



Validation of an approximate multitrait model for prediction of breeding values in dairy cattle - a stochastic simulation study

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Introduction

- Multitrait selection is used in dairy cattle
- Many traits with low h^2 has been introduced
- Information from data should be exploited
- Complete multitrait evaluation is not possible

The Project

- Simulation study
- Apply other methods to analyze non-normal data
- Real data

Objective

In a simulation study to validate an approximate multitrait model for breeding value estimation in dairy cattle

Parameters used in the simulation study

- Danish Holstein ~ 300.000 cows
- Herdsize 100 cows
- Progeny group size 100
- 15 years
- 5 replicates

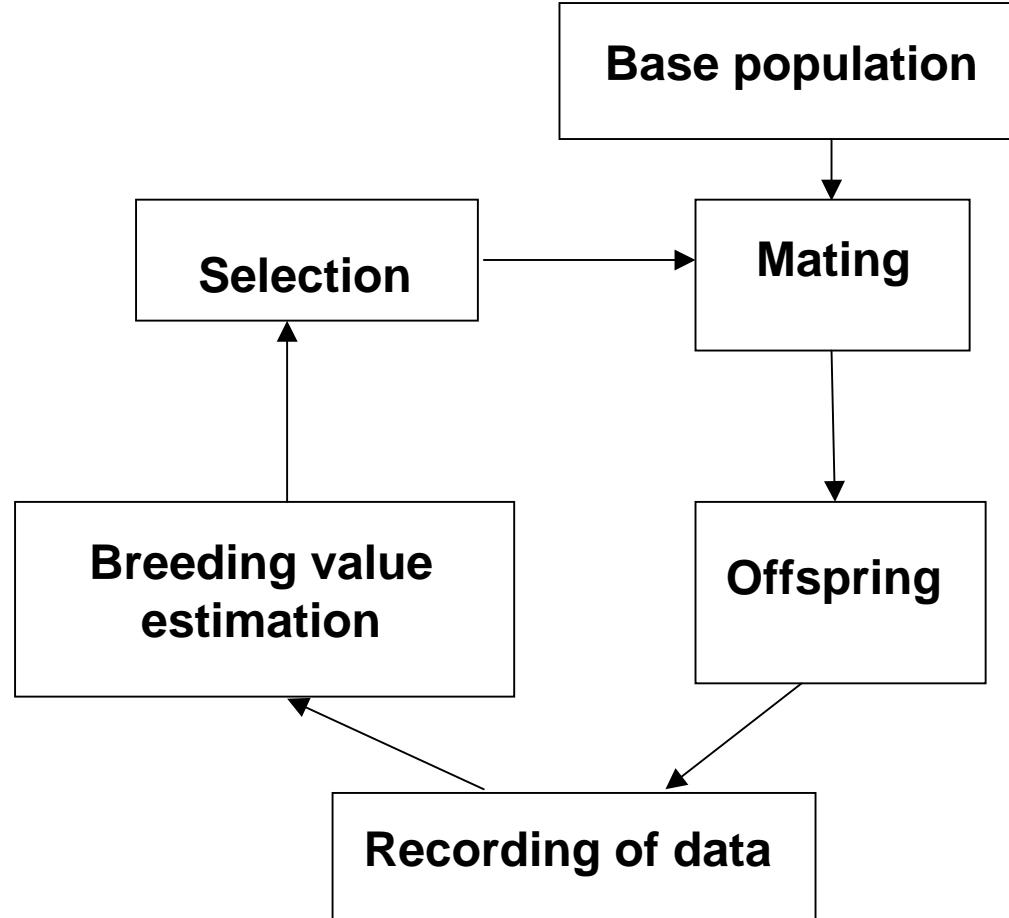
Traits

Trait	Yield	Dairy form	Udder depth	Non return rate	Mastitis Occurrence	Days Open	Somatic cell score
Abbreviation	Y	DF	UD	N	MO	DO	SCS
Type	Linear	Linear	Linear	Binary	Binary	Linear	Linear
Economic weight	400	0	100	0	200	0	0

