

Covariance Functions are Affected by Non Random Use of Sires

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Introduction

In variance component estimation environmental sensitivity (GxE) can be:

- Ignored
- Partly accounted for (heterogeneous variances)
- Completely accounted for (both het. variances and re-ranking of animals):
 - Multi trait model
 - Covariance function (Reaction norm model)

Introduction - Covariance Functions

- Covariance Functions (CF):
 - Include heterogeneous variances and re-ranking (environmental sensitivity) in model
- Genetic effect is random regression on independent variable
- Independent variable is phenotypic mean (environmental parameter; EP)



Introduction

Little is known about:

- Influence of including the animals EBV in the environmental parameter
- Effect of non random use of sires on:
 - Estimated variance components in CF
 - Poor genetic connectedness

Objective

Investigate the influence of definition of EP and preferential sire use in herds on estimated variance components and breeding values of a covariance function across the range of EP in one population.

Material and Methods

Simulated data (50,000 cows with one record each; 50 replicates):

- 25 or 100 daughters per sire
- On average 10 or 50 animals per herd
- Random versus non-random use of sires

Simulation model

- $\text{Record} = \frac{1}{2} * \text{TBV}_{\text{sire}} + \frac{1}{2} * \text{TBV}_{\text{dam}} + \text{MS} + \text{herd} + \text{residual}$
- $\text{TBV}_{\text{herd}} = \text{level}_{\text{TBV}} + \text{herd} * \text{slope}_{\text{TBV}}$
- $\text{MS}_{\text{herd}} = \text{level}_{\text{MS}} + \text{herd} * \text{slope}_{\text{MS}}$
- Level ~ TBV: $N(0, 0.4)$; MS: $N(0, 0.2)$
- Slope ~ TBV: $N(0, 0.2)$; MS: $N(0, 0.1)$
- $r(\text{level}, \text{slope}) = 0$
- Herd ~ $N(1, 1/9)$
- Residual ~ $N(0, 1 - \text{var}(\text{level}_{\text{TBV}}))$



Non-random use of sires

Group of sires (TBV for level)	Group of herds (randomly formed)				
	1	2	3	4	5
1	0.8318	0.1381	0.0247	0.0045	0.0009
2	0.1381	0.7080	0.1265	0.0229	0.0045
3	0.0247	0.1265	0.6976	0.1265	0.0247
4	0.0045	0.0229	0.1265	0.7080	0.1381
5	0.0009	0.0045	0.0247	0.1381	0.8318

Analysis of simulated data

- (Animal) Model included:
 - Mean
 - Fixed effect for herd
 - Random first order polynomial regression on EP for animal
 - Residual
- Environmental parameter
 - Phenotypic average or fixed herd effect

EP as fixed herd effect

- EP as iteratively estimated fixed effect:
 - $i=1$ EP is phenotypic herd average of the trait
 - $i>1$ EP is estimated herd effect of previous iteration
- Convergence criterion:
$$\text{MAX}(\text{ABS}(\text{EP}(i+1)-\text{EP}(i))) < 0.001$$

