

Joint Nordic Test Day Model: Variance Components

*E. A. Mäntysaari; M. Lidauer, J. Pösö, I. Strandén
P. Madsen, J. Pedersen, U.S. Nielsen,
K. Johansson, J.-Å. Eriksson,
G.P. Aamand*



Maa- ja elintarviketalouden tutkimuskeskus | Agrifood Research Finland
Forskningscentralen för jordbruk och livsmedelsekonomi

Esa Mäntysaari, Martin Lidauer, Ismo Strandén

- *MTT Agrifood Research Finland,
Biometrical Genetics, Jokioinen*

Jukka Pösö

- *Faba Breeding, Vantaa, Finland*

Per Madsen

- *Danish Institute of Agricultural Sciences, Genetics
and Biotechnology, Foulum, Denmark*

Jørn Pedersen, Ulrik Sander Nielsen

- *The Danish Agricultural Advisory Services,
Aarhus, Denmark*

Kjell Johansson, Jan-Åke Eriksson

- *Swedish Dairy Association, Stockholm, Sweden;*

Gert Pedersen Aamand

- *NAV Nordic Cattle Genetic Evaluation, Aarhus,
Denmark*

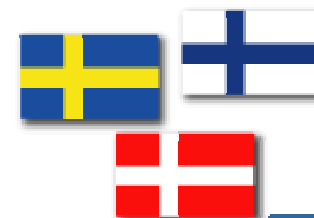


Ministry of Food, Agriculture and Fisheries
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Nordic Cattle Genetic Evaluation

Joint Nordic Test Day Model

- Development started 2002

Interbull 2004 Sousse: “Joint Nordic test day model for milk production traits”

J Pedersen, U S. Nielsen, G P. Aamand, J Pösö, EA Mäntysaari, M Lidauer, I Stranden, P Madsen, K Johansson, J-Å Eriksson, J Juga

- Model Implemented April 2006

Interbull 2006 Kuopio:

1. Joint Nordic Test Day Model: Variance components, Mäntysaari, et al.
2. Joint Nordic Test Day Model: Evaluation Model, Lidauer, et al.
3. Joint Nordic Test Day Model: Experiences with the New Model, Pösö, et al.

Nordic Test Day Model in Kuopio

1. **Joint Nordic Test Day Model: Variance components**

”Meta-Model Concept”

- Random Regression Test Day Model, Repeated traits, Unified model for 305d,...
- Variance components illustrated

2. **Joint Nordic Test Day Model: Evaluation Model**

- Model environmental effects
- Herds, breeds, cross breeding effects, breed*calving age, ...
- Adjustment for heterogenous variance

3. **Joint Nordic Test Day Model: Experiences with the New Model**

- Data, Solutions, Comparisons to used national indices

HOW TO BUILD JOINT EVALUATION?

TWO Approaches for joint evaluation

- A. Model used in population A is imported/implemented in population B
 - o Provider – customer relationship
 - o Way of technology transfer

- B. Population A and B have advanced evaluation models tailored for their local production system
 - o New evaluation model should be superset of old evaluation models
 - o Both populations will expect improved evaluation technologies plus the advantages of across populations evaluation
 - o Breeding industries in both countries have to accept compromises

In Nordic joint evaluation we started on policy B:

- that every country could keep/have their own (and justified) population specific characteristics
- every population should get a model that is better than what was in use before

Nordic Meta-Model

Year 2002

1. Finland
 - Random regression test day model
 - Multi-trait for milk-protein-fat
 - First lactation observations as different traits
 - After the first lactation, all lact. repeatability model
2. Denmark
 - Three lactation 305d repeatability animal model
 - Test day model development already started
 - Heterogenous variance adjust.
 - Heterosis accounted
3. Sweden
 - Three lactation 305d multi-trait repeatability model (2003)
 - Heterogenous variance adjust.
 - Heterosis accounted

SUPER MODEL:

- Random regression test day model
- Inclusion of 305d records needed
- Multi-trait milk-prot-fat
- Lactations 1-3 as different traits
- All lactations accounted
- Different heritabilities in populations
- Advanced environmental modelling,
 - multi-breed evaluation
 - Heterogenous variance

Meta-Model combines 3 models

For Finnish TD records

- First, second and third lactation as different traits
- Later lactations as repeated third lactation observation
- Multi-trait milk-protein-fat
 - lower heritabilities for protein and fat ?

