Joint Nordic Test Day Model: Evaluation Model

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Nordisk Avlsværdivurdering

Aim

Describing of the model

- environmental effects
- adjustment for heterogeneous variance

Data

All dairy cattle from Denmark, Finland, & Sweden

Orig. Red Danes /
Finnish Ayrshire / **Swedish Red** /
Brown Swiss / Red Holstein /
Montebeliarde / Norwegian Red /
Canadian Ayrshire / **Finncattle**

Holstein / Danish Friesian /
Finnish Friesian / Swedish Friesian /
Danish Red and White

Danish Jersey /
Swedish Jersey / US Jersey /
NZ Jersey

	Red Breeds	**Holstein**	**Jersey**
Animals	**4.1 mil.**	**6.6 mil.**	**0.6 mil.**
TD yields	**45.6 mil.**	**81.6 mil.**	**7.2 mil.**
305d yields	**1.9 mil.**	**1.6 mil.**	**-**

Model

- **Based on a meta-model approach**
  - reduced rank, random regression
  - describing TD yields and 305d yields
  - different variance components across countries

    but: genetic correlation of 1.0 across countries
- **Multiple trait: milk, protein, fat**
  - bimonthly measurements for protein and fat
- **Parities and countries are different traits**

  → 27 traits

Structure of the model

Given for one biological trait (t) and type of data (T_c, L):

$$\begin{bmatrix}\boldsymbol{\Lambda}_{T_c1t}\mathbf{y}_{T_c1t}\\ \boldsymbol{\Lambda}_{L1t}\mathbf{y}_{L1t}\\ \boldsymbol{\Lambda}_{T_c2t}\mathbf{y}_{T_c2t}\\ \boldsymbol{\Lambda}_{L2t}\mathbf{y}_{L2t}\\ \boldsymbol{\Lambda}_{T_c3t}\mathbf{y}_{T_c3t}\\ \boldsymbol{\Lambda}_{L3t}\mathbf{y}_{L3t}\end{bmatrix} = \begin{bmatrix}\mathbf{X}_{T_c1t}\mathbf{b}_{T_c1t}\\ \mathbf{X}_{L1t}\mathbf{b}_{L1t}\\ \mathbf{X}_{T_c2t}\mathbf{b}_{T_c2t}\\ \mathbf{X}_{L2t}\mathbf{b}_{L2t}\\ \mathbf{X}_{T_c3t}\mathbf{b}_{T_c3t}\\ \mathbf{X}_{L3t}\mathbf{b}_{L3t}\end{bmatrix} + \begin{bmatrix}\mathbf{K}_{T_c1t} & \mathbf{0} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{K}_{L1t} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{K}_{T_c2t} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{K}_{L2t}\\ \mathbf{0} & \mathbf{0} & \mathbf{K}_{T_c3t} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{K}_{L3t}\end{bmatrix}\begin{bmatrix}\mathbf{h}_{T_c1t}\\ \mathbf{h}_{L1t}\\ \mathbf{h}_{T_c23t}\\ \mathbf{h}_{L23t}\end{bmatrix} + \begin{bmatrix}\mathbf{L}_{T_c1t} & \mathbf{0}\\ \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{L}_{T_c1t}\\ \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{L}_{T_c3t}\\ \mathbf{0} & \mathbf{0}\end{bmatrix}\begin{bmatrix}\mathbf{s}_{T_c1t}\\ \mathbf{s}_{T_c23t}\end{bmatrix} + \begin{bmatrix}\mathbf{M}_{T_c1t} & \mathbf{0}\\ \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{M}_{T_c2t}\\ \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{M}_{T_c3t}\\ \mathbf{0} & \mathbf{0}\end{bmatrix}\begin{bmatrix}\mathbf{d}_{T_c1t}\\ \mathbf{d}_{T_c23t}\end{bmatrix}$$

