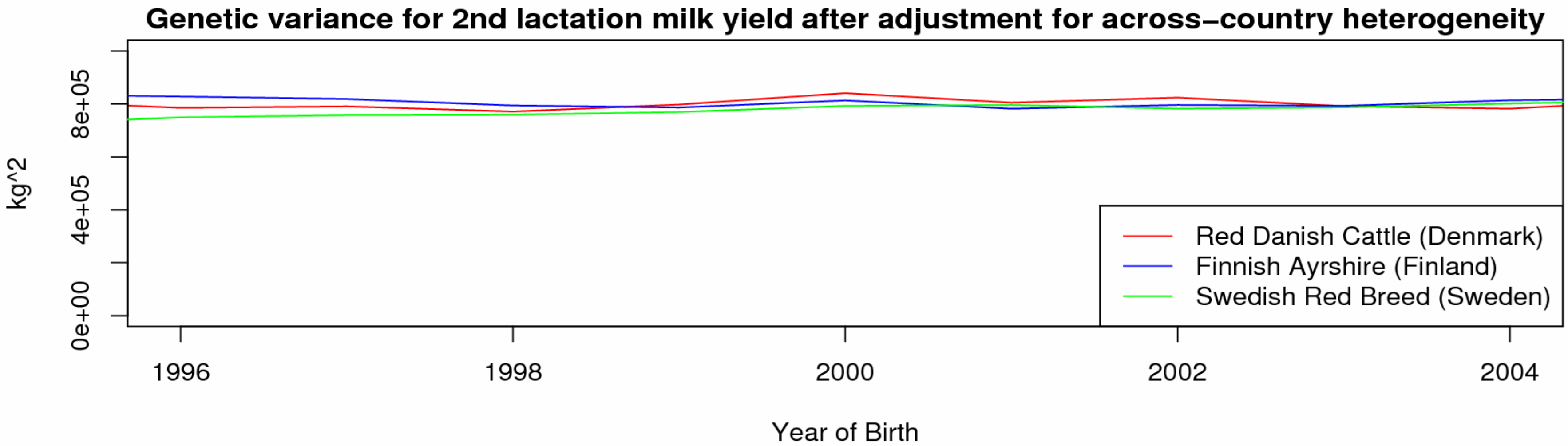

Results

- Genetic standard deviations by trait and country (in kg for 305d yields)

Trait	Milk			Protein			Fat		
Lactation	1	2	3	1	2	3	1	2	3
Finnish Ayrshire	**742**	**895**	**936**	**21.0**	**28.6**	**30.5**	**27.4**	**36.2**	**40.2**
Red Danish Cattle	**739**	**894**	**933**	**21.2**	**28.6**	**30.1**	**27.6**	**36.4**	**40.1**
Swedish Red Breed	**740**	**889**	**931**	**21.3**	**28.3**	**30.0**	**27.7**	**36.0**	**39.8**

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- Correlations between EBVs with and without across-country calibration

Across all cows born 2002 – 2007:	0.9973 – 0.9990
Finnish Ayrshire:	0.9959 – 0.9988
Red Danish Cattle:	0.9987 – 0.9995
Swedish Red Breed:	0.9998 – 0.9999

Conclusions

- Estimation of genetic variance from Mendelian sampling deviations is useful for model development and validation
- Monte Carlo sampling for PEV requires one replicate only (one additional BLUP run) when mean PEV are needed
- Calibration procedure yielded homogeneous genetic variances across countries
- And it is applicable for any heterogeneous variance adjustment method which scales the observations

THANK YOU

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faba

svenskmjölk
SWEDISH DAIRY ASSOCIATION

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