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Inferring relationships between health and fertility in Norwegian Red cows using recursive models

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Simultaneous or recursive models

- Health and fertility are complex traits
- Causal effects between phenotypes

  ➔disease in early lactation may impair a cow's ability to show heat and to conceive after insemination
- Causal relationships between phenotypes can be

  mutual (simultaneous)

  or

  one-way, i.e. a variable affects another but the reciprocal effect does not exist (recursive)

Simultaneous or recursive models

- Gianola and Sorensen (Genetics, 2004):
  extended quantitative genetics models to handle simultaneous or recursive **(SIR)** effects between phenotypes in a multivariate system.

- Wu et al. (JDS 2007; GSE 2008):
  developed software for Bayesian implementation of SIR models.

Objective

Infer phenotypic and genetic relationships between health and fertility in Norwegian Red cows using recursive models.

Traits

Fertility:

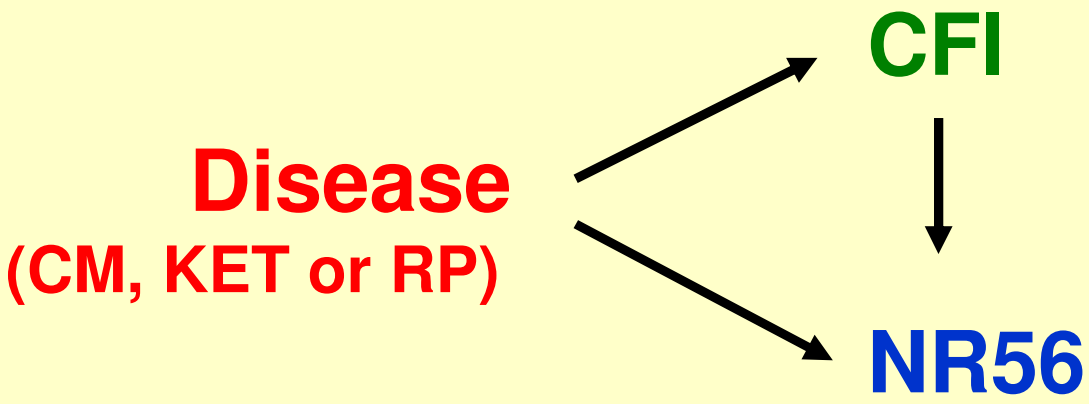
- Interval from 1st calving to 1st insemination (**CFI**)
- Non-return rate within 56 days after 1st insemination (**NR56**)

Disease:

- Clinical mastitis (**CM**)
- Ketosis (**KET**)
- Retained placenta (**RP**)

Recursive effects between fertility and disease

Disease in early lactation may affect both the cows ability to show heat (CFI) and to conceive after insemination (NR56).



Data

- 55,568 first lactation cows
- Daughters of 1,577 Norwegian Red sires

- Mean CFI, days 77
- Mean NR56, % 67
- Mean CM, % 10
- Mean KET, % 4
- Mean RP, % 2

Recursive Gaussian threshold model

$$\begin{bmatrix} \Lambda \mathbf{y}_1 \\ \Lambda \mathbf{y}_2 \\ .. \\ \Lambda \mathbf{y}_n \end{bmatrix} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}_h\mathbf{h} + \mathbf{Z}_s\mathbf{s} + \mathbf{e}$$

where $\Lambda = \begin{bmatrix} 1 & \lambda_{12} & \lambda_{13} \\ \lambda_{21} & 1 & \lambda_{23} \\ \lambda_{31} & \lambda_{32} & 1 \end{bmatrix}$ is a matrix of structural coefficients between traits 1 (CFI) , 2 (NR56), and 3 (disease), $\lambda_{ij,}$ which describes the rate of change in trait *i* with respect to trait *j*;

$\mathbf{y_1}, \mathbf{y_2}, ..., \mathbf{y_n}$ are vectors of CFI observations and liabilities of NR56 and disease (CM, KET or RP) for the n= 55,568 cows, $\mathbf{y_1} = \lfloor y_{CFI_1} \quad l_{STC_1} \quad l_{CM_1} \rfloor$;

$\boldsymbol{\beta}$: trait-specific systematic effects (age, month-year, double insemination, year-season),

h: herd-5-year of calving effects (2909 levels);

s: sire effects;