environmental effects

random animal effects

$$+\begin{bmatrix}\mathbf{R}_{T_c1t} & \mathbf{0} & \mathbf{0}\\ \mathbf{R}_{L1t} & \mathbf{0} & \mathbf{0}\\ \mathbf{0} & \mathbf{R}_{T_c2t} & \mathbf{0}\\ \mathbf{0} & \mathbf{R}_{L2t} & \mathbf{0}\\ \mathbf{0} & \mathbf{0} & \mathbf{R}_{T_c3t}\\ \mathbf{0} & \mathbf{0} & \mathbf{R}_{L3t}\end{bmatrix}\begin{bmatrix}\mathbf{f}_{1t}\\ \mathbf{f}_{2t}\\ \mathbf{f}_{3t}\end{bmatrix} + \begin{bmatrix}\mathbf{Q}_{T_c1t}\mathbf{g}_{T_c1t}\\ \mathbf{Q}_{L1t}\mathbf{g}_{L1t}\\ \mathbf{Q}_{T_c2t}\mathbf{g}_{T_c2t}\\ \mathbf{Q}_{L2t}\mathbf{g}_{L2t}\\ \mathbf{Q}_{T_c3t}\mathbf{g}_{T_c3t}\\ \mathbf{Q}_{L3t}\mathbf{g}_{L3t}\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_{aT_c1t} & \mathbf{0}\\ \mathbf{Z}_{aL1t} & \mathbf{0}\\ \mathbf{0} & \mathbf{Z}_{aT_c2t}\\ \mathbf{0} & \mathbf{Z}_{aL2t}\\ \mathbf{0} & \mathbf{Z}_{aT_c3t}\\ \mathbf{0} & \mathbf{Z}_{aL3t}\end{bmatrix}\begin{bmatrix}\mathbf{a}_{1}\\ \mathbf{a}_{23}\end{bmatrix} + \begin{bmatrix}\mathbf{Z}_{pT_c1t}\mathbf{p}_{T_c1}\\ \mathbf{Z}_{pL1t}\mathbf{p}_{L1}\\ \mathbf{Z}_{pT_c2t}\mathbf{p}_{T_c2}\\ \mathbf{Z}_{pL2t}\mathbf{p}_{L2}\\ \mathbf{Z}_{pT_c3t}\mathbf{p}_{T_c3}\\ \mathbf{Z}_{pL3t}\mathbf{p}_{L2}\end{bmatrix} + \begin{bmatrix}\mathbf{0}\\ \mathbf{0}\\ \mathbf{0}\\ \mathbf{0}\\ \mathbf{Z}_{wT_{fi}3t}\mathbf{w}_{T_{fi}3}\\ \mathbf{0}\end{bmatrix} + \begin{bmatrix}\mathbf{e}_{T_c1t}\\ \mathbf{e}_{L1t}\\ \mathbf{e}_{T_c2t}\\ \mathbf{e}_{L2t}\\ \mathbf{e}_{T_c3t}\\ \mathbf{e}_{L3t}\end{bmatrix}$$

Effects (I)

- **Calving age**
  - lin. + quad. regression on calving age

additionally for Red Breed model:

  - lin. + quad. regression on calving age x breed proportion
    - for Brown Swiss and for Holstein in Danish traits
    - for Holstein and for Finncattle in Finnish traits

Effects (II)

- **Specific to lactation yield traits**
  - calving year-month
  - regression on days open
  - preceding calving interval
- **Specific to test-day yield traits**
  - test year-month
  - days carried calf
  - days dry
  - stage of lactation

    2nd order Legendre polynomial + 2 Wilmink exp. terms nested within calving age x test-month x 4-year period

Effects (III)

- **Herd**
  - fixed herd-year
  - random herd-test-day (fixed for Danish Holstein and Jersey)
  - fixed regression on days in milk (for TD-yield traits)

    nested within herd and 5-year period

effects are considered to be the same

in 2nd and 3rd parity

Effects (IV)

- **Heterosis**
  - fixed regression on total sum of heterosis
    - modeled across countries
  - five random heterosis effects within each country
    - one for each of the most important five crosses
    - correlation structure between same heterosis effects across countries
- **Recombination loss**
  - modeled as heterosis

Effects (V)

- **Random animal effects**
  - additive genetic animal effects
    - 6 + 8 coefficients
  - none-genetic animal effects across parities
    - 6 + 6 + 6 coefficients
  - none-genetic animal effects within later parities
    - 6 coefficients for each parity from 3rd parity onwards

Heterogeneous variance adjustment

- **Simultaneous solving of evaluation model and variance-model** **(Meuwissen et al., 1996)**
- **Effects in variance-model**
  - country × year × month × parity
  - random herd-year with autoregressive correlation between herd-years
- **Across-country standardization procedure**
  - based on approx. re-estimation of genetic variances

Results: heterosis estimates

Heterosis estimates for milk yield (in % of phenotypic mean) given for two important crosses.

