



Progression of Subclinical Mastitis in Cows Using Hidden Markov Model

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ABSTRACT

Mastitis is the most important and expensive disease of dairy industry. A clear cut idea about the progression of sub 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 subclinical 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. Subclinical mastitis constituted 27.56 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 subclinical mastitis studied was $W1 \rightarrow W2 \rightarrow W1 \rightarrow W2 \rightarrow W1W2$, where $W1$ is the stage of bacterial entry and its flare up and $W2$ is the stage of leukocyte infiltration. Out of the total probability 0.1285, the viterbi probability obtained was 0.0182 for the viterbi path.

Key words: Sub clinical mastitis in cows, Hidden Markov model, Probability.

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INTRODUCTION

Mastitis is the most important and expensive disease of dairy industry [1]. 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. Inflammation can be caused by many types of injury including infectious agents and their toxins, physical trauma or chemical irritants. In the dairy cow, mastitis is nearly always caused by microorganisms; usually bacteria, that invade the udder, multiply in the milk-producing tissues, and produce toxins that are the immediate cause of injury [2].

One of the important form of bovine mastitis is the sub clinical mastitis. Subclinical infections are those in which no visible changes occur in the appearance of the milk or the udder, but milk production decreases, bacteria are present in the secretion, and composition is altered [2]. Sub-clinical mastitis limits milk production and represents an important barrier to profitable livestock economics worldwide [3]. A clear cut idea about the progression of sub 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 [4]. Hidden Markov models are important tools in estimation and analysis of biological sequences and many other systems [5]. It consists of a set of interconnected states where the connections are governed by a set of transitional probabilities. What sets a Hidden Markov model apart from a Markov model or a Markov chain is the fact that in a Markov chain the states are observable while for hidden Markov Models, the states are statistical having associated probability distributions called the observation probability density functions. Hidden Markov model can be used to

assess the disease progression as compared to the clinical stages of diseases [6]. It can also be used to determine the transition probabilities between two states [7-9].

The present study was conducted to identify the most probable sequence of stages of sub clinical form of mastitis which are hidden inside the body using the transition probabilities between the stages and also using the probabilities of possible symptoms exhibited in each stage of the disease (emission probabilities).

MATERIALS AND METHODS

The present study was conducted at the large animal clinic of Madras Veterinary College. Out of 127 cases studied, 35 were diagnosed as sub clinical mastitis. Each and every case were observed thoroughly for stages of disease and possible symptoms within 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 and the affected milk’s reaction to California mastitis Test (CMT). In the first hidden stage (W1), along with suspected milk’s trace reaction to California Mastitis Test (CMT), the symptoms shown included reduced milk production and reduced milk quality. As time advanced, the disease was progressed to the second hidden stage (W2) were milk showed positive reaction to CMT and the symptoms shown included drastic reduction in milk production along with mild clinical signs (reduced feed and water intake, increment in body temperature, signs of diarrhoea 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 subclinical mastitis, it’s 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 is 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