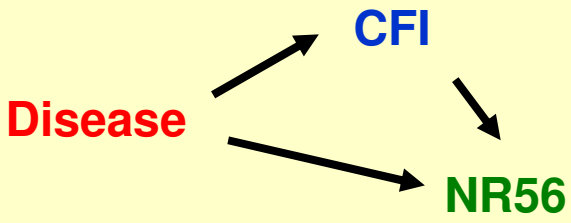
e: residuals, and $\mathbf{X}$, $\mathbf{Z_h}$, and $\mathbf{Z_u}$ are the corresponding incidence matrices.

$$\Lambda = \begin{bmatrix} 1 & 0 & \lambda_{13} \\ \lambda_{21} & 1 & \lambda_{23} \\ 0 & 0 & 1 \end{bmatrix}$$

matrix of structural coefficients between traits 1 (CFI) , 2 (NR56), and 3 (disease),

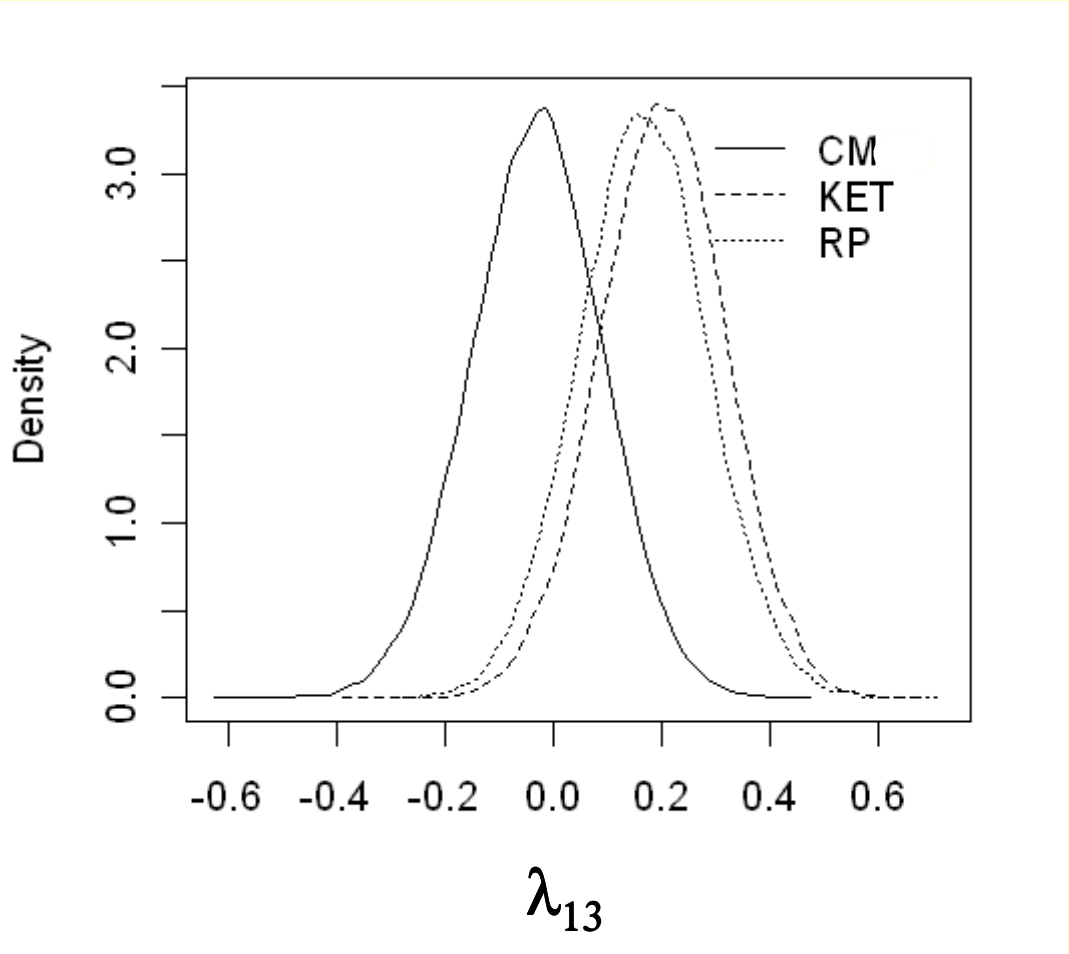
λ_{ij} = rate of change in trait *i* with respect to trait *j.*

Disease affects CFI (λ_{13}), disease affects NR56 (λ_{23}), CFI affects NR56 (λ_{21}), and all other λ_{ij}'s were set to 0



- Bayesian analysis
- Markov chain Monte Carlo (MCMC) methods
- SirBayes package

Results



Posterior mean

CM: -0.03

RP: 0.17

KET: 0.20

Figure 1. Posterior distributions of recursive effects from liability to disease (CM, KET, or RP) to CFI.

