Use of Transition Probabilities for Estimation of Mastitis Resistance

Jessica Franzén, Erling Strandberg
Jorge Urioste, Daniel Thorburn

Swedish University of Agricultural Sciences
Department of Animal Breeding and Genetics

Stockholm University
Department of Statistics

Presentation outline

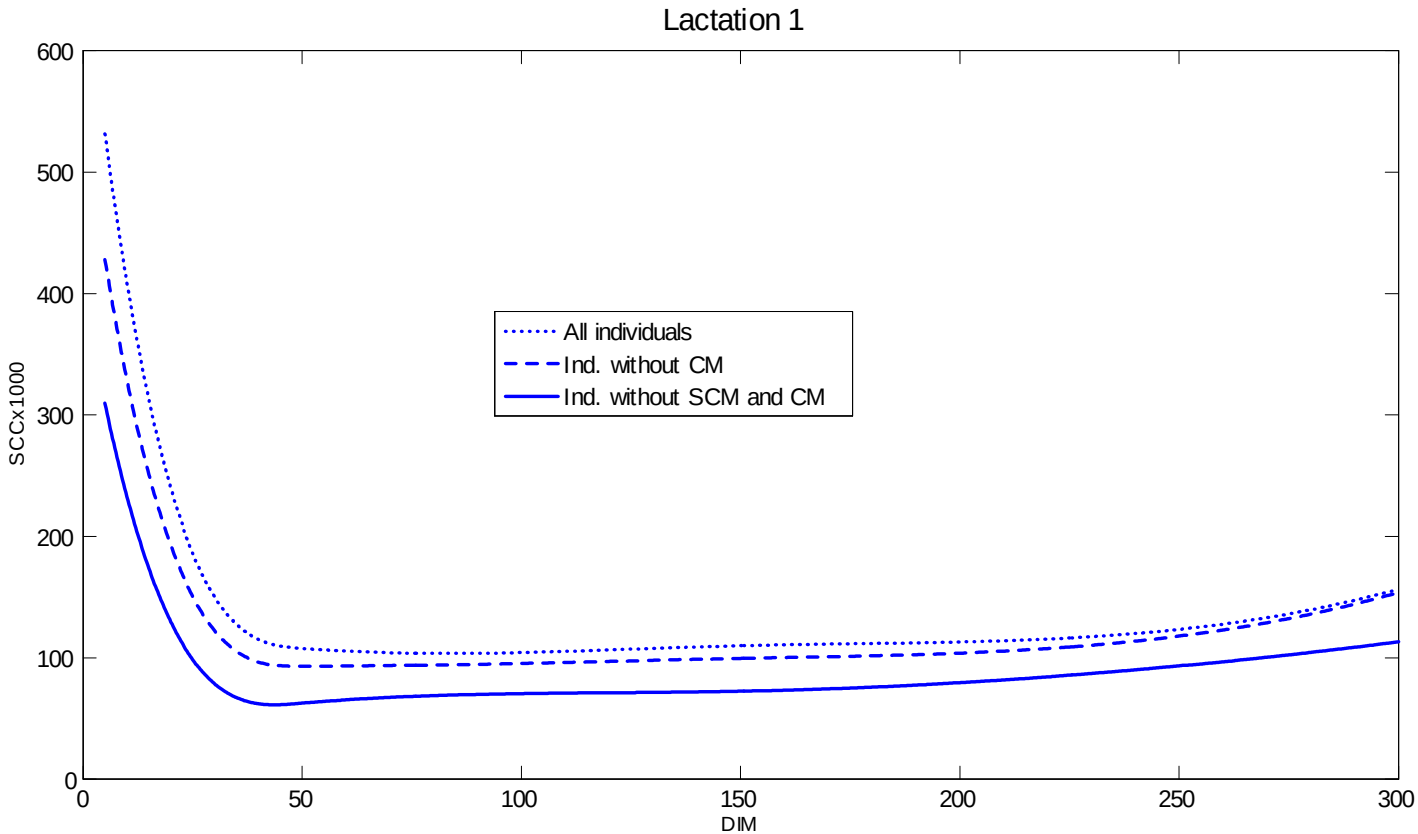
- Introduction
- Paper 1: Phenotypic and genetic characterization of novel somatic cell count traits from weekly or monthly observations
- Paper 2: Use of transition probabilities for estimation of mastitis resistance