3 traits
3 lactations
= 9 traits

For Danish TD records

- First, second and third lactation as different traits
- Multi-trait milk-protein-fat
 - lower heritabilities for second and third lactation (Red Dane)

3 traits
3 lactations
= 9 traits

For Swedish 305d lactation records

- First, second and third lactation as different traits
- Multi-trait milk-protein-fat

3 traits
3 lactations
= 9 traits

9 FI + 9 DK + 9 SE
= 27 traits

Meta-Model I

RED BREEDS

Sub-model types:

- Swedish Red (SRB)
- Red Danes (RDM)
 - with ABS, RH, SRB,...
- Finnish Ayrshire (FAY)
 - Finnish Holstein
 - Finncattle

- SRB has 3 lact * 3 trait
MT model for lactation yields
- RDM has 3 lact * 3 trait
MT model for TD observations
- FAY has 3 lact * 3 trait
MT model for TD yields
with repeated observations for
3th lact.

$$9 \text{ FI} + 9 \text{ DK} + 9 \text{ SE} \\ = 27 \text{ traits}$$

Meta-Model II

HOLSTEIN

- Swedish Holstein
- Danish Holstein
- Finnish Holstein
 - Finnish Ayrshire
 - Finncattle

- Sweden has 3 lact * 3 trait
MT model for lactation yields
- Denmark has 3 lact * 3 trait
MT model for TD observations
- Finland has 3 lact * 3 trait
MT model for TD yields
with repeated observations for
3th lact.

BUT HERE THE
"BIOLOGICAL TRAITS"
ARE THE SAME IN EACH MODEL

9 FI + 9 DK + 9 SE
= 27 traits

Meta-Model III

JERSEY

- Danish Jersey
 - Few Swedish herds
- Denmark has 3 lact * 3 trait
MT model for TD observations

9 DK TD
= 9 traits



Meta-Model Example

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Nordisk Avlsværdiurdering

RED Breeds Meta-Model

$$\begin{pmatrix} \mathbf{y}^{dk} \\ \mathbf{y}^{fi} \\ \mathbf{y}^{se} \end{pmatrix} = \begin{pmatrix} \boldsymbol{\beta}^{dk} \\ \boldsymbol{\beta}^{fi} \\ \boldsymbol{\beta}^{se} \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_a^{dk} \\ \mathbf{Z}_a^{fi} \\ \mathbf{Z}_a^{se} \end{pmatrix} \mathbf{a} + \begin{pmatrix} \mathbf{Z}_p^{dk} & 0 & 0 \\ 0 & \mathbf{Z}_p^{fi} & 0 \\ 0 & 0 & \mathbf{Z}_p^{se} \end{pmatrix} \begin{pmatrix} \mathbf{p}^{dk} \\ \mathbf{p}^{fi} \\ \mathbf{p}^{se} \end{pmatrix} + \begin{pmatrix} \mathbf{e}^{dk} \\ \mathbf{e}^{fi} \\ \mathbf{e}^{se} \end{pmatrix}$$

where:

$\boldsymbol{\beta}^m$ environmental effects in the country m

**BV coefficients
are across countries**

$\mathbf{Z}_a^m \mathbf{a}$ Breeding Value (BV) function in the country m

$\mathbf{Z}_p^m \mathbf{p}^m$ non-genetic cow function in the country m

**PE coefficients
are within countries**

\mathbf{e}^m measurement errors

RED Breeds Meta-Model Danish TD records

$$\begin{pmatrix} \mathbf{y}_{1i}^{dk} \\ \mathbf{y}_{2i}^{dk} \\ \mathbf{y}_{3i}^{dk} \end{pmatrix} = \begin{pmatrix} \boldsymbol{\beta}_{1i}^{dk} \\ \boldsymbol{\beta}_{2i}^{dk} \\ \boldsymbol{\beta}_{3i}^{dk} \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{a1i}^{dk} & 0 \\ 0 & \mathbf{Z}_{a2i}^{dk} \\ 0 & \mathbf{Z}_{a3i}^{dk} \end{pmatrix} \begin{pmatrix} \mathbf{a}_{1i} \\ \mathbf{a}_{23i} \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{p1i}^{dk} & 0 & 0 \\ 0 & \mathbf{Z}_{p2i}^{dk} & 0 \\ 0 & 0 & \mathbf{Z}_{p3i}^{dk} \end{pmatrix} \begin{pmatrix} \mathbf{p}_{1i}^{dk} \\ \mathbf{p}_{2i}^{dk} \\ \mathbf{p}_{3i}^{dk} \end{pmatrix} + \begin{pmatrix} \mathbf{e}_{1i}^{dk} \\ \mathbf{e}_{2i}^{dk} \\ \mathbf{e}_{3i}^{dk} \end{pmatrix}$$

