Use of Transition Probabilities for Estimation of Mastitis Resistance

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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
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
Introduction

SCC base curve

Lactation 1

- All individuals
- Ind. without CM
- Ind. without SCM and CM
Introduction

Individual SCC patterns
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

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

\[
T_i = \begin{bmatrix}
S & H \\
S & 1 - P_{i}^{SH} & P_{i}^{HS} & 1 - P_{i}^{HS} \\
1 - P_{i}^{SH} & P_{i}^{SH}
\end{bmatrix}
\]
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

  \[
P_i^{HS} = P_i (\text{sick} \mid \text{healthy } \tau \text{ days ago}) = 1 - \exp \left(-\lambda_i^{(S)} \tau \right)
\]

  \[
\lambda_i^{(S)} = b^{(S)} X + a^{(S)} Z + e_i^{(S)}
\]

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

  \[
P_i^{SH} = P_i (\text{healthy} \mid \text{sick } \tau \text{ days ago}) = 1 - \exp \left(-\lambda_i^{(H)} \tau \right)
\]

  \[
\lambda_i^{(H)} = b^{(H)} X + a^{(H)} Z + e_i^{(H)}
\]
Use of transition probabilities for estimation of mastitis resistance

Transition probabilities for two different transition intensities $\lambda_1$ and $\lambda_2$.

$$P_{i}^{HS} = P_i \left( \text{sick} \mid \text{healthy } \tau \text{ days ago} \right) = 1 - \exp \left( -\lambda_i^{(S)} \tau \right)$$
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 $\implies$ Multilevel \textit{continuous time} survival model

- Irregular spaced intervals and/or "long" intervals $\implies$ Multilevel \textit{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

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

\[ P_{i}^{HS} = P_i (\text{healthy} | \text{sick last test day}) \]

\[ Y_{it} \sim \text{Ber}(P_{i}^{HS}) \]

\[ \log \left( \frac{P_{i}^{HS}}{1 - P_{i}^{HS}} \right) = \log it(P_{i}^{HS}) = b^{(S)} X + a^{(S)} Z + e_{i}^{(S)} \]
Use of transition probabilities for estimation of mastitis resistance

Example with sire and herd effects:

\[ Y_{tij} \sim \text{Ber}(P_{ij}^{HS}) \]

\[
\log \left( \frac{P_{ij}^{HS}}{1 - P_{ij}^{HS}} \right) = \log \text{it}(P_{ij}^{HS}) = f(t) + s_j + h_k + e_{ij} \]

\[ s_j \sim N(0, \sigma_s^2) \]
\[ h_j \sim N(0, \sigma_h^2) \]
\[ e_{ij} \sim N(0, \sigma_e^2) \]
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: $p(\sigma^2) \sim \Gamma^{-1}(\epsilon, \epsilon)$
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!