# A Multilevel Multistate Competing Risks Model for the Prediction of Bulk Milk Somatic Cell **Count from Individual Cow Characteristics**

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# Introduction

In the UK, a threshold of 200,000 cells/mL is commonly used to categorise cows as having a Low or a High somatic cell count (SCC) (Bradley and Green, 2005). The main factor increasing SCC is mastitis. However, variations in SCC with stage of lactation and parity have been demonstrated (Schepers et al., 1997). In turn, individual cow SCC impact bulk milk somatic cell counts (BMSCC) which farmers have a strong interest in controlling because they determine milk price and saleability. As a consequence, supposedly infected cows are more likely to be dried off or culled early. Low and High SCC levels, drying off or culling can be seen as competing risks. The probability of being in one of these states depends on the state a cow was in on her previous milk recording, her stage of lactation and her parity. This can be modelled using multistate competing risks model for event history data (Steele et al., 2004).

**Aims**: ➤ To model the probability of transition between two SCC levels, drying off and culling

> To determine whether BMSCC can be predicted from these state transitions using data milk recording data

# Materials and Methods

 $State_{ijk} \sim Multinomial(\pi_{iik})$ 

 $u_{ik}^{i'} \sim MVN(0, \Sigma_u)$ 

#### Data

- Monthly collected milk recording data
- January 2004 to December 2006
- 100 herds 7 consecutive test-days dataset 1

# · First 6 test-days: training data

- dataset 2
- 7th test-day: validation data
  - dataset 3
- 100 herds 1 test-day: validation

### Multilevel multistate competing risks model

- · Multinomial logit model
- Outcome: State (Low; High; Dry; Culled)
- Covariates:  $\sum I[State_{i(j-1)k}^{i'}](\alpha_i^{i'} + \sum X_{ijk}\beta_i^{i'} + u_{ik}^{i'})$ 
  - > Previous state (Low; High; Dry; First)
  - ➤ Days in milk
  - > Parity (1 or > 1)
  - · Herd random effects

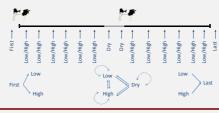
#### **Multilevel Linear model**

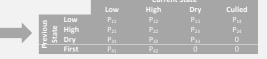
$$BMSCC_{ij} = \alpha + \sum X_{ij}\beta^T + u_j + e_{ij}$$
$$u_j \sim N(0, \sigma_j^2)$$
$$e_{ij} \sim N(0, \sigma_{ij}^2)$$

- Outcome: BMSCC
- Covariates:
  - % of the herd in each state transition
- Herd random effect

### Cow categories

- First recording
- · Lactating cows
  - Threshold T of 200,000 cells/mL
    - Low when ≤ T
    - High when > T
- Dry cows
- Culled cows



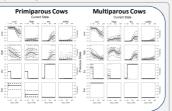


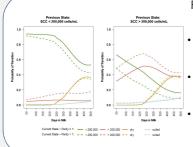
# Results

### Multilevel multistate competing risks model

#### Probabilities of transition between states /day in milk (dataset 1)

- Grey dots: observed probabilities
- · Black continuous lines: Median probabilities of transition as predicted by the model
- Black dashed lines: 95 % credibility interval for each probability of transition.



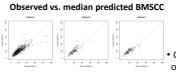


### Probabilities of transition from Low (left) and High (right) to Low, High, dry and

#### culled.

- Multiparous likely to cows more become or to stay High than primiparous cows
- Calving to 250 days in milk: sharp increase/decrease in the probability of staying High/becoming Low
- 250 to 450 days in milk: increase in the risk of moving to dry which resulted in a decrease in the probability to move to Low or High

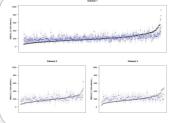
## **Multilevel Linear model**



BMSCC predicted from the percentage of lactating cows undergoing each transition

 Good agreement between observed and predicted values

## State transition & BMSCC



#### **BMSCC** predicted by combining the state transition model and the BMSCC model

- Black dots: observed BMSCC
- Blue dots: median predicted BMSCC
- Grey lines: 95 % credibility intervals for the predicted values
- Predictions not useful in ranking individual BMSCC

A Bayesian multilevel multistate competing risks model was shown to predict transitions between 4 states during dairy cows career correctly. However, the prediction of BMSCC from the predicted SCC states was not accurate. The reasons for this are unclear, It is possible that the model could anticipate physiological variation such as an SCC increase with stage of lactation and parity correctly but that infection, which might contribute more to BMSCC, is inherently less predictable. Such models could have a wide range of applications in Veterinary Epidemiology. The ease of generating predictions for model checking in WinBUGS makes a Bayesian approach appealing in this respect.

References

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