here the TD yields \mathbf{y}_{2i}^{dk} include all the traits in lact. 2 for cow i

coefficients in BV function $\mathbf{Z}_{a1i}^{dk} \mathbf{a}_{1i}$ are different in first lact but the same $\mathbf{Z}_{a23i}^{dk} \mathbf{a}_{23i}$ in second and third lactation

$\mathbf{Z}_{a1i}^{dk} \mathbf{a}_{1i}$ is a Reduced Rank RR function of order **6**

- reduced from 12 [= 3*traits*(3 polynomials+Wilmlink term)]

$\mathbf{Z}_{a23i}^{dk} \mathbf{a}_{23i}$ is a Reduced Rank RR function of order **8**

- reduced from 24 [= 6*traits*(3 polynomials+Wilmlink term)]

RED Breeds Meta-Model Danish TD records

$$\begin{pmatrix} \mathbf{y}_{1i}^{dk} \\ \mathbf{y}_{2i}^{dk} \\ \mathbf{y}_{3i}^{dk} \end{pmatrix} = \begin{pmatrix} \boldsymbol{\beta}_{1i}^{dk} \\ \boldsymbol{\beta}_{2i}^{dk} \\ \boldsymbol{\beta}_{3i}^{dk} \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{a1i}^{dk} & 0 \\ 0 & \mathbf{Z}_{a2i}^{dk} \\ 0 & \mathbf{Z}_{a3i}^{dk} \end{pmatrix} \begin{pmatrix} \mathbf{a}_{1i} \\ \mathbf{a}_{23i} \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{p1i}^{dk} & 0 & 0 \\ 0 & \mathbf{Z}_{p2i}^{dk} & 0 \\ 0 & 0 & \mathbf{Z}_{p3i}^{dk} \end{pmatrix} \begin{pmatrix} \mathbf{p}_{1i}^{dk} \\ \mathbf{p}_{2i}^{dk} \\ \mathbf{p}_{3i}^{dk} \end{pmatrix} + \begin{pmatrix} \mathbf{e}_{1i}^{dk} \\ \mathbf{e}_{2i}^{dk} \\ \mathbf{e}_{3i}^{dk} \end{pmatrix}$$

coefficients in non-genetic function $\mathbf{Z}_{pti}^{dk} \mathbf{p}_{ti}$ are different in every lactation

$\mathbf{Z}_{pti}^{dk} \mathbf{p}_{ti}$ are a Reduced Rank RR functions of order 6

- reduced from 12 similar to the BV functions

RED Breeds Meta-Model Finnish TD records

$$\begin{pmatrix} \mathbf{y}_{1i}^{fi} \\ \mathbf{y}_{2i}^{fi} \\ \mathbf{y}_{3i}^{fi} \\ \mathbf{y}_{4i}^{fi} \end{pmatrix} = \begin{pmatrix} \boldsymbol{\beta}_{1i}^{fi} \\ \boldsymbol{\beta}_{2i}^{fi} \\ \boldsymbol{\beta}_{3i}^{fi} \\ \boldsymbol{\beta}_{4i}^{fi} \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{a1i}^{fi} & 0 \\ 0 & \mathbf{Z}_{a2i}^{fi} \\ 0 & \mathbf{Z}_{a3i}^{fi} \\ 0 & \mathbf{Z}_{a4i}^{fi} \end{pmatrix} \begin{pmatrix} \mathbf{a}_{1i} \\ \mathbf{a}_{23i} \end{pmatrix} + \begin{pmatrix} \mathbf{Z}_{p1i}^{fi} & 0 & 0 & 0 & 0 \\ 0 & \mathbf{Z}_{p2i}^{fi} & 0 & 0 & 0 \\ 0 & 0 & \mathbf{Z}_{p3i}^{fi} & \mathbf{Z}_{p3i}^{fi} & 0 \\ 0 & 0 & \mathbf{Z}_{p4i}^{fi} & 0 & \mathbf{Z}_{p4i}^{fi} \end{pmatrix} \begin{pmatrix} \mathbf{p}_{1i}^{fi} \\ \mathbf{p}_{2i}^{fi} \\ \mathbf{p}_{3i}^{fi} \\ \mathbf{w}_{3i} \\ \mathbf{w}_{4i} \end{pmatrix} + \begin{pmatrix} \mathbf{e}_{1i}^{fi} \\ \mathbf{e}_{2i}^{fi} \\ \mathbf{e}_{3i}^{fi} \\ \mathbf{e}_{4i}^{fi} \end{pmatrix}$$