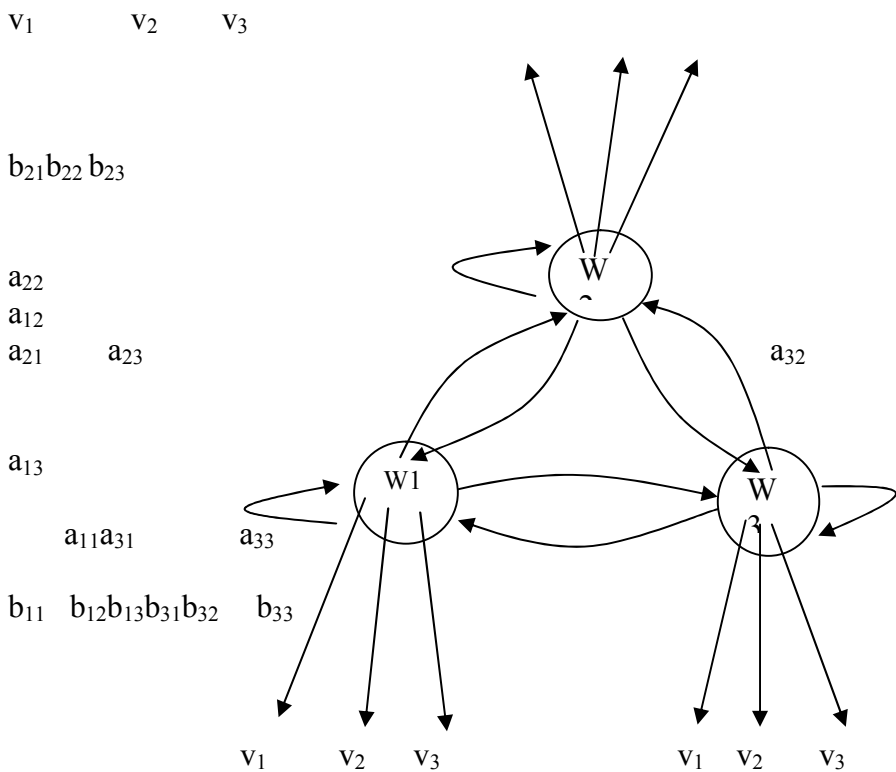


Figure 1: Three hidden units in hidden Markov model with their transition and emission probabilities

Computation of hidden Markov Model

Evaluation

Hidden Markov model (HMM) is effective in uncovering underlying statistical patterns in disease progression by considering HMM states as disease stages [6]. 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 $P(V^T) = \sum P(V^T | W_r^T) P(w_r^T)$

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.

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

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^{5,10}. 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

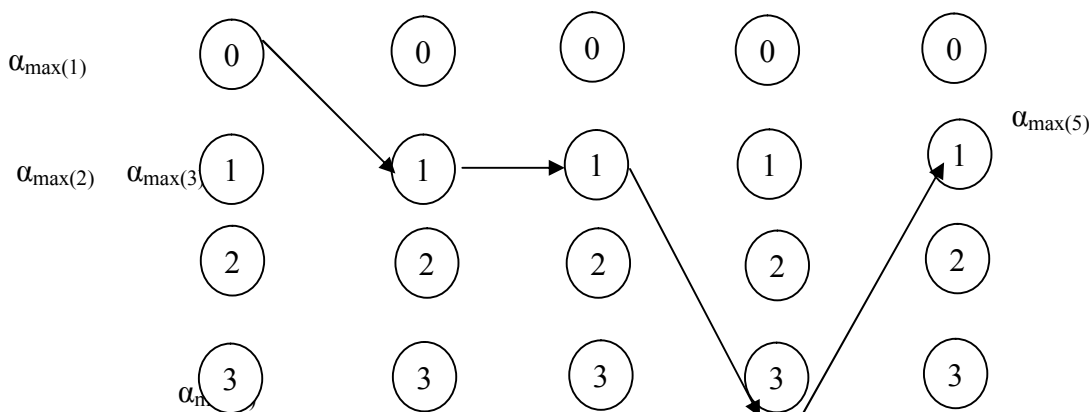


Figure 2: The decoding algorithm finds at each step, the state that has the highest probability of having come from the previous step and generated the observed visible state v_k . The full path is the sequence of such states.

RESULTS AND DISCUSSION

Transition probability matrix Emission probability matrix

| | | | | |
|-------------|-------------|-------------|-------------|-------------|
| 0.23 | 0.74 | 0.94 | 0.86 | 0.74 |
| 0.44 | 0.36 | 1.00 | 0.83 | 0.71 |