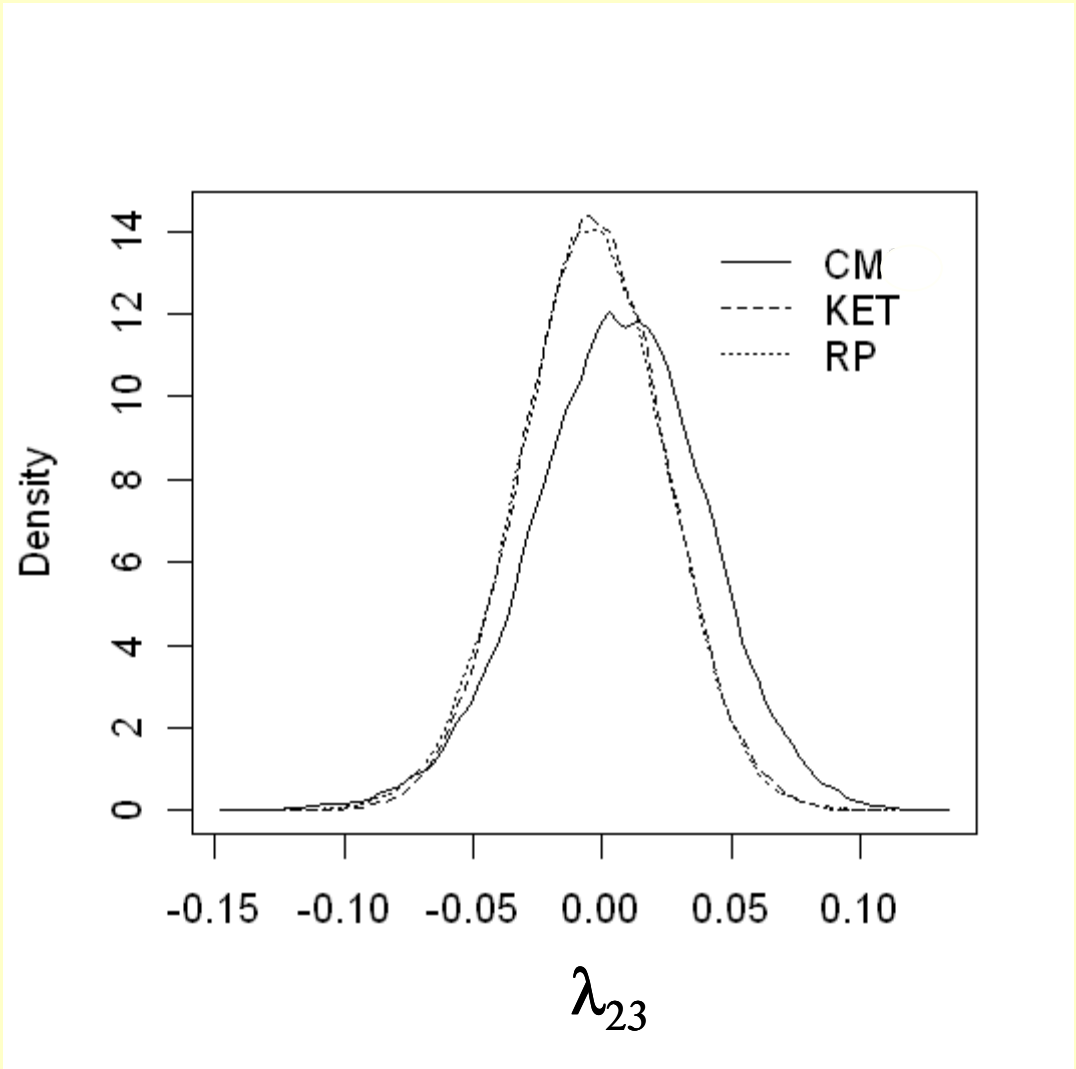