		Lactation		
Traits		**1.**	**2.**	**3.**
Danish	**RDMxSRB**	**4.4**	**3.9**	**2.9**
Swedish	**SRBxRDM**	**4.6**	**3.7**	**2.9**
Swedish	**SRBxFAY**	**2.6**	**2.9**	**2.2**
Finnish	**FAYxSRB**	**2.1**	**2.5**	**1.7**

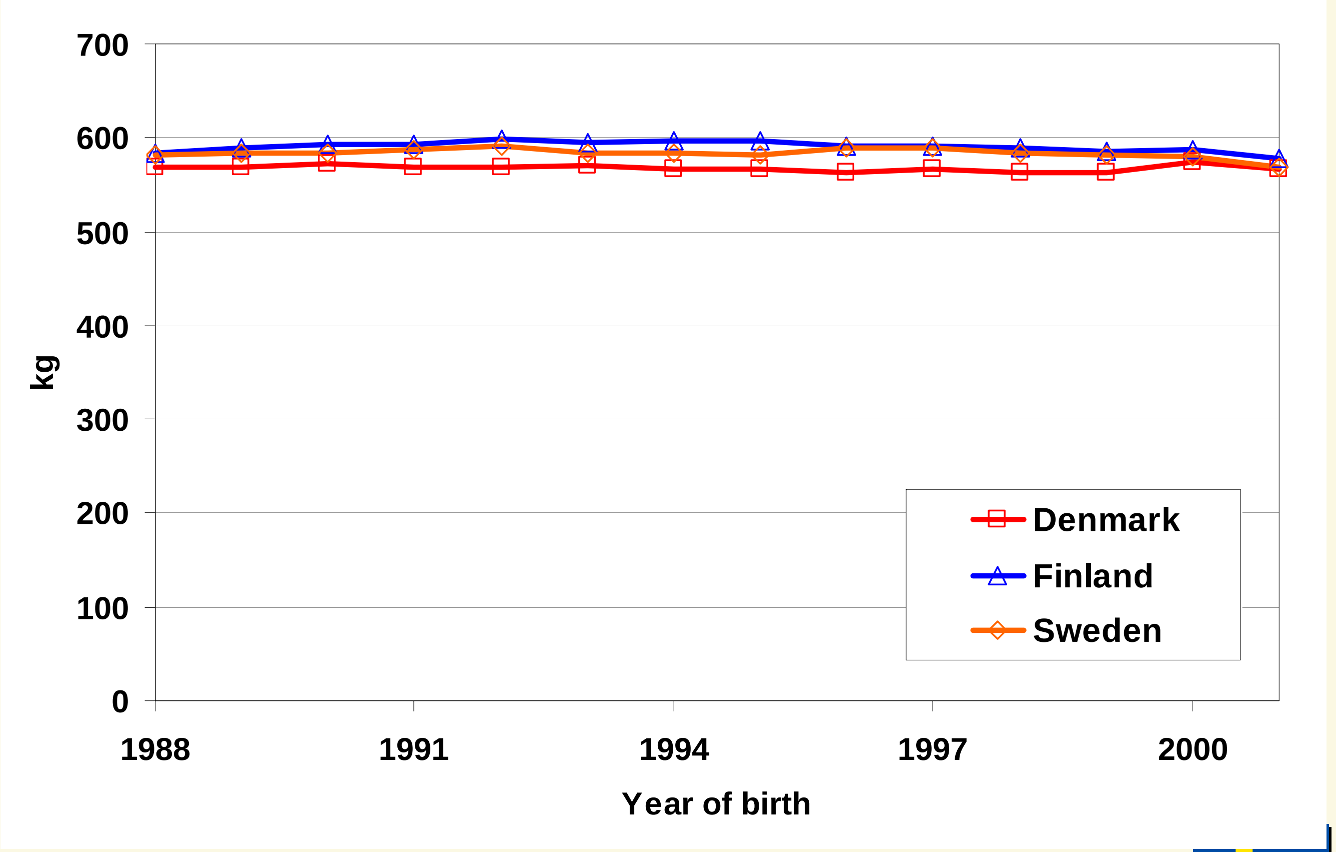
Results: heterogeneous variance

Re-estimated genetic standard deviation for NAV index (in kg), obtained from Red Breed sires.

