

Detection of Progression of Clinical Mastitis in Cows Using Hidden Markov Model

Safeer M. Saifudeen^{1*}, S. Selvam², A. Serma Saravana Pandian³, R. Venkataramanan³ and A. Mohamed Safiullah⁴

¹PG scholar, ²Professor and Head (Retd.), ³Assistant Professor, ⁴Professor and Head, Department of Animal Husbandry Statistics and Computer Applications, Madras Veterinary College, Chennai, Tamil Nadu Veterinary and Animal Sciences University, Chennai-600051

*Corresponding Author E-mail: safeermsaifudeen@gmail.com

Received: 20.04.2017 | Revised: 28.05.2017 | Accepted: 1.06.2017

ABSTRACT

Mastitis is the most important and expensive disease of dairy industry. A clear cut idea about the progression of clinical cases of mastitis in a herd is essential for effective mastitis prevention and control program. Hidden Markov model is a doubly stochastic process with an underlying stochastic process that is not observable (it is hidden), but can only be observed through another set of stochastic processes that produce the sequence of observed symbols. The present study reveals the most probable sequence of stages of bovine clinical mastitis which are hidden inside the body using the transition probabilities between the stages and also using the emission probabilities of possible symptoms exhibited in each stage of the disease as an application of hidden Markov model. Clinical mastitis constituted 46.8 percent of the total mastitis cases presented. The sequence of progression of the stages of mastitis obtained as viterbi path from the overall cases of bovine clinical mastitis studied was $W1 \rightarrow W2 \rightarrow W1 \rightarrow W2 \rightarrow W1$, where $W1$ is the stage of inflammatory response and $W2$ is the stage of bacterial flare up and production of toxins.

Key words: Mastitis in cows, Hidden Markov model, Probability.

INTRODUCTION

Mastitis is the most important and expensive disease of dairy industry¹. This disease is characterized by inflammation of mammary gland in response to injury for the purpose of destroying or neutralizing the infectious agents and to prepare the way for healing and return to normal function. In the dairy cow, mastitis is nearly always caused by micro organisms; usually bacteria, that invade the udder,

multiply in the milk-producing tissues, and produce toxins that are the immediate cause of injury². Clinical mastitis is presented with five gross signs of udder inflammation namely redness, heat, swelling, pain, and clots or discoloration of milk. A clear cut idea about the progression of clinical cases of mastitis in a herd is essential for effective mastitis prevention and control program.

Cite this article: Saifudeen, S.M., Selvam, S., Pandian, A.S.S., Venkataramanan, R. and Safiullah, A.M., Detection of Progression of Clinical Mastitis in Cows Using Hidden Markov Model, *Int. J. Pure App. Biosci.* 5(5): 436-441 (2017). doi: <http://dx.doi.org/10.18782/2320-7051.2877>

Hidden Markov model is a doubly stochastic process with an underlying stochastic process that is not observable (it is hidden), but can only be observed through another set of stochastic processes that produce the sequence of observed symbols³. Hidden Markov models are important tools in estimation and analysis of biological sequences and many other systems⁴. It consists of a set of interconnected states where the connections are governed by a set of transitional probabilities. Hidden Markov model can be used to assess the disease progression as compared to the clinical stages of diseases⁵. It can also be used to determine the transition probabilities between two states⁶⁻⁸. The present study was conducted to identify the most probable sequence of stages of bovine clinical mastitis which are hidden inside the body using the transition probabilities between the stages and also using the emission probabilities of possible symptoms exhibited in each stage of the disease.

MATERIALS AND METHODS

The present study was conducted at the large animal clinic of Madras Veterinary College. Out of 127 cases studied, 60 were found to be clinical mastitis. Each and every case was observed thoroughly including the stages of disease and the possible symptoms occurred in each stage. The particular stage of the disease (which was hidden) and the change in stage of disease were identified by the symptoms shown by the affected animals. In the first hidden stage (W1), three types symptoms including reduced milk production, udder inflammation⁹ (swelling, heat, hardness,

redness, pain), mild clinical signs (reduced feed and water intake, increment in body temperature, signs of diarrhoea etc.) were noted. As time advanced, the disease was progressed to the second hidden stage (W2) showing abnormality in milk (watery appearance, flakes, clots or pus), abnormality in udder and major clinical signs (fever, reduction in mobility, sunken eyes, dehydration etc.). The probability of transition from one stage to other stage or itself (transition probability) and the probability of showing particular symptoms at different stages (emission probability) were calculated. Detailed description of hidden stages of mastitis, its transition probabilities, the observed symptoms along with the emission probabilities were given in table 1 and 2. Using the above said probability values both transition and emission probability matrices were constructed.