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

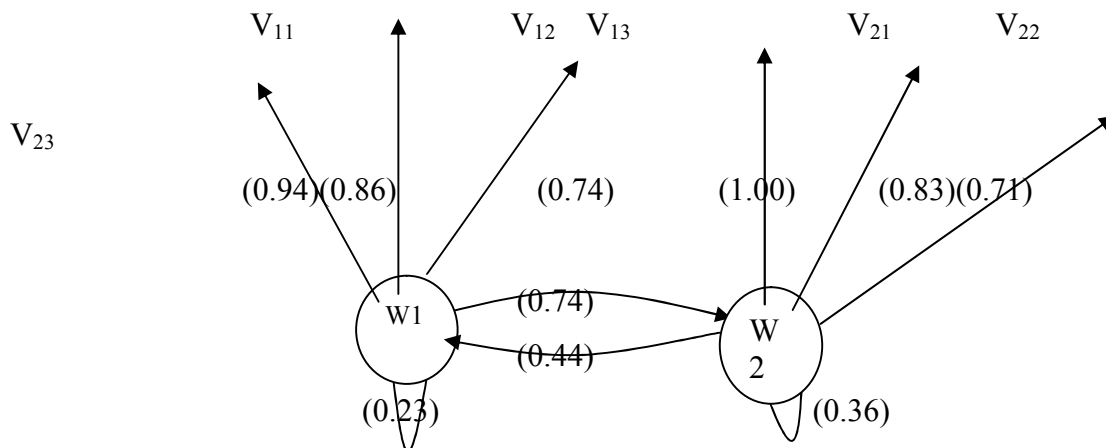


Figure:3W-Hidden stages of mastitis. V-Symptoms produced by each stage (visual observations). Transition and emission probabilities were given in the parenthesis.

Table 1: Stages of mastitis with the observed symptoms

| Labels for Hidden Observation | Observed parameters | Probability of occurrence noted (in percentage) |
|--|---|---|
| Stage of Bacterial entry and its flare up (W1) | Trace reaction to CMT (V ₁₁) | 94.28 |
| | Reduced milk production (V ₁₂) | 85.71 |
| | Reduced milk quality (V ₁₃) | 74.28 |
| Stage of leukocyte infiltration(W2) | Positive reaction to CMT (V ₂₁) | 100 |
| | Drastic reduction in milk production (V ₂₂) | 83.33 |
| | Mild clinical signs(V ₂₃) | 70.83 |

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 Bacterial entry and its flare up (W1) | W1 to W1 | 22.86 |
| | W1 to W2 | 74.28 |
| Stage of leukocyte infiltration (W2) | W2 to W1 | 44 |
| | W2 to W2 | 36 |

Table 3: End probabilities obtained from decoding using viterbi algorithm

| Total probability | Viterbi probability | Viterbi path |
|-------------------|---------------------|---------------------------------|
| 0.0605 | 0.0605 | W1 + W1 |
| 0.1948 | 0.1948 | W1 + W2 |
| 0.0988 | 0.0857 | W1 + W2+ W1 |
| 0.1122 | 0.0701 | W1 + W2 + W2 |
| 0.0707 | 0.0309 | W1 +W2 + W2 + W1 |
| 0.1091 | 0.0596 | W1 + W2 + W1 + W2 |
| 0.0633 | 0.0262 | W1 + W2 + W1 + W2 + W1 |
| 0.0885 | 0.0215 | W1 + W2 + W2 + W1 + W2 |
| 0.0526 | 0.0094 | W1 +W2 + W2 + W1 +W2+ W1 |
| 0.0759 | 0.0182 | W1 +W2 + W1 + W2 +W1+ W2 |
| *0.1285 | 0.0182 | W1 +W2 + W1 + W2 +W1+ W2 |

*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 mastitis studied was W1 → W2 → W1 → W2 → W1W2, where W1 is the stage of bacterial entry and its flare up and W2 is the stage of leukocyte infiltration.

Subclinical mastitis constituted 27.56 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. The bacteria entered the mammary gland and the body mechanism failed to eliminate the causative organisms and it got flared up. An inflammatory response was initiated when bacteria entered the mammary gland and this was body's second line of defence. The stage of bacterial entry and its flare up (W1) is followed by stage of leukocyte infiltration (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 time advanced. In this way, overall progression of disease in the herd could be evaluated through the viterbi path and remedy measures for prevention and control could be suggested. As subclinical form of 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 sub clinical mastitis in dairy cattle. Subclinical mastitis constituted 27.56 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 sub clinical mastitis revealed that the disease was initiated with the bacterial entry and its continuous flare up. It was succeeded by the stage of leukocyte infiltration. 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 bacterial entry and its flare up and W2 is the stage of leukocyte infiltration. Applications of Hidden Markov model in disease progression aspects were exploited.

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