Introduction

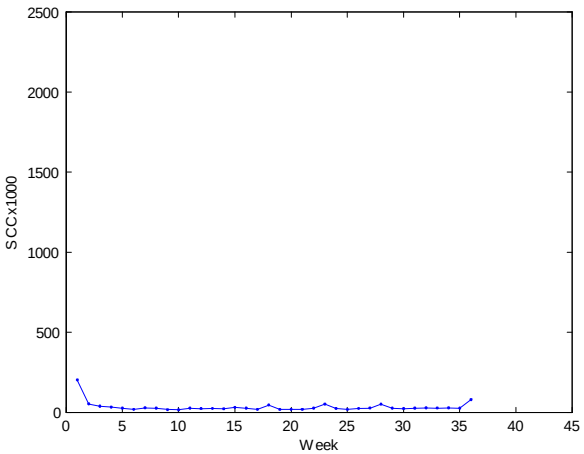
Some approaches for studying mastitis:

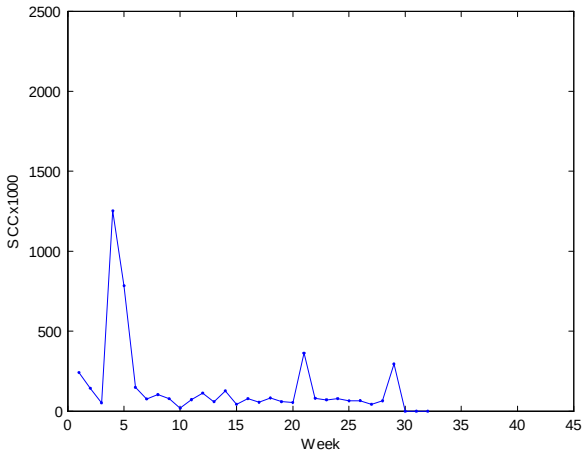
- Binary trait, presence/absence (0 -1)
- Survival analysis, time to first case
- Nr of cases model
- Patterns over a few consecutive test days
- New indicator traits
- Transition behavior

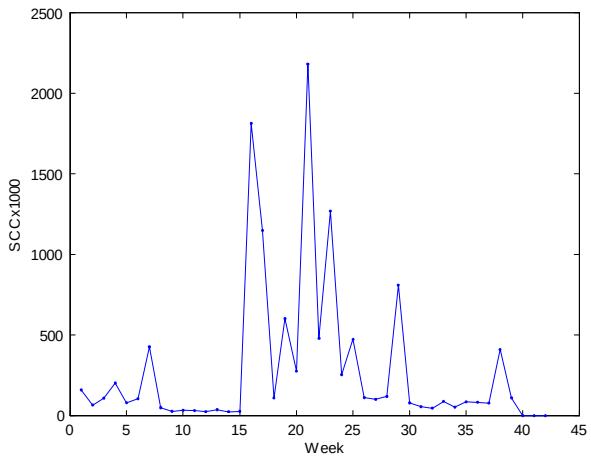
SCC base curve



Individual SCC patterns







Phenotypic and genetic characterization of novel somatic cell count traits from weekly or monthly observations

- Suggest traits that better capture changes in SCC than does the commonly used lactation average SCC or the 0 - 1 binary trait
- Estimate heritabilities and relationships to clinical mastitis
- Determine if these traits are feasible for use also in monthly data

Phenotypic and genetic characterization of novel somatic cell count traits from weekly or monthly observations