Representation of a three state ergodic hidden Markov model was given in figure 1. In a sequence of states at successive times, the hidden state at any time denoted by $W(t)$ emits some visible symptoms $v(t)$. The system can revisit a state at different steps and not every state need to be visited. The model was explained in such a way that at any state $W(t)$, probability of emitting a particular visible state $v(t)$. The particular sequence of visible states are given by $V^T = \{v(1), v(2), \dots, v(T)\}$. The transition probabilities are denoted by a_{ij} among hidden states and the emission probabilities as b_{jk} (emission of a visible state).

$$a_{ij} = P(W_j(t+1)|W_i(t))$$

$$b_{jk} = P(v_k(t)|W_j(t))$$

Three state Ergodic Hidden Markov model

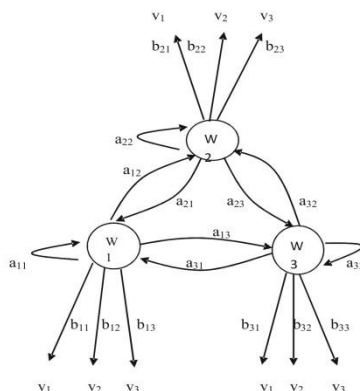


Fig. 1: Three hidden units in hidden Markov model with their transition and emission probabilities

Computation of hidden Markov Model

$$P(V^T) = \sum P(V^T | W_r^T) P(w_r^T)$$

Evaluation

Hidden Markov model (HMM) is effective in uncovering underlying statistical patterns in disease progression by considering HMM states as disease stages⁵. The probability that a particular sequence of hidden states W^T that led to those observations should be determined.

The probability that the model produces a sequence V^T of visible states is

$$\alpha_i(t) = \begin{cases} 0 & t = 0 \text{ and } i \neq \text{initial state} \\ 1 & t = 0 \text{ and } i = \text{initial state} \\ \sum_j \alpha_j(t-1) a_{ij} b_{jk} v(t) & \text{otherwise,} \end{cases}$$

The probability of a particular visible sequence is merely the product of the corresponding (hidden) transition probabilities (a_{ij}) and the (visible) output probabilities (b_{jk}) of each step. Forward algorithm could be used for doing evaluation.

Decoding

The decoding problem could be used to find the most probable sequence of hidden states provided a sequence of visible states V^T . For this every possible path should be enumerated and calculate the probability of the visible sequence observed. Simple decoding algorithm could be used. Viterbi algorithm is

most commonly used for decoding^{4,10}. Algorithm works by doing iteration with all the possible sequence of stages. These algorithms can be used to decode an unobserved hidden semi-Markov process and it is the first time that the complexity is achieved to be the same as in the Viterbi for Hidden Markov models⁴.

Most likely sequence of Hidden states

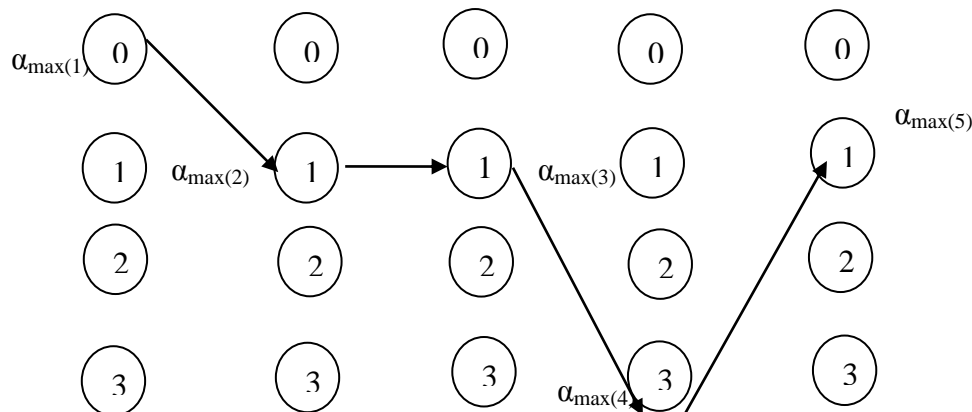


Fig. 2: The decoding algorithm finds at each step, the state that has the highest probability of having come from the previous step and generated the observed visible state v_k . The full path is the sequence of such states

