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Random regression models for clinical mastitis in dairy cattle

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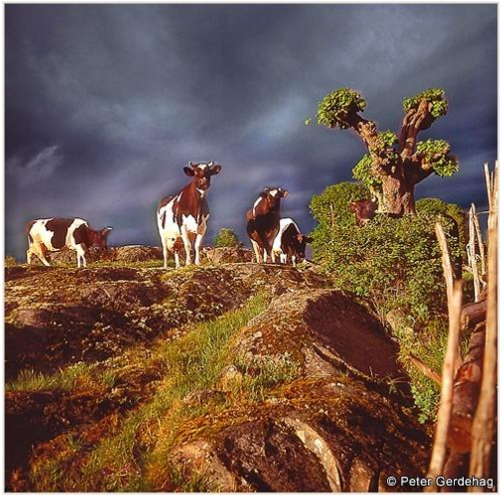
Objectives

- Estimate genetic parameters and predict breeding values for a longitudinal binary clinical mastitis trait with linear random regression models
- Compare these results with those from linear longitudinal multivariate and cross-sectional models



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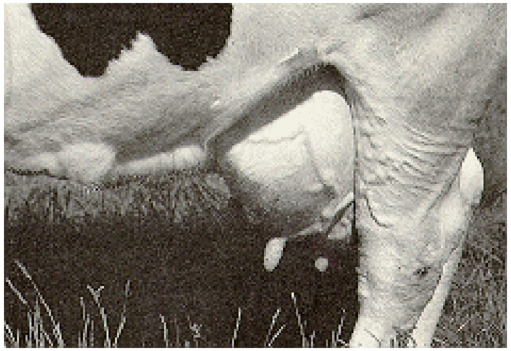
Background

- Clinical mastitis (CM) is one of the most common and costly diseases in dairy cattle
- In the Nordic countries, veterinary treatments of CM are recorded and used in the genetic evaluation (with SCC and udder conformation)
- CM is defined as an all-or-none trait during certain time periods of the lactations and linear cross-sectional models (CSM) are applied



Background

Main disadvantages with the linear CSM:

- Multiple cases and timing of cases ignored
- Ongoing and incomplete records not treated properly

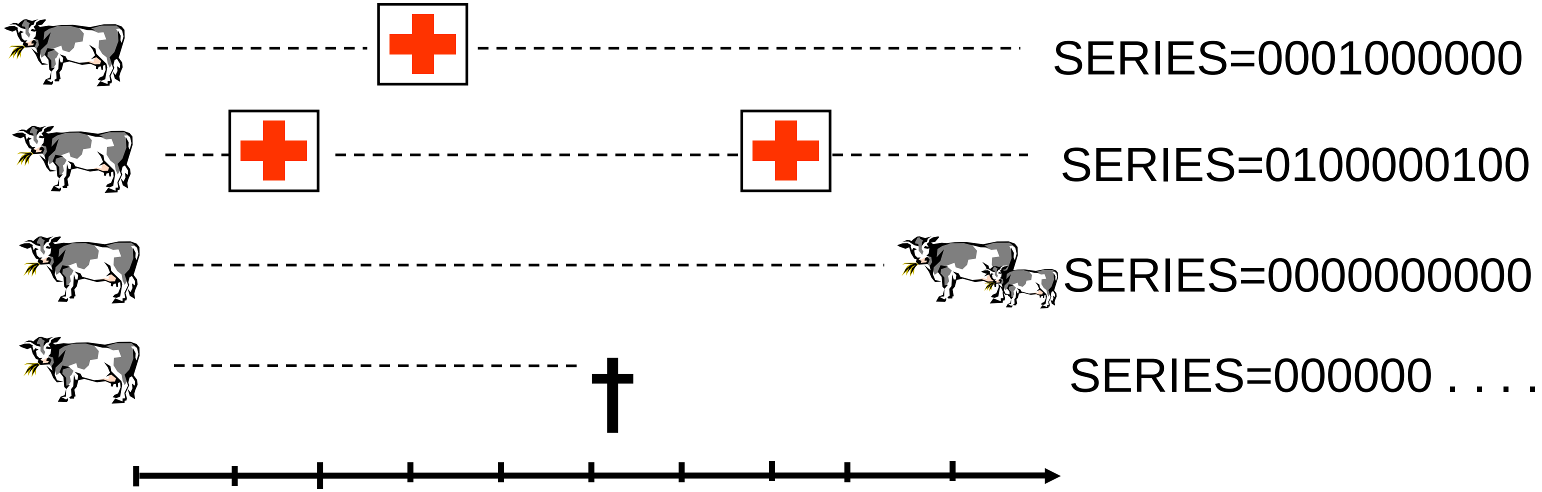
Alternatives:

- Threshold models – appropriate in theory
- Survival models - time to first mastitis
- Longitudinal models
  - multivariate
  - random regression

Random regression models

- RRM suitable for longitudinal data, e.g. test-day records
- Binary longitudinal data: survival (Veerkamp et al., 2001) and CM (Heringstad et al., 2003)

- ”TD-mastitis” = healthy or not in defined intervals



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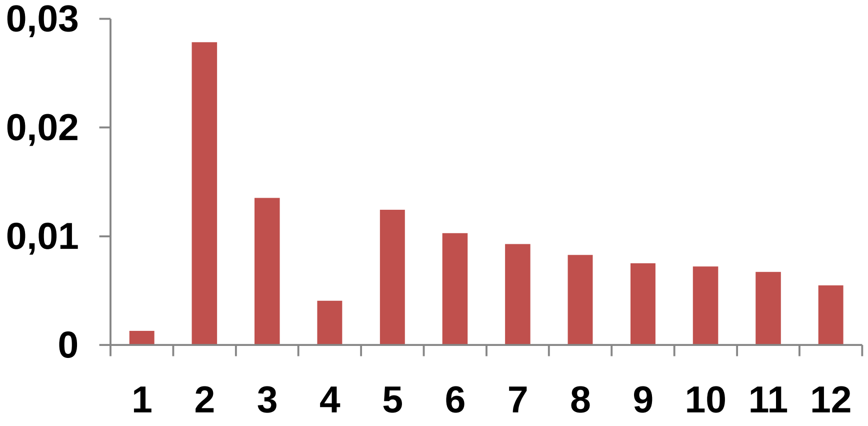
Data and trait definition

- 90,000 first-parity Swedish Holstein cows calving between 1998 and 2000
- Pedigree file with 759 sires
- Period from -10 to 241 d divided into four 1-week intervals followed by eight 4-week intervals
- Mastitis=0 at mid-point; Mastitis=1 at treatment day

Mastitis freqency per interval



RR model

$$CM_{|t} = age + month + ls + hy + cow + \sum_{i=0}^{3} sire_i \,\mathrm{lg}_i \;\; t \; + e$$

Average phenotypic ”curve” of CM over time:

- Lactation stage (fixed)

Random regression function with Legendre polynomials (cubic):