Variable acronym	Description
	SCC general levels/time of infection
SCC150D	Average test day SCC between 1 - 150 days in milk (DIM)
SCC150-305D	Average test day SCC between 151 – 305 DIM
LTSCC	Log of total amount of SCC in milk
DIMSCC>150	Average DIM until SCC observations >150,000 cell/mL
	Variation in SCC curve
SCCSD	SCC standard deviation
	Level of infection/inflammation
TD<40	Test day SCC <40,000 cell/mL (0,1)
TD41-80	Test day SCC between 41 and 80,000 cell/mL (0,1)
TD81-150	Test day SCC between 81 and 150,000 cell/mL (0,1)
TD151-500	Test day SCC between 151 and 500,000 cell/mL (0,1)
TD>500	Test day SCC>500,000 cell/mL (0,1)
NTD<40	Number of test days with SCC<40,000 cell/mL
NTD41-80	Number of test days with between 41 and 80,000 cell/mL
NTD81-150	Number of test days with between 81 and 150,000 cell/mL
NTD151-500	Number of test days with between 151 and 500,000 cell/mL
NTD>500	Number of test days with SCC>500,000 cell/mL
NTD>150	Number of test days with SCC>150,000 cell/mL
NPeak	Number of peaks (SCC>150,000 cell/mL)
	Time of recovery
DWidest	Days in the widest peak
DSick	Total number of days sick (sum up the days sick for each peak)
ADSick	Average days sick over peaks
	Production traits
AVMilk	Average test day milk yield
AVFPR	Average fat/protein ratio
	Mastitis
CM	Presence (1) or absence (0) of clinical mastitis during the lactation

Phenotypic and genetic characterization of novel somatic cell count traits from weekly or monthly observations

Data:

- Test-day records collected at weekly intervals in the Jälla research herd
- 1006 cow-lactation records
- Swedish Red (648) and Swedish Holstein (358)

Methods for trait selection:

- Cluster analysis
- Logistic regression

Method for genetic evaluation:

- General mixed animal model, Bayesian inference

Phenotypic and genetic characterization of novel somatic cell count traits from weekly or monthly observations

Conclusions:

- Significant new traits:
  1. Standard deviation of SCC over the lactation (W, M)
  2. Test day with SCC>500 000 (W, M)
  3. Number of days in the widest peak (W)
  4. Number of SCC peaks (M)
  5. Average number of days in SCC peaks (M)
- Heritability estimates for these new traits were 10 - 16% (4% for 0-1 CM)
- Heritabilities were as high in the monthly as in the weekly dataset

