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A dynamic Bayesian network for diagnosing ventilator-associated pneumonia in ICU patients ☆

Theodore Charitos [a], Linda C. van der Gaag [a,*], Stefan Visscher [b], Karin A.M. Schurink [b], Peter J.F. Lucas [c]

[a] Department of Information and Computing Sciences, Utrecht University, The Netherlands
[b] Department of Internal Medicine and Infectious Diseases, University Medical Center Utrecht, The Netherlands
[c] Institute for Computing and Information Sciences, Radboud University, Nijmegen, The Netherlands

Abstract

Diagnosing ventilator-associated pneumonia in mechanically ventilated patients in intensive care units is seen as a clinical challenge. The difficulty in diagnosing ventilator-associated pneumonia stems from the lack of a simple yet accurate diagnostic test. To assist clinicians in diagnosing and treating patients with pneumonia, a decision-theoretic network had been designed with the help of domain experts. A major limitation of this network is that it does not represent pneumonia as a dynamic process that evolves over time. In this paper, we construct a dynamic Bayesian network that explicitly captures the development of the disease over time. We discuss how probability elicitation from domain experts served to quantify the dynamics involved and how the nature of the patient data helps reduce the computational burden of inference. We evaluate the diagnostic performance of our dynamic model for a number of real patients and report promising results.

Keywords: Ventilator-associated pneumonia; Diagnosis; Dynamic Bayesian networks; Stochastic processes; Inference

1. Introduction

Many patients admitted to an intensive care unit (ICU) need respiratory support by a mechanical ventilator; in addition, many of these patients are affected by severe disease which may result in depression of their immune system. Both conditions promote the development of ventilator-associated pneumonia (VAP) in these patients. Because of the wide-spread dissemination of multiresistant bacteria at the ICU, effective and fast treatment of VAP is seen as an issue of major significance. The difficulty of the diagnosis of VAP is in the lack of a gold standard; VAP is therefore diagnosed by taking a number of clinical features into account (Schurink, 2003). To support ICU clinicians in diagnosing and treating VAP, a probabilistic and decision-theoretic network, representing the uncertainties and preferences involved, was constructed by Lucas, de Bruijn, Schurink, and Hoepelman (2000). The network was developed with the help of two infectious disease experts, who assessed both its qualitative structure and its numerical part. The goal of the network was to prescribe an optimal antimicrobial therapy for treating patients with VAP.

Two stochastic processes play a prominent role in the domain of pneumonia: the colonisation of the laryngotracheobronchial tree by pathogens and the onset and development of pneumonia. Although both processes evolve dynamically, these dynamics were not explicitly modelled by means of temporal transitions in the network of Lucas et al. Instead, the dynamics of the processes were modelled implicitly by additional interactions between the duration of hospital stay and the duration of mechanical ventilation

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* Corresponding author. Tel.: +31 30 253 4113; fax: +31 30 251 3791.
E-mail address: linda@cs.uu.nl (L.C. van der Gaag).

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of a patient with the colonisation by pathogens. The main motivation for this simplification was the large amount of data needed to specify the probability distribution underlying the stochastic processes and the increase in computational requirements. The network of Lucas et al. thus constitutes a static simplification of the domain. The static network was used for every patient for each day on the ICU separately, without taking into account the patient's characteristics from earlier days. Consequently, its diagnostic performance was suboptimal and even confusing for patients without VAP. As the development of VAP is a dynamic process, we feel that time needs to be modelled in a more explicit way to improve the diagnosis.

In this paper, we alleviate the problems associated with the static representation of the domain by modelling VAP as a dynamic process. More specifically, we develop a dynamic Bayesian network (DBN) that explicitly captures the temporal relationships between the variables (Murphy, 2002); our focus thereby is initially on the diagnostic part of the network. We use the method of van der Gaag, Renooij, Witteman, Aleman, and Taal (1999, 2002) for the elicitation, from domain experts, of the probability distribution of the underlying stochastic process. This method transcribes probabilities and uses a scale with both numerical and verbal anchors that allows experts to assess many probabilities in little time. Moreover, we discuss how the computational burden of inference with our model can be eased by exploiting the nature of the observations involved and the properties of the transitional relationships of the model with just a small loss in accuracy.