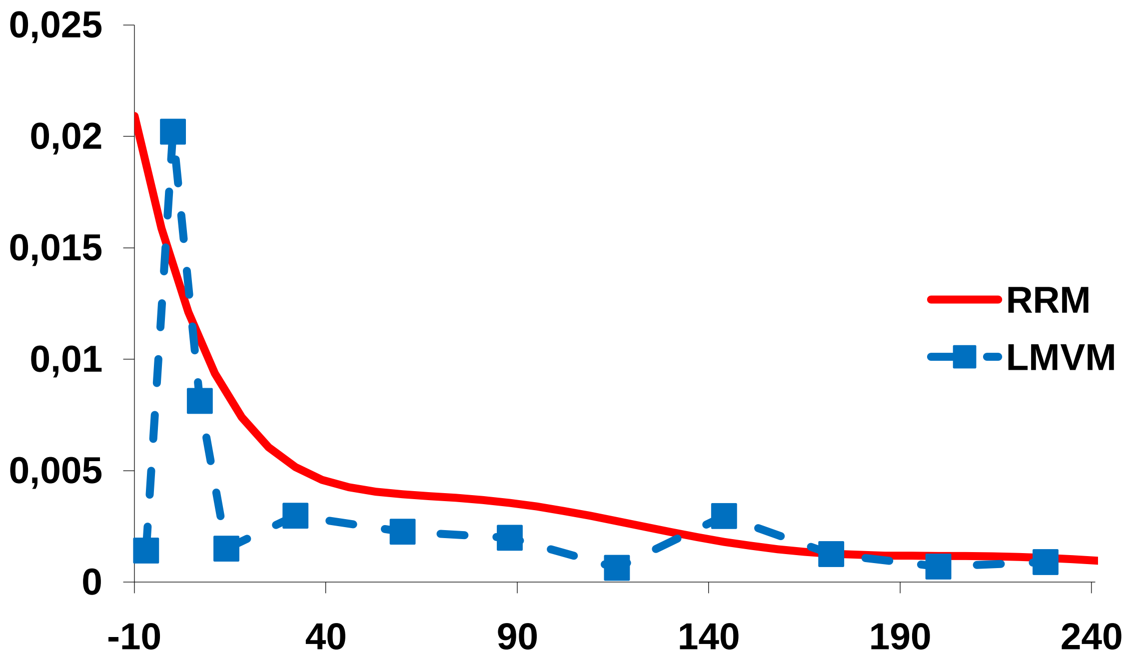
- Sire (genetic)

Time-independent effects:

- Age and month at calving (fixed)
- Herd-year at calving (random)
- Permanent environment of cow (random)
- Residual

Genetic parameters

Heritability of CM over time from random regression models (RRM) and longitudinal multivariate models (LMVM)

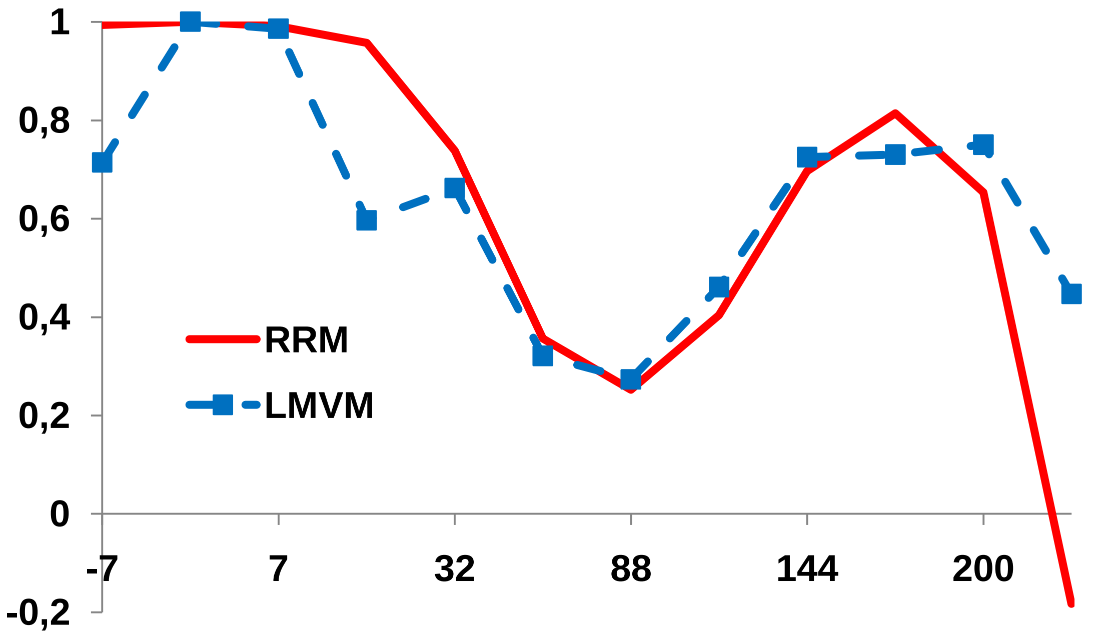


→ Low heritability because of low mastitis frequency

→ Good agreement except for first interval

Genetic parameters

Genetic correlations between CM in different time periods from RRM and LMVM– Day of calving