The Finnish sub-model for a cow i that has 4 lactations

In $\mathbf{Z}_{a1i}^{fi} \mathbf{a}_{1i}$ the BV coefficients \mathbf{a}_{1i} are the "same" as in Danish model, but the \mathbf{Z}_{a1i}^{fi} eigen function covariables are different

For later lactations, the non-genetic cow effects are described by two functions:

by $\mathbf{Z}_{p3i}^{fi} \mathbf{p}_{3i}$ where \mathbf{p}_{3i} is the same in every lactation and

by $\mathbf{Z}_{p3i}^{fi} \mathbf{w}_{3i}$ where \mathbf{w}_{3i} is different in each later lactation

RED Breeds Meta-Model Swedish 305d lactation yields

$$\begin{pmatrix} y_{1i}^{305} \\ y_{2i}^{305} \\ y_{3i}^{305} \end{pmatrix} = \begin{pmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \end{pmatrix} + \begin{pmatrix} \mathbf{z}_{a1}^{305} & \mathbf{0} \\ \mathbf{0} & \mathbf{z}_{a2}^{305} \\ \mathbf{0} & \mathbf{z}_{a3}^{305} \end{pmatrix} \begin{pmatrix} \mathbf{a}_{1i} \\ \mathbf{a}_{23i} \end{pmatrix} + \begin{pmatrix} \rho_{1i}^{305} \\ \rho_{2i}^{305} \\ \rho_{3i}^{305} \end{pmatrix} + \begin{pmatrix} e_{1i}^{305} \\ e_{2i}^{305} \\ e_{3i}^{305} \end{pmatrix}$$

here the function $\mathbf{z}_{a1}^{305} \mathbf{a}_{1i}$ is a single 305d BV, and

the \mathbf{z}_{a1}^{305} covariables are sums of standard test days $\mathbf{z}_{at}^{305} = \tau_t \sum_{j=1}^{10} \mathbf{z}_{j\ ati}^{dk}$

correspondingly ρ_{ti}^{305} are permanent environment effects, equal to $\mathbf{z}_{pti}^{dk} \mathbf{p}_{3i}$

The coefficient τ_t in \mathbf{z}_{at}^{305} is used to scale the appropriate heritability for Swedish traits

GENETIC PARAMETERS

Estimated using 2- step approach:

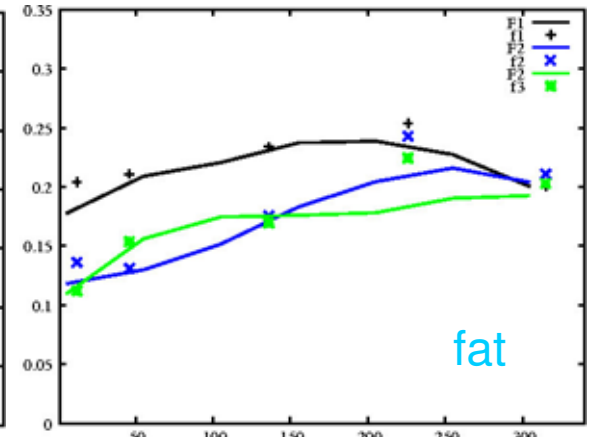
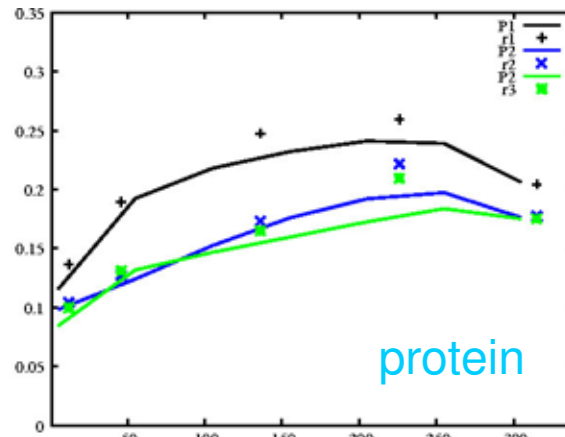
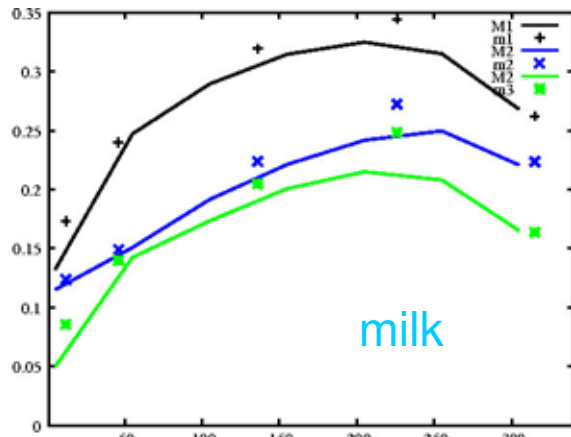
- 1) MT REML runs with
3 lact, 3 trait, 5 lactation stages
- 2) Reduced Rank covariance function
fits