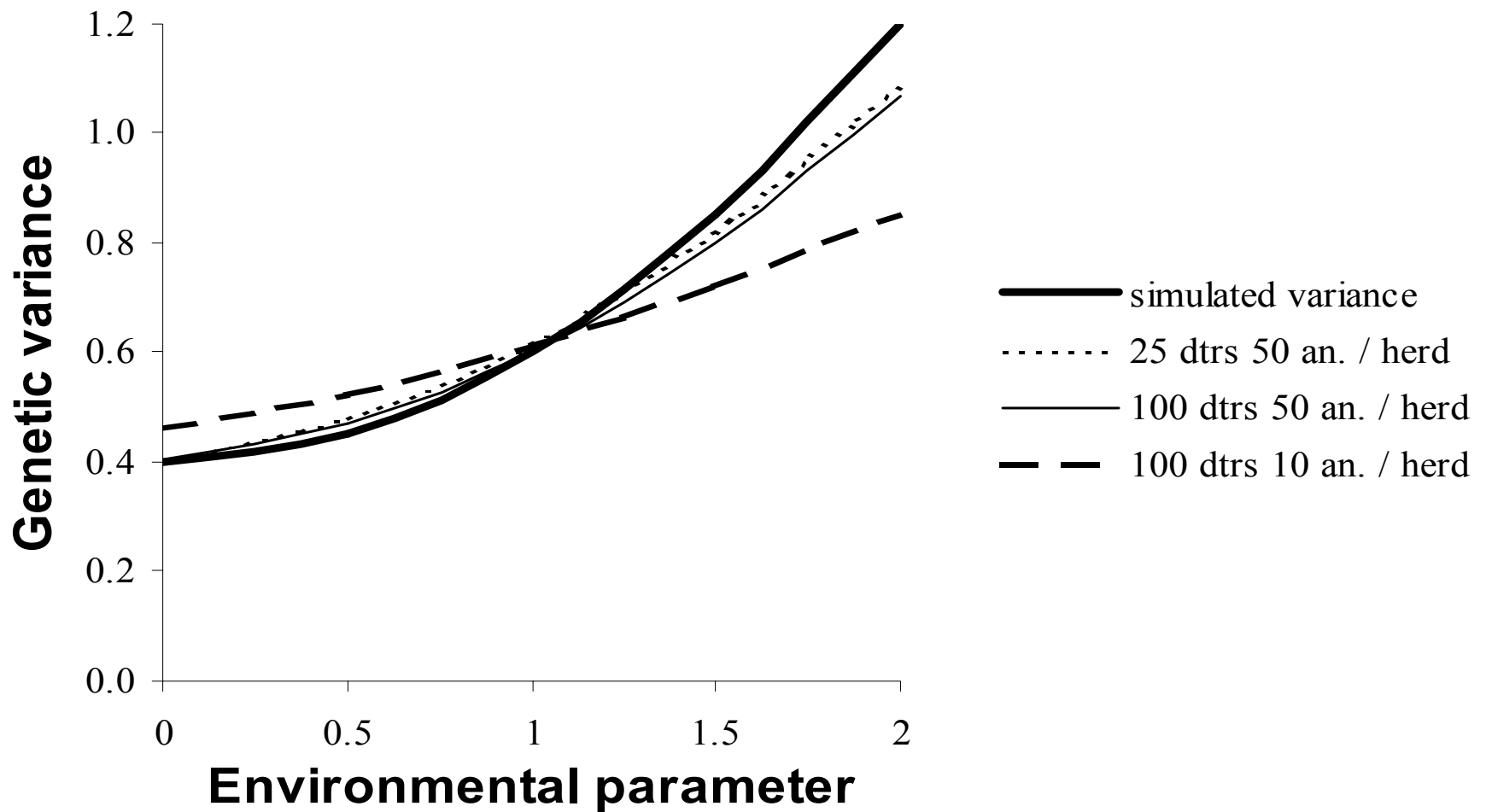
Results - EP as fixed herd effect

- EP converged in two or three iterations
- Definition of EP hardly influenced estimated variance components

