

# Robust Models for Approximate Multitrait Evaluations

Lassen, J.<sup>1</sup>, Sørensen, M. K.<sup>1</sup>, P. Madsen<sup>1</sup> and V. Ducrocq<sup>2</sup>

<sup>1</sup>Danish Institute of Agricultural Sciences, P.O. box 50, DK-8830 Tjele, <sup>2</sup>Station de Génétique Quantitative et Appliquée, INRA, 78352 Jouy-en-Josas, France

---

## Abstract

This study is a part of a bigger study to validate an approximate multitrait model for prediction of breeding values. The approximate multitrait model is a two-step procedure where solutions for fixed effects from single trait models are subtracted from the phenotypes and a multitrait model is applied on these preadjusted data. The main focus in this presentation is to quantify the effect on genetic gain of adding or not a year effect into the approximate multitrait model. This is done in a stochastic simulation study of a dairy cattle population.

There was a significant effect of adding a year effect into the model on genetic gain for total merit. Genetic correlations between production and the other traits in the breeding goal were estimated with the models corresponding to the ones used for prediction of breeding values. These showed considerable differences with the ones used in the simulation and with the ones obtained from an approximate multitrait model without the year effect. Adding a year effect in the model provided more robust genetic trends and took selection bias into account. These conclusions might also apply for international breeding evaluations.

---

## Introduction

Multitrait selection is used in most countries with a dairy cattle breeding program. This is done using breeding values from single trait models combining these with economic values, or at most doing multitrait evaluations on groups of traits. Over the last years increasing focus has been put on low heritable traits leading to breeding values with low accuracies and thereby instability. A way to reduce this problem is to use multitrait breeding value estimation by exploiting the data and combine direct and indirect information on correlated traits in the breeding goal. An approximate method was proposed by Ducrocq *et al.* (2001) analyzing records adjusted for fixed effects so each record contained an overall mean a genetic term and a residual term for all animals in a multitrait setting. Using this method the accuracy for longevity on newly proven bulls increased substantially.

Another benefit of using multitrait evaluation is to take account for the fact that the main selection over the past years has been on production. Predicted breeding values from single trait analysis therefore might be biased

since the covariance structure of the traits is not accounted for.

The aim of this study is to propose an approximate multitrait model that is robust to over- and underestimation of genetic parameters by adding a year effect in the model. Thereby selection is taken into account when predicting breeding values. This is done in a stochastic simulation study of a dairy cattle population.

## Materials and Methods

A population of approximately 100 000 animals was simulated for a 30 years period using a modified version of the stochastic simulation program DairySim (Sørensen *et al.*, 1999). The simulation was setup to mimic a dairy cattle population and included 7 traits. The genetic and phenotypic parameters for the traits (table 1) were chosen so they correspond to production (**P**), udder depth (**UD**), mastitis occurrence (**MO**), non return rate (**NRR**), dairy character (**DC**), days open (**DO**) and somatic cell score (**SCS**). These traits were chosen to represent different types of traits of interest in a total merit breeding goal.

**Table 1.** Heritabilities (diagonal), genetic (below diagonal) and phenotypic (above diagonal) correlations for traits<sup>a)</sup> in the simulation.

Trait	P	UD	MO	N	DF	DO	SCS
P	<b>.30</b>	-.20	0	-.10	.25	.20	-.15
UD	-.35	<b>.30</b>	-.05	0	0	-.10	-.05
MO	.35	-.60	<b>.04</b>	0	0	0	.20
N	-.35	.30	-.10	<b>.03</b>	0	.05	0
DF	.45	-.10	.25	0	<b>0.25</b>	.10	0
DO	.55	-.10	.05	-.10	.45	<b>.04</b>	0
SCS	.15	-.30	.75	-.20	.25	-.25	<b>.10</b>

<sup>a)</sup>P=production, UD=udder depth, MO= mastitis occurrence, N=non return rate, DF=dairy form, DO=days open , SCS=somatic cell score