45 traits

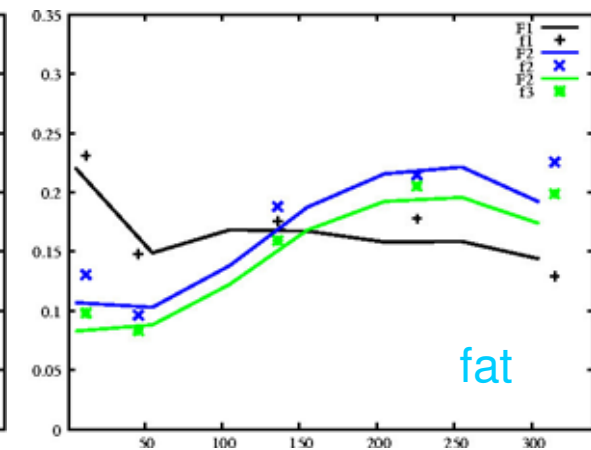
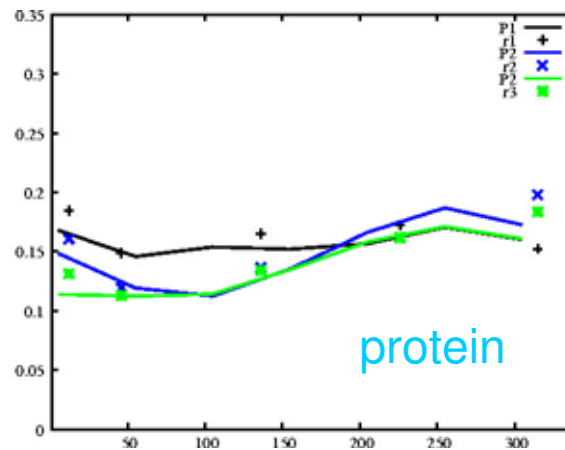
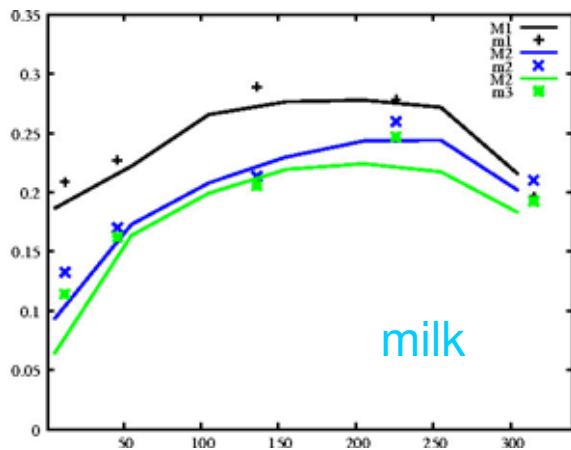
14
rank
for G