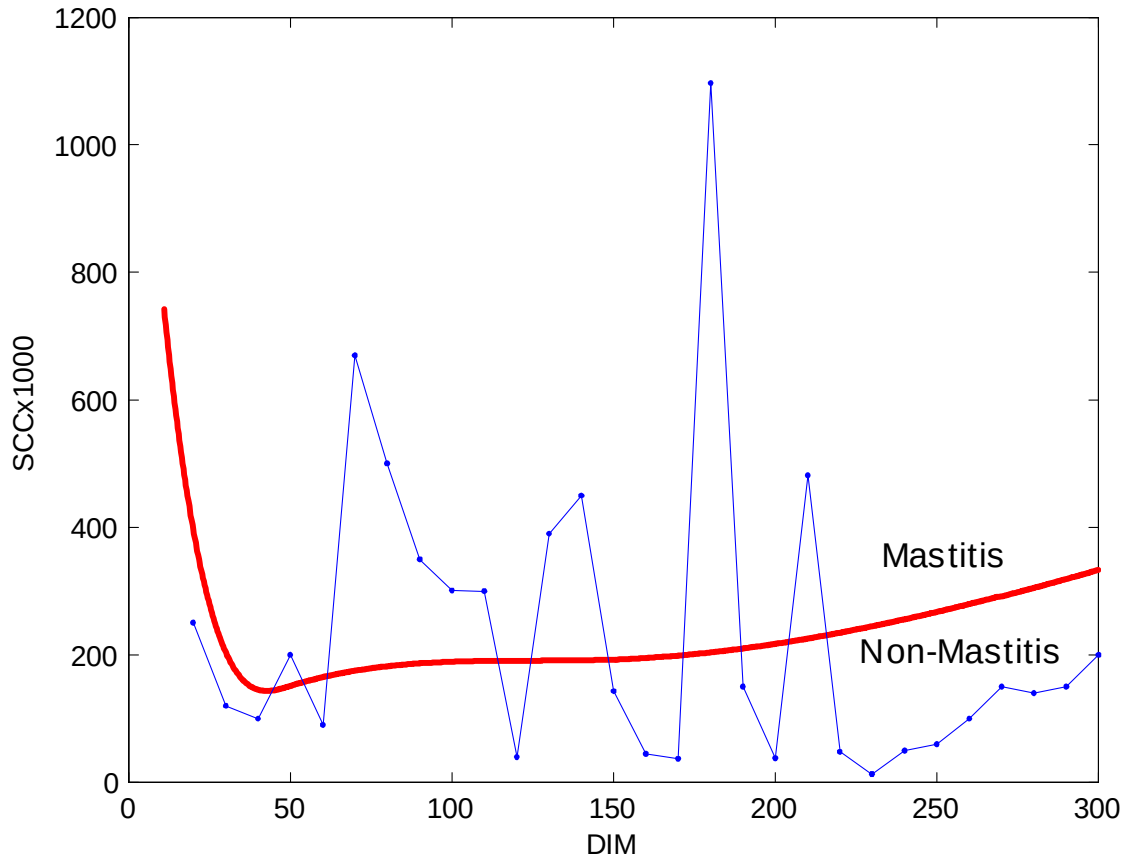
Use of transition probabilities for estimation of mastitis resistance

Another attempt to capture possible genetic information in SCC lactation pattern.

SCC movements are captured by modelling transition probabilities between states of mastitis (S) and non-mastitis (H).

$$T_i = \begin{array}{c} \\ H \\ S \end{array} \begin{array}{c} \begin{array}{cc} S & H \end{array} \\ \begin{bmatrix} P_i^{HS} & 1 - P_i^{HS} \\ 1 - P_i^{SH} & P_i^{SH} \end{bmatrix} \end{array}$$

Use of transition probabilities for estimation of mastitis resistance



Use of transition probabilities for estimation of mastitis resistance

The transition probabilities are modeled by a multilevel continuous time survival model:

- The probability of going from non-mastitis to mastitis (Healthy to Sick) is expressed as

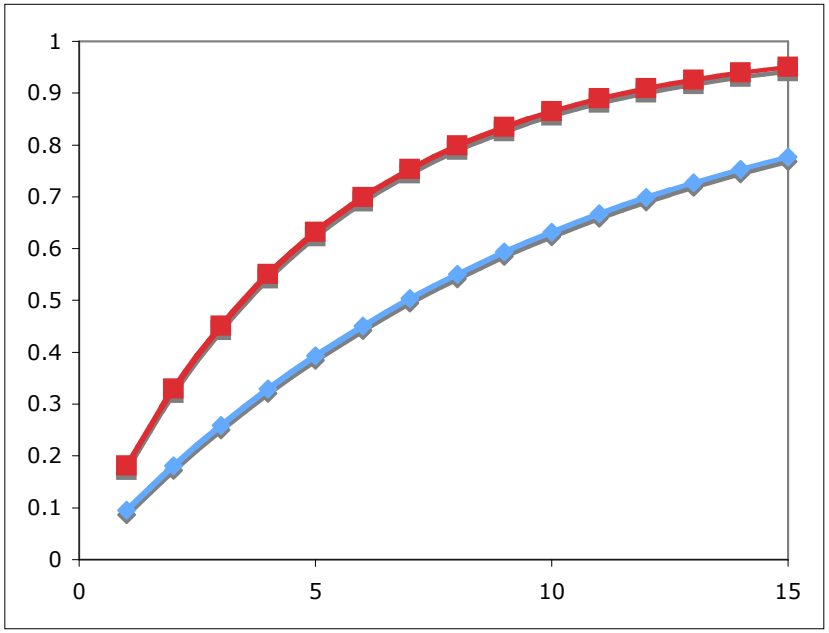
$$\begin{aligned} P_i^{HS} &= P_i\left(\text{sick} \,|\text{healthy } \tau \text{ days ago}\right) = 1 - \exp\left(-\lambda_i^{(S)}\tau\right) \\ \lambda_i^{(S)} &= b^{(S)}X + a^{(S)}Z + e_i^{(S)} \end{aligned}$$