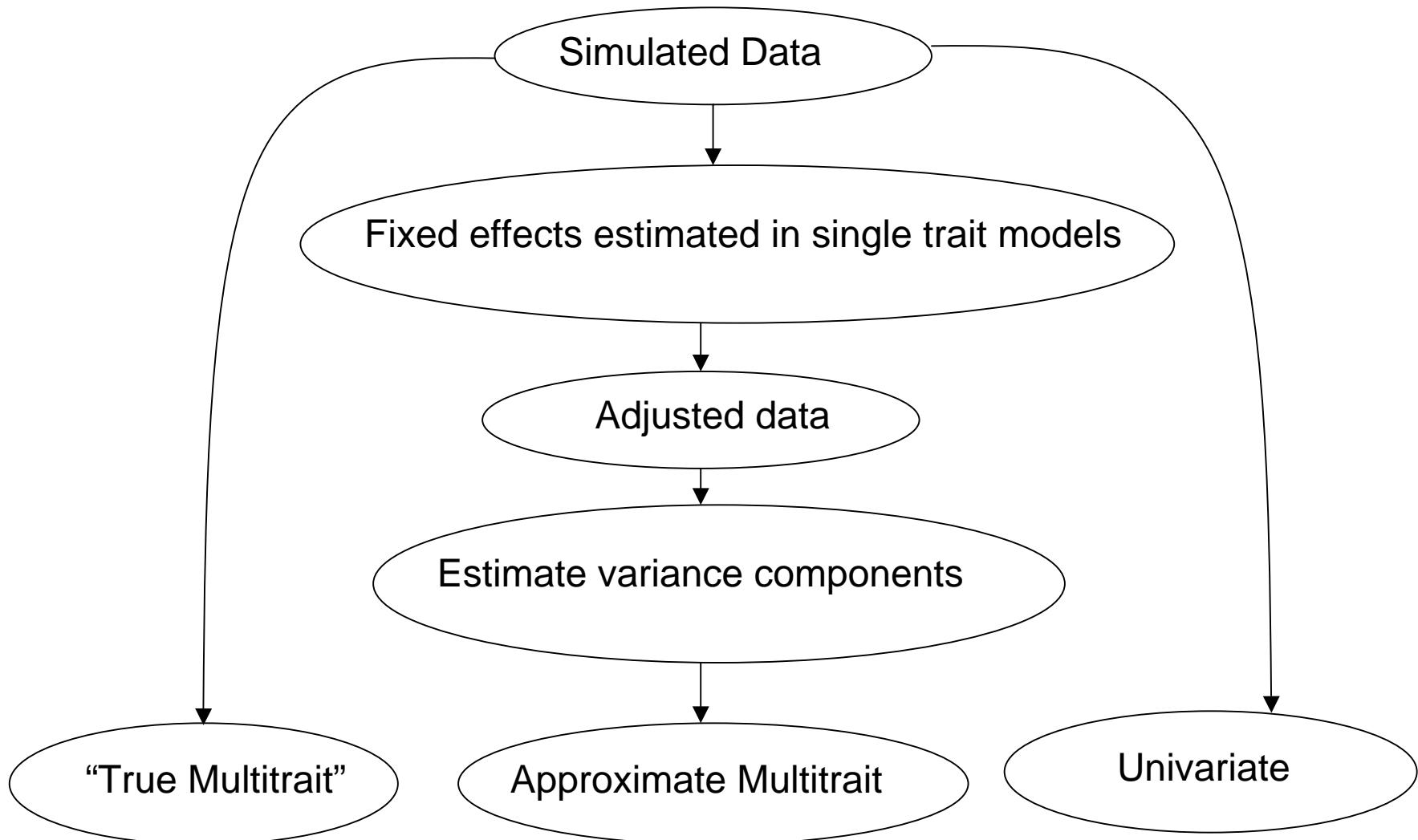
Heritabilities (diagonal), **genetic** (below diagonal) and **phenotypic** (above diagonal) correlations for traits in the simulation study

Trait	Y	DF	UD	N	MO	DO	SCS
Y	0.30	0.25	-0.20	-0.10	0	0.20	-0.15
DF	0.45	0.25	0	0	0	0.10	0
UD	-0.35	-0.10	0.30	0	-0.05	-0.10	-0.05
N	-0.35	0	0.30	0.03	0	0.05	0
MO	0.35	0.25	-0.60	-0.10	0.04	0	0.20
DO	0.55	0.45	-0.10	-0.10	0.05	0.04	0
SCS	0.15	0.25	-0.30	-0.20	0.75	-0.25	0.10

Simulating the population



Estimation procedure



Linear Model

- $y^*_{i,m} = \mu_i + a_{i,m} + e_{i,m}$
- $\text{Var}(e_i) = (W_i)^{-1} \sigma_{e_i}^2$
- Where, $W_{i,m} = (1 - p_{ev_{i,m}})/\sigma_{a_i}^2$
is standardized to mean 1

Results

Correlation between true predicted breeding values
(mean of 5 replicates)

	True multitrait	Approximate Multitrait	Univariate
Yield	0.91 ± 0.01	0.91 ± 0.02	0.56 ± 0.02
Udder depth	0.67 ± 0.02	0.67 ± 0.02	0.54 ± 0.03
Mastitis	0.33 ± 0.02	0.13 ± 0.04	0.07 ± 0.04
Dairy form	0.78 ± 0.02	0.78 ± 0.02	0.45 ± 0.04
Days open	0.81 ± 0.01	0.78 ± 0.02	0.22 ± 0.05
SCS	0.58 ± 0.01	0.58 ± 0.01	0.34 ± 0.03
Non return rate	0.29 ± 0.05	0.19 ± 0.05	0.09 ± 0.05

Conclusion

- The approximate model works well on normal data
- On all traits the approximate model gives higher r_{ia} than using a univariate model