18
rank
for R

Test Day yield heritabilities



Holstein



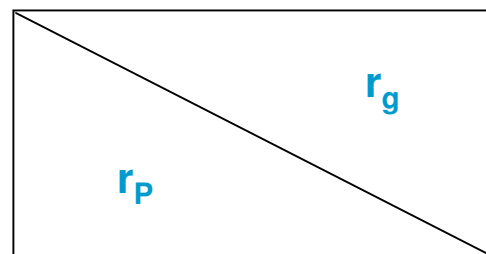
Finnish Ayrshire

Heritabilities for (derived) 305d yields

Trait / lactation	Jersey	Red breeds			Holstein	
		Red Dane RDM	Finnish Ayrshire FAY	Swedish Red SRB	Danish Finnish test day	Swedish
Milk 1	0.44	0.41	0.38	0.38	0.33	0.43
Protein 1	0.38	0.35	0.26	0.36	0.31	0.35
Fat 1	0.35	0.41	0.27	0.37	0.33	0.36
Milk 2	0.47	0.24	0.30	0.27	0.28	0.29
Protein 2	0.23	0.21	0.23	0.30	0.28	0.25
Fat 2	0.22	0.28	0.27	0.31	0.35	0.29
Milk 3	0.27	0.20	0.30	0.22	0.29	0.27
Protein 3	0.23	0.19	0.23	0.27	0.28	0.25
Fat 3	0.23	0.25	0.24	0.26	0.35	0.29

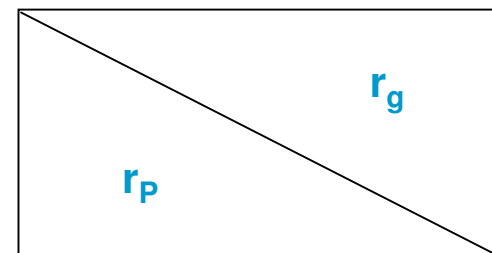
Genetic parameters for (derived) 305d yields in Holstein

	Lactation 1			Lactation 2			Lactation 3		
	Milk	Prot	Fat	Milk	Prot	Fat	Milk	Prot	Fat
Milk 1		0.86	0.46	0.85	0.71	0.23	0.81	0.63	0.09
Prot 1	0.93		0.67	0.75	0.85	0.46	0.71	0.81	0.33
Fat 1	0.77	0.85		0.42	0.68	0.85	0.43	0.70	0.78
Milk 2	0.48	0.45	0.36		0.84	0.42	0.99	0.78	0.32
Prot 2	0.44	0.48	0.43	0.95		0.72	0.84	0.99	0.62
Fat 2	0.32	0.39	0.49	0.82	0.89		0.47	0.76	0.98
Milk 3	0.43	0.41	0.33	0.43	0.41	0.33		0.79	0.37
Prot 3	0.39	0.43	0.40	0.39	0.44	0.39	0.94		0.69
Fat 3	0.24	0.31	0.42	0.30	0.37	0.44	0.83	0.88	



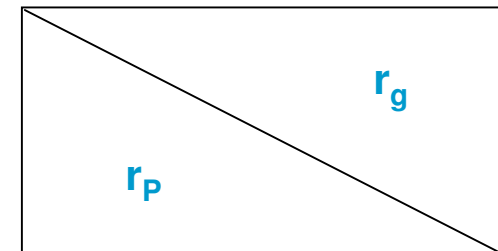
Genetic parameters for (derived) 305d yields Finnish Ayrshire

	Lactation 1			Lactation 2			Lactation 3			Lactation 4		
	Milk	Prot	Fat	Milk	Prot	Fat	Milk	Prot	Fat	Milk	Prot	Fat
Milk 1		0.86	0.46	0.85	0.71	0.23	0.81	0.63	0.10	0.81	0.63	0.10
Prot 1	0.92		0.68	0.75	0.85	0.47	0.71	0.81	0.33	0.71	0.81	0.33
Fat 1	0.69	0.79		0.42	0.68	0.84	0.43	0.70	0.78	0.43	0.70	0.78
Milk 2	0.71	0.68	0.49		0.84	0.43	0.99	0.78	0.32	0.99	0.78	0.32
Prot 2	0.65	0.70	0.58	0.91		0.72	0.84	0.99	0.63	0.84	0.99	0.63
Fat 2	0.42	0.52	0.65	0.63	0.75		0.47	0.77	0.98	0.47	0.77	0.98
Milk 3	0.61	0.58	0.43	0.56	0.48	0.32		0.79	0.38	1.00	0.79	0.38
Prot 3	0.54	0.59	0.52	0.47	0.51	0.41	0.88		0.69	0.79	1.00	0.69
Fat 3	0.31	0.41	0.56	0.28	0.37	0.50	0.62	0.76		0.38	0.69	1.00
Milk 4	0.61	0.58	0.43	0.56	0.48	0.32	0.55	0.47	0.30		0.79	0.38
Prot 4	0.54	0.59	0.52	0.47	0.51	0.41	0.47	0.50	0.38	0.88		0.69
Fat 4	0.31	0.41	0.56	0.28	0.37	0.50	0.30	0.38	0.47	0.62	0.76	