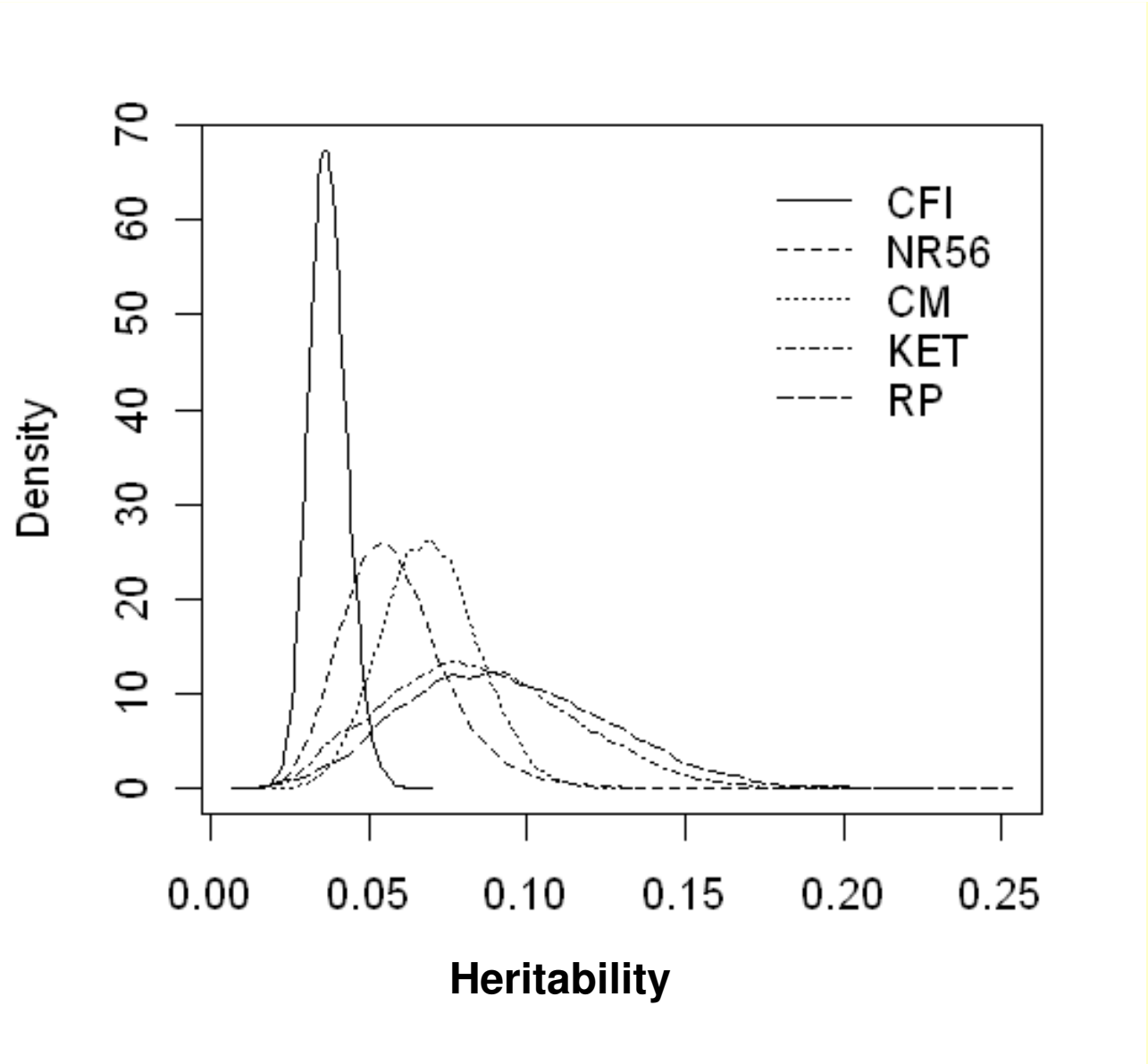