RESULTS AND DISCUSSION

Transition probability matrix

$$\begin{bmatrix} 0.22 & 0.57 \\ 0.5 & 0.24 \end{bmatrix}$$

Emission probability matrix

$$\begin{bmatrix} 0.9 & 0.9 & 0.85 \\ 0.88 & 0.82 & 0.76 \end{bmatrix}$$

Stages of mastitis represented as two-state left-to-right hidden Markov model

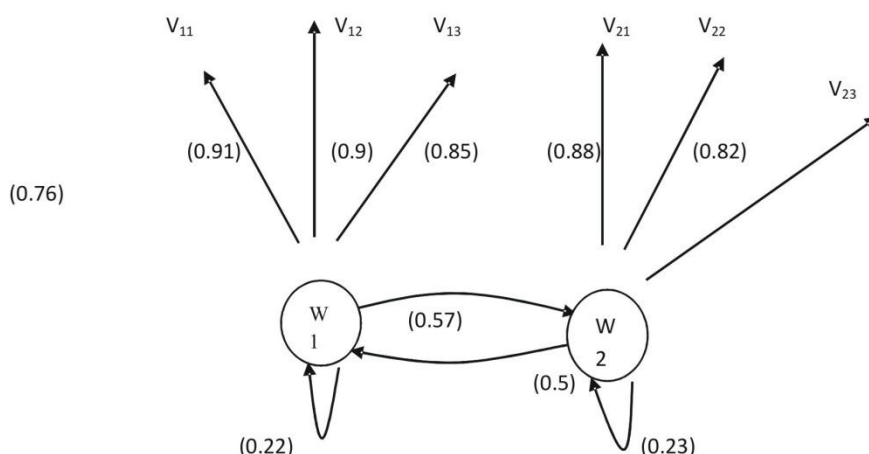


Fig. 3: W-Hidden stages of mastitis. V-Symptoms produced by each stage (visual observations). Transition and emission probabilities were given in the parenthesis

Table 1: Stages of mastitis with the observed symptoms

Labels for Hidden Observation	Observed symptoms	Probability of occurrence noted (in percentage)
Stage of inflammatory response (W1)	Reduced milk production(V ₁₁)	91.60
	Udder inflammation(V ₁₂)	90
	Mild clinical signs(V ₁₃)	85
Stage of bacterial flare up and production of toxins (W2)	Abnormal milk(V ₂₁)	88.24
	Abnormal udder(V ₂₂)	82.30
	Major clinical signs(V ₂₃)	76.47

Table 2: Transition stages of mastitis along with its probability of occurrence

Labels for Hidden Observation	Possible transitions	Probability of occurrence noted (in percentage)
Stage of inflammatory response (W1)	W1 to W1	21.66
	W1 to W2	56.66
Stage of bacterial flare up and production of toxins (W2)	W2 to W1	50
	W2 to W2	23.5

Table 3: End probabilities obtained from decoding using viterbi algorithm

Total probability	Viterbi probability	Viterbi path
0.0878	0.0878	W1 + W1
0.2384	0.2384	W1 + W2
0.1213	0.1049	W1 + W2+ W1
0.0970	0.0524	W1 + W2 + W2
0.0653	0.0230	W1 +W2 + W2 + W1
0.0828	0.0532	W1 + W2 + W1 + W2
0.0486	0.0234	W1 + W2 + W1 + W2 + W1
0.0513	0.0117	W1 + W2 + W1 + W2 + W2
*0.1000	0.0234	W1 + W2 + W1 + W2 + W1

*overall iteration result of the viterbi algorithm showing the most probable sequence of hidden stage.