The simulation was done in two steps, each covering a 15 years time period. In the first step a narrow breeding goal (**BG1**) with weight on production and mastitis occurrence was used. The economic weights in BG1 were 19.4 for P and -50 for MO. Predictions of breeding values were based on a single trait analysis for production and a trivariate analysis for mastitis, using MO, UD and SCS as sources of information. For the second step, 6 different scenarios were setup in order to quantify the effect of changing method/model for prediction of breeding values and/or changing to a broader breeding goal (**BG2**) with economic weights on P (19.4), UD (4.2), MO (-50), NRR (13) and DO (-16.75).

Three different multitrait models were used. Model 1 was an approximate multitrait model as proposed by Ducrocq *et al.*, (2001). This is a two-step procedure, where the first step is applying single trait models for all traits. In the second step the individual observations are adjusted for the fixed effects ( $\hat{F}$ ) obtained from the single trait analyses. On these preadjusted data a multitrait model with an overall mean, an additive genetic effect and a residual effect was applied.

$$y = F + a + e \rightarrow y - \hat{F} = y^* = mean + a^* + e^*, (1)$$

Model 2 was also an approximate multitrait model, where the model for  $y^*$  was augmented with a year effect. The purpose of this was to test the idea of Ducrocq *et al.*, (2003) of including a year effect to account for biases in genetic trends. Model 3 was a full multitrait model on  $y$  (unadjusted observations). The combinations of breeding goal and evaluation model are described in table 2.

**Table 2.** Description of model (1= approximate multitrait, 2= 1+ a year effect, 3=full multitrait) and breeding goal (BG1, BG2 = narrow, broad breeding goals, respectively) combinations used in the 6 different scenarios.

	Model 1	Model 2	Model 3
BG1	1	3	5
BG2	2	4	6

Before starting simulation of the last 15 years, covariance components were estimated on subsets of the data, using models corresponding to the models used for breeding value estimation in each scenario. These parameters were applied in the evaluation models for the last 15 years. The estimation was conducted using the DMU software (Madsen & Jensen, 2000). The covariance components used for the simulation were the same in the last 15 years as in the first 15 years.

For each of the 6 scenarios, 20 replicates were simulated all starting from the same population simulated in step 1.

Effects of changing breeding goal and/or evaluation model were quantified as regression of true (simulated) and predicted breeding values on year for total merit based on BG2.

## Results

Including a year effect in the approximate multitrait model improved the genetic merit significantly both when comparing the true and the predicted breeding values (table 3).

**Table 3.** True and predicted genetic trends per year for total merit in simulation using the economic values from breeding goal 2 with standard errors in brackets.

Scenario	Predicted TM	True TM
1	1.52 (0.08)	1.80 (0.07)
2	2.57 (0.08)	2.82 (0.05)
3	1.76 (0.07)	1.83 (0.06)
4	2.94 (0.07)	2.98 (0.06)
5	1.90 (0.05)	1.97 (0.06)
6	3.02 (0.05)	3.06 (0.07)

This effect was more pronounced with a broad breeding goal than with a narrow breeding goal. Using the full multitrait model gave the highest genetic merit, but it was not significantly better than the approximate multitrait model with a year effect. Using a broad breeding goal gave the highest genetic

merit. An approximate multitrait model without a year effect gave the biggest difference between the true and the predicted breeding values for total merit. In other words, the estimated genetic gain was biased downwards compared to the true one. Within breeding goal among models there was very little difference across models in true genetic progress or decline for the individual traits (table 4), though these small differences sum up to substantial differences in total merit. In general using a broader breeding goal and a more advanced model gave a more favourable genetic merit for the individual traits. Similar pattern were found for genetic merit in predicted breeding values. Table 5 shows the genetic correlations between production and the 6 individual traits that were used in the simulation and estimated on the data after 15 years of simulation.

