



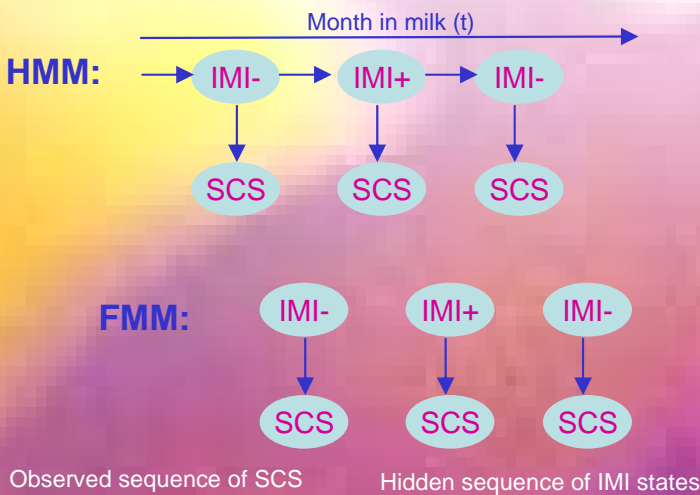
Introduction

In genetic studies, information on intra-mammary infection (IMI) is usually based on somatic cell scores (SCS). One important difficulty in using SCS to find animals most tolerant to IMI is that factors known to influence SCS are different in healthy from infected cows such that estimates obtained from the traditional linear models are biased. To solve this issue, several authors have proposed the finite mixture model (FMM) to infer the cow's putative probability of being infected based on their individual SCS.

Here, we proposed a generalization of the FMM : the Hidden Markov Model (HMM). It has the advantages – not provided by the FMM - to also predict the cow's putative probabilities of recovery (from IMI+ to IMI-) and of new infection (from IMI- to IMI+). The validity of both the FMM and HMM is assessed on SCS simulated from parameters published in the literature for mastitis associated with *Escherichia coli* and *Staphylococcus aureus*.

Materials and Methods

General formulation of the model (Diacyclic graph)



Parameters for the simulated data sets

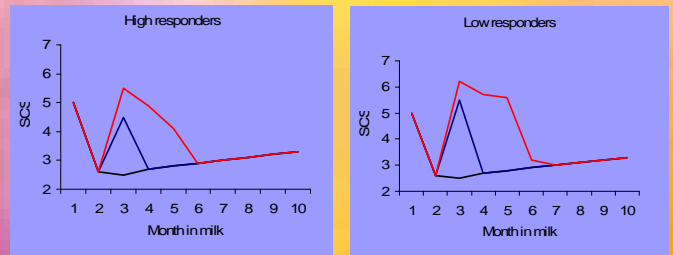
If IMI- $SCS_{0,k}^t = \mu_0^t + e_{0,k}^t$ $e_{0,k}^t \sim N(0, I\sigma_0^2)$

If IMI+ $SCS_{1,k}^t = \mu_1^t + e_{1,k}^t$ $e_{1,k}^t \sim N(0, I\sigma_1^2)$

$\sigma_0^2 = 1$ or 1.4

% cows IMI+ = 20% or 50%

% *E. coli* among IMI+ = 0%, 50% or 100%



Per-MIM means of SCS for lactations without clinical mastitis (μ_0^t ; black) and with clinical mastitis (μ_1^t) associated with *S. aureus* (red) or *E. coli* (blue) occurring on the 3rd (median) MIM for multiparous cows (adapted from de Haas et al., JDS 2002).

Results

Maximum likelihood Estimates

HMM:

$$\mu_0^t = \frac{\sum_{k=1, N} \text{pr}(z_k^t = 0 | \text{obsv.seq}_k)}{\sum_{k=1, N} \text{pr}(z_k^t = 0 | \text{obsv.seq}_k)}$$

$$\sigma_0^2 = \frac{\sum_{k=1, N} \sum_{t=1, T} p(z_k^t = 0 | \text{obsv.seq}_k) (SCS_k^t - \mu_0^t)^2}{\sum_{k=1, N} \sum_{t=1, T} p(z_k^t = 0 | \text{obsv.seq}_k)}$$

$$a_{00}^k = \frac{\sum_{t=1, T} p(z_k^t = 0 \cap z_k^{t+1} = 0 | \text{obsv.seq}_k)}{\sum_{t=1, T} p(z_k^t = 0 | \text{obsv.seq}_k)}$$

FMM:

$$\mu_0^t = \frac{\sum_{k=1, N} \text{pr}(z_k^t = 0 | SCS_k^t) SCS_k^t}{\sum_{k=1, N} \text{pr}(z_k^t = 0 | SCS_k^t)}$$

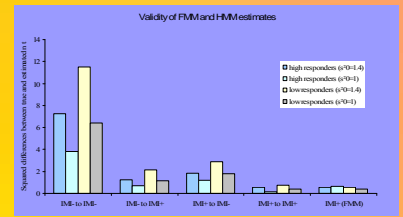
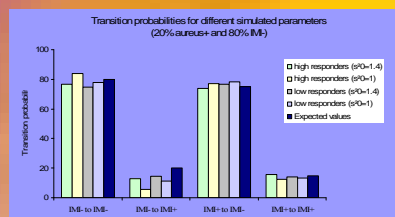
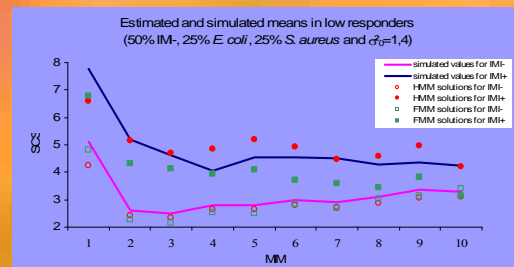
$$\sigma_0^2 = \frac{\sum_{k=1, N} \sum_{t=1, T} p(z_k^t = 0 | SCS_k^t) (SCS_k^t - \mu_0^t)^2}{\sum_{k=1, N} \sum_{t=1, T} p(z_k^t = 0 | SCS_k^t)}$$

$$\lambda^k = \frac{\sum_{t=1, T} p(z_k^t = 0 | SCS_k^t)}{T}$$

$z_k^t = 0$ if IMI- at MIM = t on the kth cow
 $z_k^t = 1$ if IMI+ at MIM = t on the kth cow
 for k = 1 to N cows and t = 1 to T MIM

Solutions from the simulated data

(1000 iterations in the EM algorithm; T=10; N=500)



Conclusions

Both FMM and HMM are useful tools to estimate cow's putative IMI status based on the available monthly SCS:

- FMM is better adapted to the analysis of whole lactations
- HMM is better adapted to the analysis of individual MIM