Genetic evaluation of mastitis liability and recovery through longitudinal models of somatic cell count

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Introduction

- Mastitis is most frequent and costly diseases.
- Genetic evaluation is performed either with cross sectional or longitudinal methods[1].
- Cross-sectional methods are the most commonly used.
- In cross-sectional methods lactations are considered as a static process.

[1] *Franzén et al*. 2012

Introduction

- Longitudinal methods enable us to model changes throughout a lactation:
  - Getting infected
  - Recovery after infection
- SCC (Somatic Cell Count) is used as a proxy to label clinical mastitis.

Objective

Develop better longitudinal models that capture as much genetic information as possible in both directions of the disease.

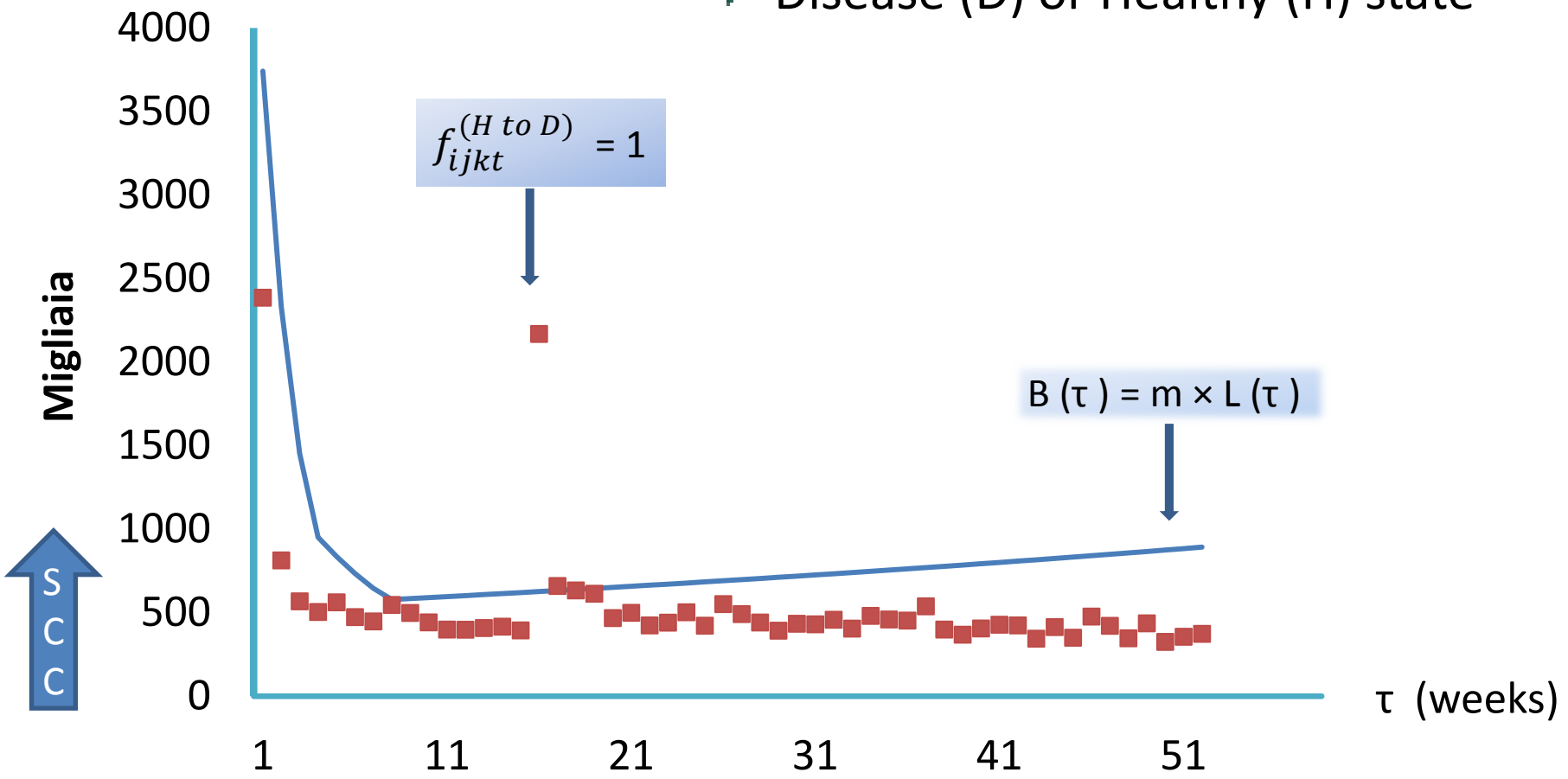
Material and Methods

- Data with five dairy traits were generated in Fortran.
  - SCC and TBV for mastitis liability and recovery
- Two population sizes:
  - 24 000 and 60 000 first-parity cows from 1200 herds
  - 400 unrelated sires (60 or 150 daughter/sire)
- 28% and 95% mastitis incidence rates per lactation
- Genetic correlations between infection and recovery:
  - rg = 0.00. rg = 0.02. rg = -0.02
- Designed to generate a representative of the real life dairy population and alternative herd structure[1].