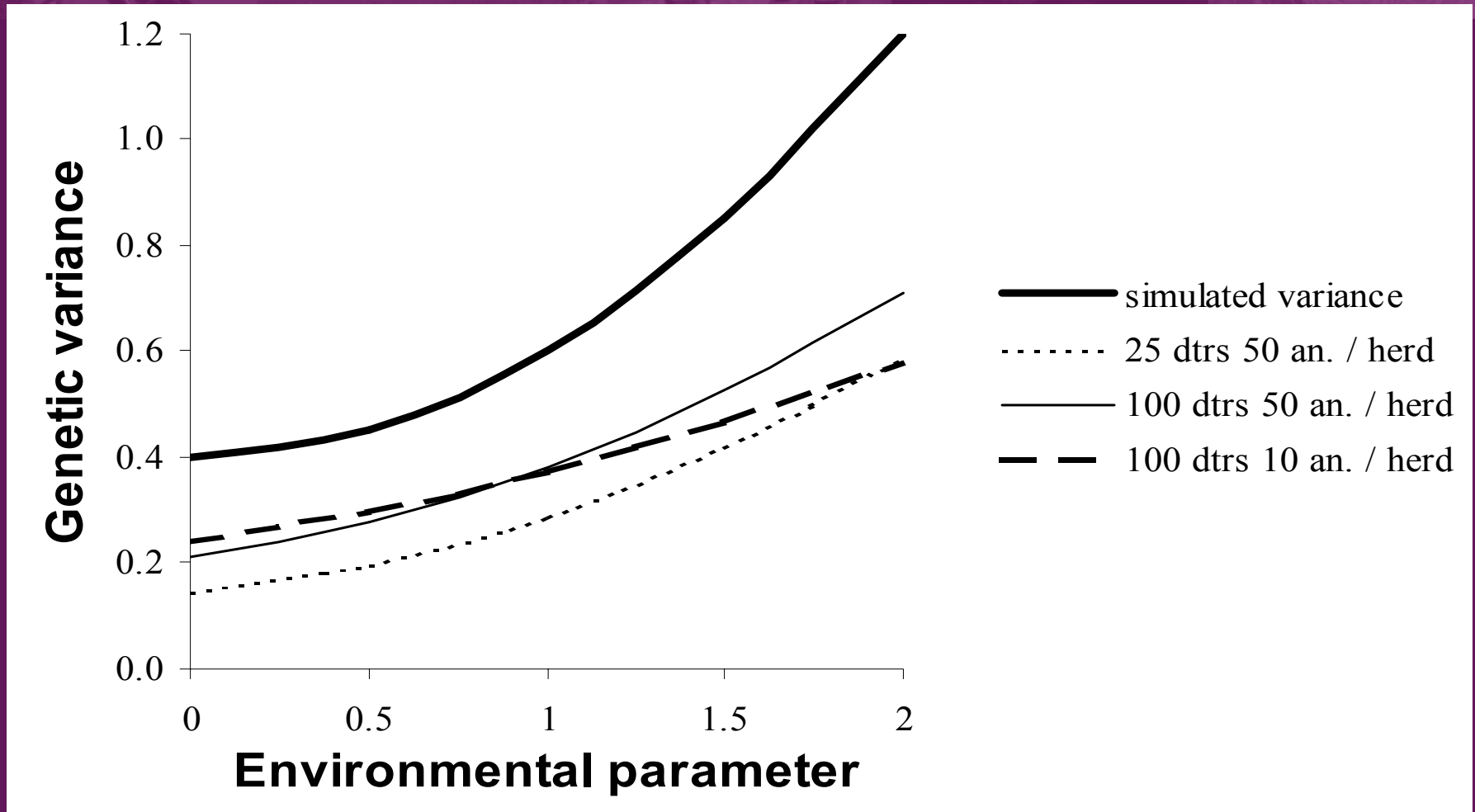
Results - Population structure

- $\text{Var}(\text{slope})$ stronger underestimated if herds were smaller
- $\text{Cov}(\text{level}, \text{slope})$ was overestimated
- Correlation between simulated and estimated effects:
 - EP influenced by nr. animals per herd
 - Level and slope influenced by nr. dtrs per sire

Genetic variance - Random use of sires



Genetic variance - Non random use of sires



Results - EBV across environments

- The course of EBV was overall flatter than the course of TBV
- The course of EBV became flatter if the data became more complex (i.e. non-random use of sires)
- Genetic correlations across environments were estimated closer to 1 than simulated

Discussion

- Alternative method did not properly correct for genetic influence on EP
- Possibly due to absorption of (part of) genetic effects in the herd effect:
 - Fixed effects can lead to loss of information
 - Alternative EP is ‘genetically biased’

Discussion

- Alternative EP with RANDOM herd effect:
 - Underestimated herd variance
 - Overestimated genetic variance
- Handling poor genetic connectedness across herds:
 - Only one generation of unrelated sires

Conclusions

- Phenotypic averages as EP can lead to problems with variance component estimation
- Alternative model does not solve this problem
- Covariance functions can not easily overcome poor genetic connectedness

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