Figure 2. Posterior distributions of recursive effects from liability to disease (CM, KET, or RP) to NR56.



Posterior mean
CFI: 0.04
NR56 0.06
CM: 0.07
RP: 0.09
KET: 0.09

Figure 3. Posterior distributions of (from the left) heritability of CFI and of liability to NR56, CM, KET and RP.

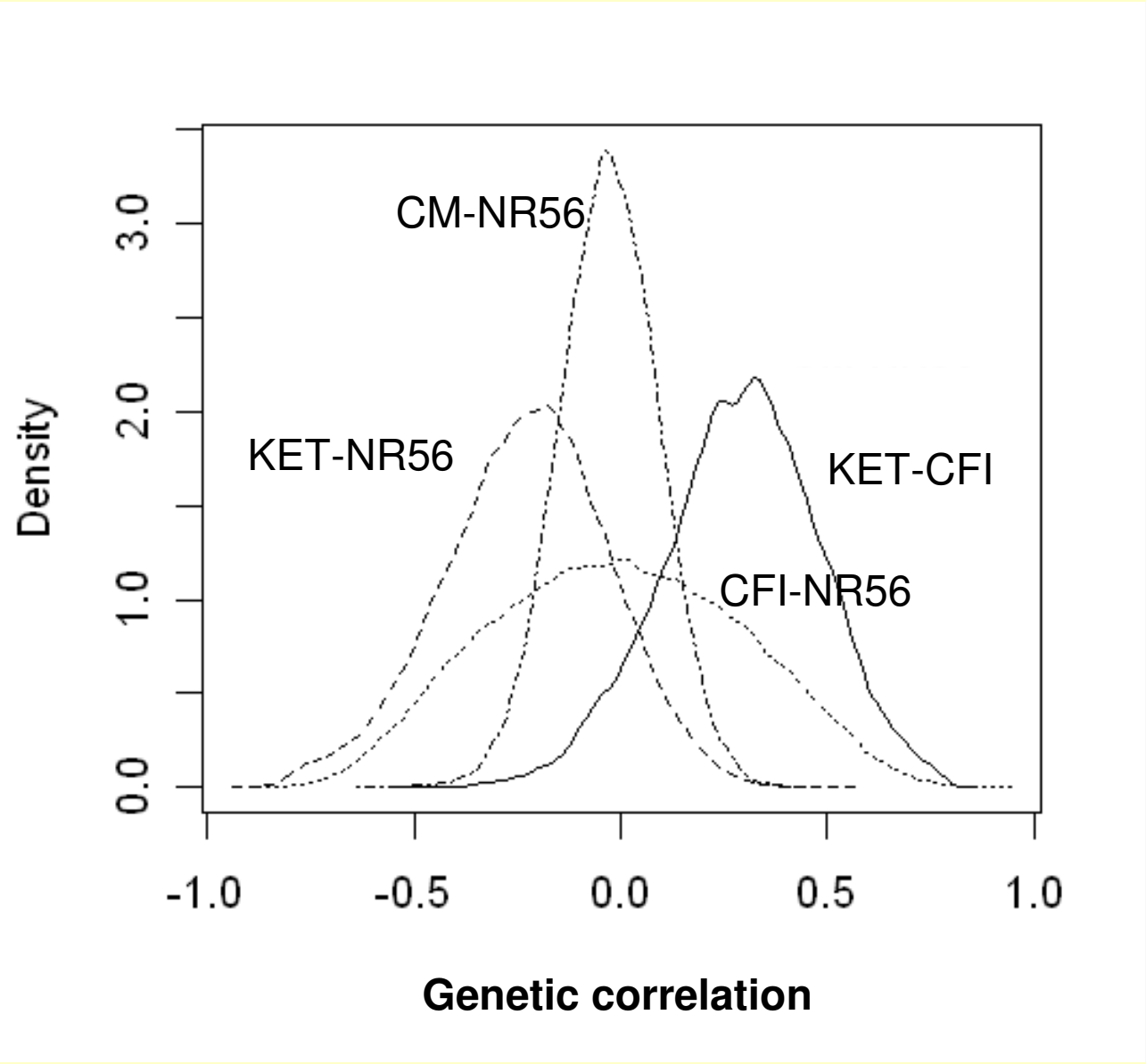


Figure 4. Posterior distributions of genetic correlations between health and fertility.

Conclusions

- Increased liability to KET or RP elevates CFI
- No causal effects from mastitis to fertility
- Recursive effects from disease to NR56, and from CFI to NR56 were close to zero
- Low to moderate, favorable genetic correlations between health and fertility
  - selection against disease expected to result in a small improvement of fertility as a correlated response

Conclusions

Structural-equation models

- distinguishing between causal effects between phenotypes and genetic relationships between traits
- may be useful to attain better understanding of complex relationships between traits.