	Denmark	Finland	Sweden
Milk	568.6	568.9	565.4
Protein	15.0	14.9	14.9
Fat	24.0	24.0	23.9

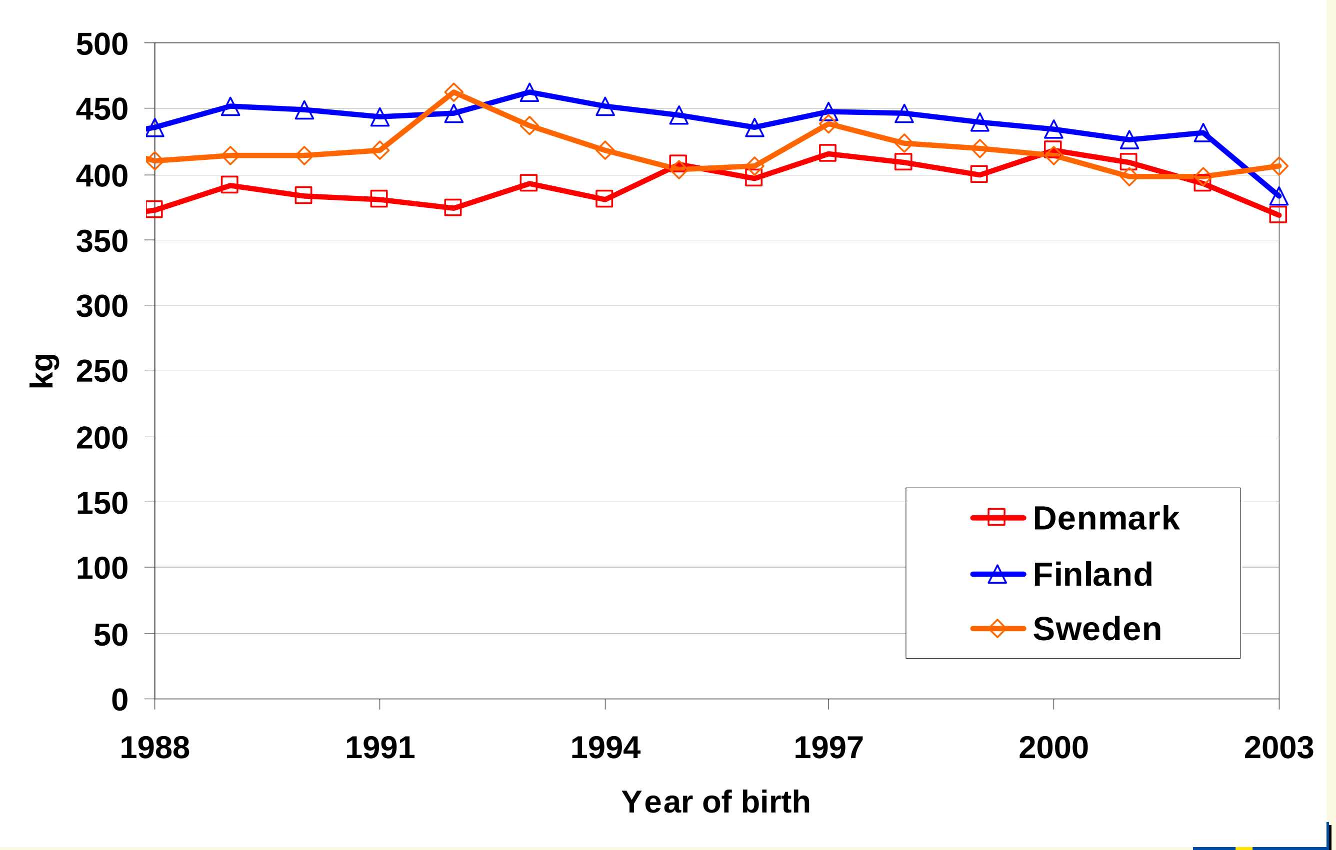
Results: heterogeneous variance

Re-estimated genetic standard for NAV milk index, obtained from Red Breed cows.



Results: **breeding values**

Standard deviation of NAV milk index for Red Breed cows.



Conclusions

- **Across-country evaluation based on raw data is preferable over MACE**
- **Complexity of the model bears own risks**
    - sensitivity of across-country evaluation to modelling of cross breeding effects
    - across-country standardization of heterogeneous variance
- **Solving of these problems enabled official implementation of the Nordic yield model**