[1] *Franzén et al*. 2012

Data Creation

- Binary data {0, 1} were created to define:
  - Disease (D) or Healthy (H) state



Transition probability model

- Possibilities of mastitis contract and recovery model
  - $T_i = \begin{bmatrix} \pi^{(H\ to\ D)} & 1-\pi^{(H\ to\ D)} \\ 1-\pi^{(D\ to\ H)} & \pi^{(D\ to\ H)} \end{bmatrix}$
  - T_i = transition probabilities for individual i going from a healthy (H) to a disease (D) state or the other way.
- A desired structure of the transition matrix is
  - High values of $\pi^{(H\ to\ H)}$ and $\pi^{(D\ to\ H)}$
  - Low values $\pi^{(H\ to\ D)}$ and $\pi^{(D\ to\ D)}$

Statistical Model

- The transition probability of getting infected:
  - $f_{ijkt}^{(H\ to\ D)} \sim Ber\left(\pi^{(H\ to\ D)}{}_{ijk}\right)$ and
  - $\boldsymbol{Probit\left(\pi^{(H\ to\ D)}{}_{ijk}\right) = \beta^{(H\ to\ D)} + S_j^{(H\ to\ D)} + h_k^{(H\ to\ D)} + e_{ijk}^{(H\ to\ D)}}$
    - $f_{ijkt}^{(H\ to\ D)}$ = 1 if a transition in time interval t. otherwise = 0.
    - β = liability of mastitis during period i for an average cow
    - h_j = fixed herd effect ; s_k = random sire effect
    - e_{ijkl} = random residual effect for a cow
- The transition probability of recovery $\pi^{(D\ to\ H)}{}_{ijk}$:
  - $f_{ijkt}^{(D\ to\ H)} \sim Ber\left(\pi^{(D\ to\ H)}{}_{ijk}\right)$ and
  - $\boldsymbol{probit\left(\pi^{(D\ to\ H)}{}_{ijk}\right) = \beta^{(D\ to\ H)} + S_j^{(D\ to\ H)} + h_k^{(D\ to\ H)} + e_{ijk}^{(D\ to\ H)}}$

Statistical Analysis

- Breeding values were estimated.
- RJMC[1] package in DMU
  - single trait genetic analysis
- MCMCglmm[2] package in R
  - multitrait genetics analysis.
- Correlations between TBV and EBV were calculated as the reliability of estimates.

[1]Madsen *et al*. 2010

[2]Hadfield, 2010

Results and Discussion

- More reliable estimates in the HD direction

Cases per lactation	Scenario 1 (28%)		Scenario 2 (95%)	
Transition direction	HD	DH	HD	DH
r_g= 0	0.73	0.40	0.81	0.61
rg= 0.2	0.72	0.37	0.82	0.62
rg= -0.2	0.71	0.56	0.82	0.59

- So far: single-trait analysis, ignoring genetic correlation between contracting and recovery.