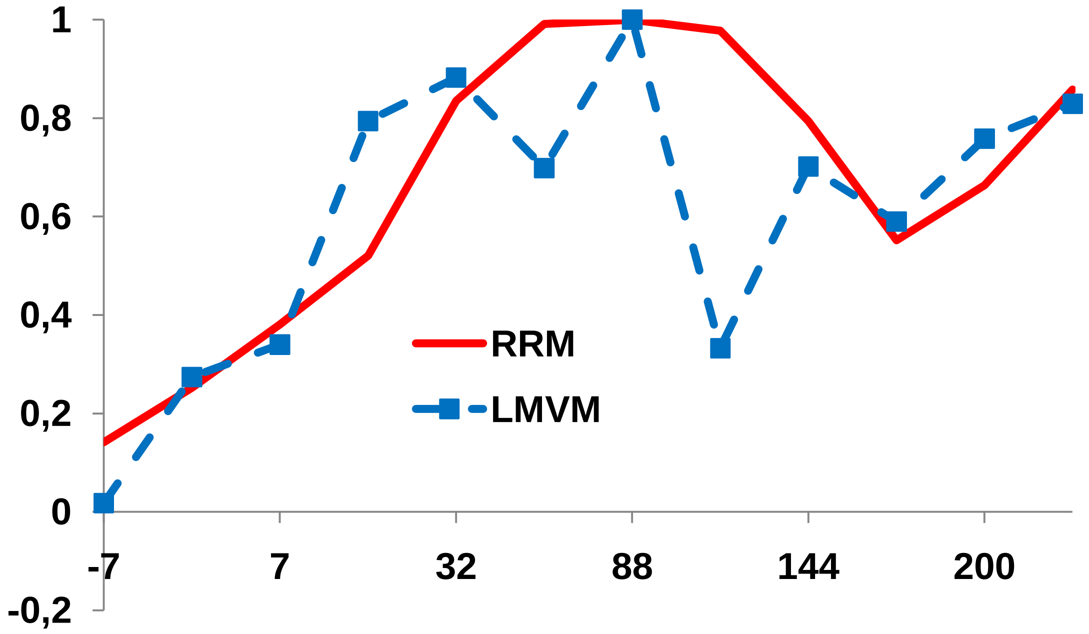


→ Very good agreement between methods

→ CM not same trait genetically throughout lactation

Genetic parameters

Genetic correlations between CM in different time periods from RRM and LMVM – Day 88



→ Good agreement but LMVM more unstable results

→ ”Mirror image” of previous graph

Predicted breeding values

- Summarized PBV from RRM for the periods -10 to 150 d, -10 to 50 d and 51 to 150 d

$$PBV_{RRM} = \sum_{t=i}^{j} 1 \quad \lg 1(t) \quad \lg 2(t) \quad \lg 3(t) \quad s_0 \quad s_1 \quad s_2 \quad s_3 \quad ^{T}$$

- Correlations between sire PBV from RRM and CSM

-10 to 150 d	-10 to 50 d	51 to 150 d
0.96	0.92	0.74

→ Re-ranking of sires occured

Conclusions

- Method of RRM rather unstable and sensitive when used for parameter estimation of binary CM data

  - very low mastitis frequency and variation in some periods

  - high correlations between RR coefficients

- Fairly good agreement between chosen RRM and LMVM/CSM and could work well for prediction of breeding values

- More research needed!

  - heterogeneity of residual variance, mastitis intervals, time-dep function....

Magnus J Stark

Questions or comments?

Thanks for your attention!