**Table 4.** True genetic trends in genetic standard deviation units per year for individual traits in simulation using the economic values from breeding goal 2. Desired direction for each trait is in brackets. Standard errors are between 0.001 and 0.011.

Scenario	P(+)	UD(+)	MO(-)	NRR(+)	DC(0)	DO(-)	SCS(-)
1	0.134	-0.036	-0.001	-0.010	0.048	0.051	-0.011
2	0.113	0.027	-0.009	-0.001	0.032	0.016	-0.023
3	0.131	-0.0004	-0.002	-0.007	0.056	0.046	-0.009
4	0.122	0.038	-0.011	0.001	0.024	0.009	-0.029
5	0.121	0.015	-0.003	-0.004	0.059	0.037	-0.019
6	0.118	0.040	-0.014	0.003	0.032	0.011	-0.030

**Table 5.** Genetic correlations between production and the 6 individual traits used in the simulation and estimated on the data using the 3 different models.

	"True"	Model 1	Model 2	Model 3
Udder depth	-0.35	-0.16	-0.38	-0.41
Mastitis	0.35	0.17	0.42	0.39
Non return rate	-0.35	-0.22	-0.27	-0.36
Dairy character	0.45	0.31	0.48	0.47
Days open	0.55	0.24	0.32	0.34
SCC	0.15	0.12	0.16	0.18

## Discussion

In this study the effect of adding a year effect into an approximate multitrait model on genetic progress for total merit has been quantified. The genetic progress improved significantly and one reason was the difference in the genetic correlations between production and the other traits in the simulation that was

estimated after the first 15 years. Including a year effect in the model gave correlations very close to the ones used in the simulation and also very close to the ones estimated in the full multitrait model. One reason for this is the selection done on production in the first part of the simulation. Including a year effect in the model to correct for selection bias leads to more robust genetic trends as shown in this and

other studies (Ducrocq *et al.*, 2003). This study was done selecting on a national total merit index, but the same problems of estimating consistent genetic trends applies for international evaluations as well, where problems concerning robustness of genetic trends have been raised (Ducrocq *et al.*, 2003). Correlations used are only estimates and they are often estimated with high uncertainty. Villanueva *et al.* (1993) showed that response to selection depends highly on precision of the estimated variance components. Therefore sometimes even univariate models can provide more precise estimates than multitrait models.

The approximate multitrait model with a year effect as proposed in this study will lead to more robust genetic trends and it will give genetic progress at nearly the same level as a full multitrait model. The proposed model would also be able to handle more traits and more animals than exemplified in this study, which makes the model appealing to implement for national breeding evaluations.

## References

- Ducrocq, V., Boichard, D., Barbat, A. & Larroque, H. 2001. Implementation of an approximate multitrait BLUP to combine production traits and functional traits into a total merit index. *52<sup>nd</sup> annual meeting EAAP*, Budapest, Hungary.
- Ducrocq, V., Delaunay, I., Boichard, D. & Mattalia, S. 2003. A general approach for international genetic evaluations robust to inconsistencies of genetic trends in national evaluations. *Interbull workshop 2003*.
- Madsen, P. & Jensen, J. 2004. *DMU: a user's guide*. A package for analysing multivariate mixed models. Version 6, release 4.5, DJF, Foulum, Denmark.
- Sørensen, M.K., Berg, P., Jensen, J. & Christensen, L.G. 1999. Stochastic simulation of breeding schemes for total merit in dairy cattle. *GIFT Seminar on Genetic Improvement of Functional Traits in Cattle*, Wageningen, The Netherlands, 7-9. November. *Interbull Bulletin 23*, 183-192.
- Villanueva, B., Wray, N.R. & Thompson, R. 1993. Prediction of asymptotic rates of response to selection on multiple traits using univariate and multivariate best linear unbiased predictors. *Anim. Prod.* 57, 1-13.