Genetic parameters for (derived) 305d yields in Jersey

	Lactation 1			Lactation 2			Lactation 3		
	Milk	Prot	Fat	Milk	Prot	Fat	Milk	Prot	Fat
Milk 1		0.91	0.74	0.88	0.84	0.49	0.90	0.84	0.49
Prot 1	0.95		0.86	0.78	0.90	0.65	0.81	0.90	0.66
Fat 1	0.87	0.92		0.65	0.83	0.86	0.67	0.83	0.86
Milk 2	0.56	0.52	0.47		0.86	0.57	0.99	0.86	0.53
Prot 2	0.53	0.54	0.51	0.95		0.80	0.88	1.00	0.78
Fat 2	0.41	0.46	0.51	0.87	0.93		0.58	0.79	0.99
Milk 3	0.50	0.46	0.40	0.55	0.51	0.43		0.88	0.55
Prot 3	0.46	0.48	0.44	0.51	0.54	0.48	0.95		0.77
Fat 3	0.34	0.39	0.44	0.41	0.47	0.51	0.86	0.92	



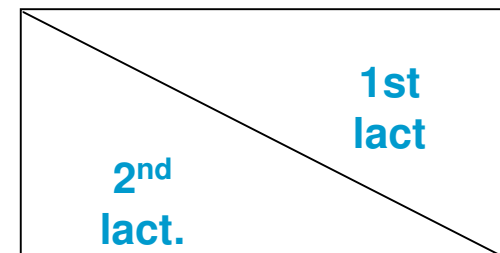


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Genetic correlations for TD milk yields within lactation in Holstein

DIM	10	50	90	130	170	210	250	290	330
10		0.96	0.91	0.87	0.83	0.79	0.76	0.73	0.70
50	0.96		0.99	0.97	0.95	0.92	0.90	0.87	0.84
90	0.90	0.99		0.99	0.98	0.97	0.95	0.93	0.90
130	0.86	0.97	0.99		1.00	0.99	0.98	0.96	0.93
170	0.81	0.94	0.98	1.00		1.00	0.99	0.98	0.96
210	0.77	0.91	0.96	0.99	1.00		1.00	0.99	0.97
250	0.73	0.88	0.94	0.97	0.99	1.00		1.00	0.99
290	0.69	0.85	0.92	0.95	0.97	0.99	1.00		1.00
330	0.64	0.81	0.88	0.92	0.95	0.97	0.99	1.00	

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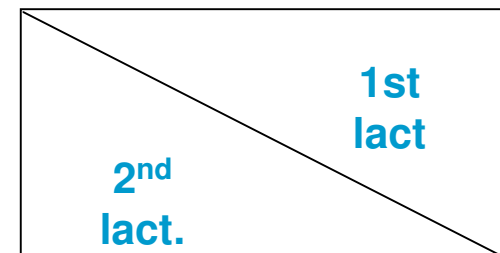


MTT

Genetic correlations for TD milk yields within lactation in Red breeds

DIM	10	50	90	130	170	210	250	290	330
10		0.96	0.91	0.86	0.80	0.73	0.67	0.59	0.50
50	0.89		0.99	0.96	0.93	0.88	0.83	0.77	0.69
90	0.82	0.99		0.99	0.97	0.94	0.90	0.85	0.77
130	0.78	0.98	1.00		0.99	0.98	0.95	0.90	0.84
170	0.75	0.96	0.99	1.00		0.99	0.98	0.94	0.89
210	0.71	0.94	0.97	0.99	1.00		0.99	0.97	0.93
250	0.67	0.91	0.95	0.98	0.99	1.00		0.99	0.96
290	0.63	0.88	0.93	0.95	0.97	0.99	1.00		0.99
330	0.57	0.83	0.89	0.93	0.95	0.97	0.99	1.00	

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Nordic Test Day Model SUMMARY

- Combines TD records and 305d records
- Provides different heritabilities and repeatabilities in different countries/populations, BUT assumes $r_g = 1.00$ across countries
- Allows repeated observations for some traits
- Because of rank reduction:
Feasible for large population!



THANK YOU

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