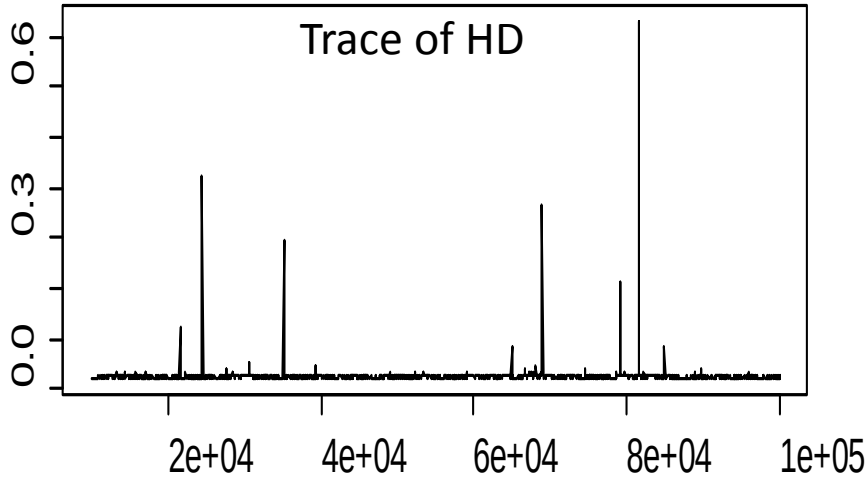
Results and Discussion

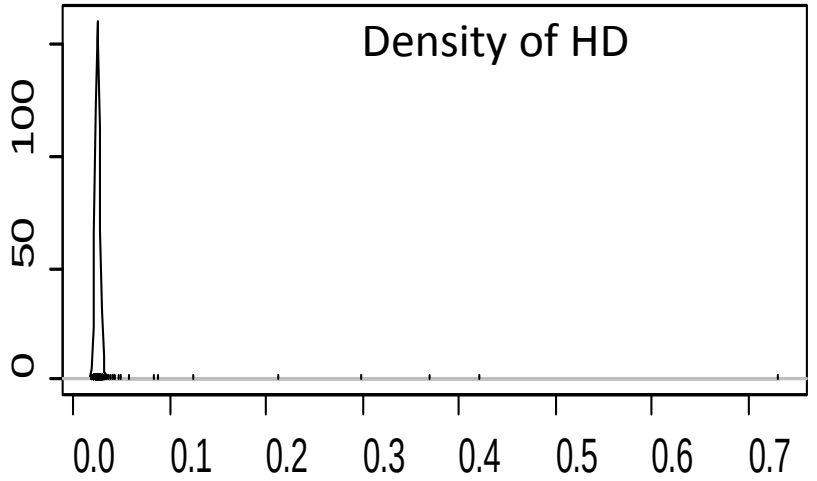
- Estimates from the MCMCglmm analysis

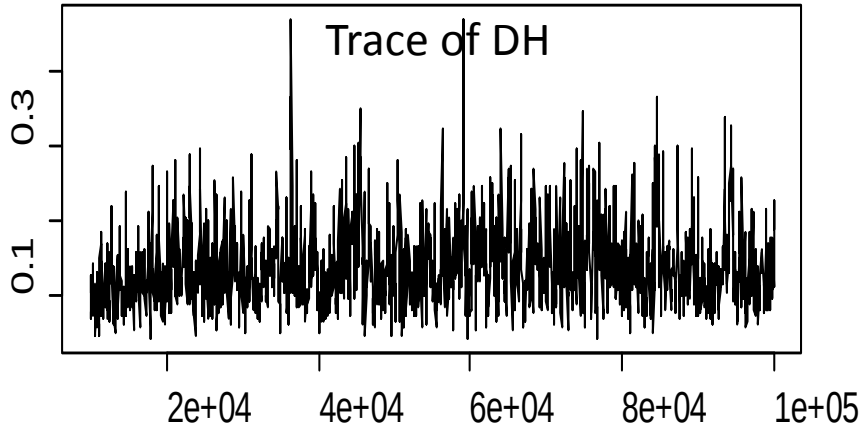
Direction	rTBV,EBV	h^2	correlation
HD	**0.543**	**0.191**	**0.119**
DH	**0.240**	**0.001**	

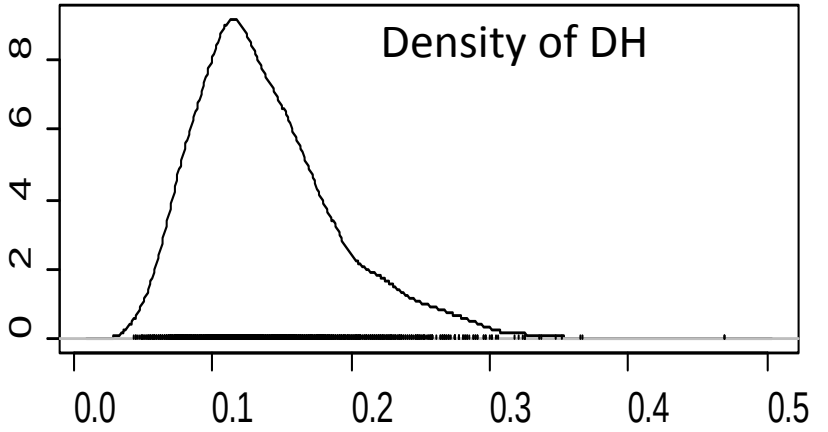
- Bivariate model considering both traits at the same time enable us to calculate the possible genetic correlation between the traits.

MCMC trace plots









Conclusions

- Selection accuracy as good as the estimations based on clinical mastitis for the HD direction.
- The transition probability model enables us to generate breeding values for DH direction.
- An option to include the whole disease course in the genetic evaluation of udder health.