The sequence of progression of the stages of mastitis obtained as viterbi path from the overall cases of clinical mastitis studied was $W1 \rightarrow W2 \rightarrow W1 \rightarrow W2 \rightarrow W1$, where W1 is the stage of inflammatory response and W2 is the stage of bacterial flare up and production of toxins.

Clinical mastitis constituted 46.8 percent of the total mastitis cases present. It was considered as the start probability of the study. The most probable symptoms shown by the mastitis affected animals in each stage were identified. These paved the way to determine the most likely sequence of hidden states of mastitis. An inflammatory response (W1) was initiated when bacteria entered the mammary gland and this was body's second line of defence. These bacteria were multiplied and produced toxins, enzymes etc in the second stage (W2). These stages happened as a series. The immune status of the body along with the treatment given reduced the severity of the disease and the symptoms were reduced and observed as seen in the first stage. In this way, overall progression of disease in the herd could be evaluated and remedy measures for prevention and control can be suggested. As mastitis is the most prevalent production disease in dairy herds worldwide it is important to control the disease as much as possible.

CONCLUSION

The present study revealed the most likely sequence of hidden stages of clinical mastitis in dairy cattle. Clinical mastitis constituted 46.8 percent of the total mastitis cases present. Each stage of the disease were separately analysed and the probability of occurrence of each symptoms were studied. The sequence of progression of the stages of mastitis obtained as viterbi path from the overall cases of clinical mastitis revealed that the disease was initiated with the inflammatory response as body's second line of defence. It was succeeded by the stage of bacterial flare up and production of toxins. The progression of the disease could be represented in a sequence of stages of mastitis represented as W1 and

W2, where W1 is the stage of inflammatory response and W2 is the stage of bacterial flare up and production of toxins. Applications of Hidden Markov model in disease progression aspects were exploited.

Acknowledgements

The authors are thankful to Dean and to Head of Department of Clinics of Madras Veterinary College for providing the necessary facilities to conduct the research work.

REFERENCES

1. Sharif, A., and Muhammad, G., Mastitis control in dairy animals. *Pakistan Vet. J*, **29 (3)**: 145-148 (2009).
2. Jones, G. M., and Bailey, T. L., Understanding the basics of mastitis. (2009).
3. Rabiner, L., and Juang, B., An introduction to hidden Markov models. *IEEE ASSP magazine*, **3(1)**: 4-16 (1986).
4. Pertsinidou, C. E., and Limnios, N., Viterbi algorithms for Hidden semi-Markov Models with application to DNA Analysis. *RAIRO-Operations Research*, **49(3)**: 511-526 (2015).
5. Sukkar, R., Katz, E., Zhang, Y., Raunig, D., and Wyman, B.T., Disease progression modeling using hidden Markov models. *In Engineering in Medicine and Biology Society (EMBC), Annual International Conference of the IEEE* (pp. 2845-2848). (2012).
6. Bartolomeo, N., Trerotoli, P., and Serio, G., Progression of liver cirrhosis to HCC: an application of hidden Markov model. *BMC medical research methodology*, **11(1)**: 38 (2011).
7. Robertson, C., Sawford, K., Gunawardana, W.S.N., Nelson, T.A., and Nathoo, F., A Hidden Markov Model for Analysis of Frontline Veterinary Data for Emerging Zoonotic Disease Surveillance. *PLoS ONE*, **6(9)**: (2011).
8. Jackson, C. H., Sharples, L. D., Thompson, S. G., Duffy, S. W., and Couto, E., Multistate Markov models for

- disease progression with classification error. *Journal of the Royal Statistical Society: Series D (The Statistician)*, **52(2)**: 193-209 (2003).
9. Nguyen, V. T., Nguyen, T. H., Nguyen, N. S., Bui, V.D., and Miyamoto, A., A study about mastitis infection characteristics in dairy cow of Bavi, Hanoi, Vietnam. *Asian J Pharm Clin Res*, **8(3)**: 165-168 (2015).
10. Lou, H. L., Implementing the Viterbi algorithm. *IEEE signal processing magazine*, **12(5)**: 42-52 (1995).