- In the same way, the probability of going from mastitis to non-mastitis is expressed as,

$$\begin{aligned} P_i^{SH} &= P_i\left(\text{healthy} \,|\text{sick } \tau \text{ days ago}\right) = 1 - \exp\left(-\lambda_i^{(H)}\tau\right) \\ \lambda_i^{(H)} &= b^{(H)}X + a^{(H)}Z + e_i^{(H)} \end{aligned}$$

Use of transition probabilities for estimation of mastitis resistance

Transition probabilities for two different transition intensities λ_1 and λ_2.



$$P_i^{HS} = P_i\left(\text{sick} \,\middle|\, \text{healthy } \tau \text{ days ago}\right) = 1 - \exp\left(-\lambda_i^{(S)}\tau\right)$$

Use of transition probabilities for estimation of mastitis resistance

Considerations:

- Interval censored data
  - Although the underlying event process is in continuous time, data collection may lead to interval censored data.
- Regular or irregular spaced intervals
- Interval length

Guidelines for interval censored data:

- Approx. regular spaced intervals and "short" intervals $\Longrightarrow$ Multilevel *continuous time* survival model
- Irregular spaced intervals and/or "long" intervals $\Longrightarrow$ Multilevel *discrete time* survival model

Use of transition probabilities for estimation of mastitis resistance

In the discrete case, the probability of transition is modeled through a standard multilevel binary response model with a logit link function

$$Y_{it} = \begin{cases} 1 \text{ if state transition in interval } t \\ 0 \text{ if no state transition in interval } t \end{cases}$$

$$P_i^{HS} = P_i\left(\text{healthy} \,|\text{sick last test day}\right)$$

$$Y_{it} \sim Ber(P_i^{HS})$$

$$\log\left(\frac{P_i^{HS}}{1-P_i^{HS}}\right) = \log it(P_i^{HS}) = b^{(S)}X + a^{(S)}Z + e_i^{(S)}$$

Use of transition probabilities for estimation of mastitis resistance

Example with sire and herd effects:

$$\begin{aligned} i &= cow \\ j &= sire \\ k &= herd \end{aligned}$$

$$Y_{tijk} \sim Ber(P_{ijk}^{HS})$$

$$\log\left(\frac{P_{ijk}^{HS}}{1-P_{ijk}^{HS}}\right) = \log it(P_{ijk}^{HS}) = f(t) + s_j + h_k + e_{ijk}$$

$$\begin{aligned} s_j &\sim N\left(0, \sigma_s^2\right) \\ h_j &\sim N\left(0, \sigma_h^2\right) \\ e_{ijk} &\sim N\left(0, \sigma_e^2\right) \end{aligned}$$

Use of transition probabilities for estimation of mastitis resistance

Parameter estimation in MLwiN software package

- Bayesian estimation using MCMC method
- Gibbs sampler and Metropolis Hastings algorithm
- Vague prior distributions
  - Fixed parameters: $p(\beta) \propto 1$
  - Variances: $p(\sigma^2) \sim \Gamma^{-1}(\varepsilon, \varepsilon)$

Use of transition probabilities for estimation of mastitis resistance

Future work:

- Both the continuous and discrete models will be tested on simulated data with known breeding values.
- Depending on the outcome, real data from our research herd and data from Swedish Milk will be used
- Expand the model to a 3 state model (NM, SCM, CM)
- Estimate the threshold between states within the model
- Comparison with other methods

Thank you for listening!