We evaluated our dynamic network on a group of patients, drawn from the files of the ICU of the University Medical Center Utrecht in the Netherlands. Our results indicate that the dynamic model is capable of distinguishing between patients with VAP and without VAP. By exploiting all available past information of a patient, it in fact yields at least as good or even better predictions than the static model. Specifically for patients without VAP, we noticed that the use of previous information leads to lower estimates for VAP than the ones obtained from the static network.

The paper is organised as follows. In Section 2, we briefly describe the static decision-theoretic network that had been developed before for the management of VAP. In Section 3, we discuss the construction of a dynamic network for VAP and present computational methods for performing efficient inference with the model. In Section 4 we present the results of an experimental evaluation of our network. Conclusions and directions for further research are given in Section 5.

2. A static network for VAP

Ventilator-associated pneumonia is a low-prevalence disease occurring in mechanically ventilated patients in critical care and involves infection of the lower respiratory tract (Bonten, 2004). In contrast to infections of more frequently involved organs (such as the urinary tract), for which mortality is low, ranging from 1% to 4%, the mortality rate for VAP ranges from 24% to 50% and can reach 76% for some high-risk pathogens. VAP therefore has been associated with increased morbidity, attributable mortality and increased health care costs. Important causes related to the development of VAP include the duration of hospitalisation and of mechanical ventilation of the patient; important symptoms that indicate the presence of VAP include an increased body temperature, an abnormal amount of coloured sputum, signs on the chest X-ray, an abnormal ratio between the amount of oxygen in the arterial blood and the fractional inspired oxygen concentration, that is, pO_2/FiO_2, and an abnormal number of leukocytes.

As diagnosing VAP and deciding upon treatment can be a hard task for clinicians, a decision-theoretic network was constructed as part of a decision-support system to assist clinicians in their task in the ICU (Lucas et al., 2000, 2003). Fig. 1 (left) illustrates the global structure of the network, which we call the static VAP network, or sVAP network for short. Dashed arcs denote temporal probabilistic relationships; solid arcs represent stochastic dependency without a special temporal meaning. Boxes in the figure indicate collections of stochastic variables; the collection of therapy variables is shown by thick lines; ellipses indi-

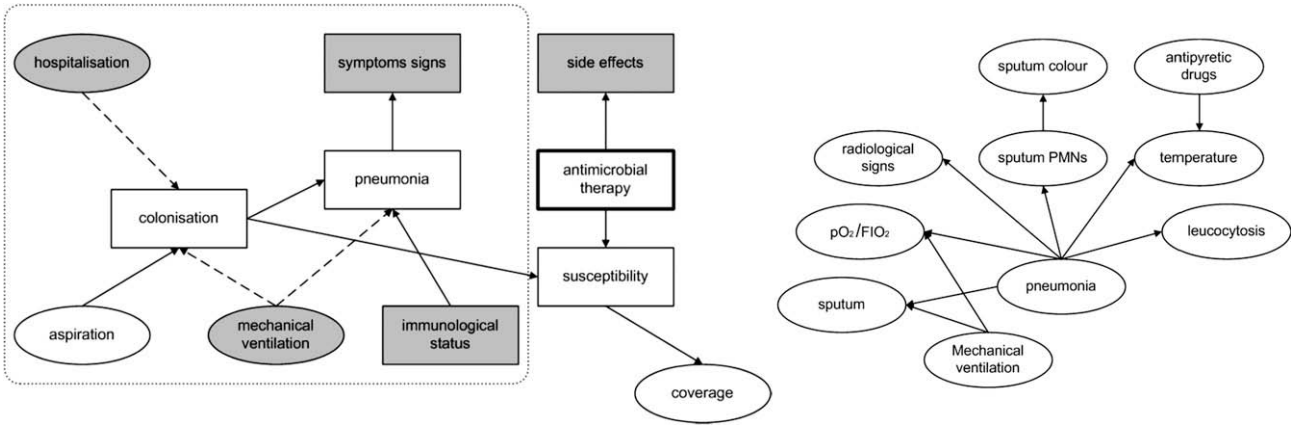

Fig. 1. (left) Global structure of the sVAP network. The dotted box indicates the network's diagnostic part. (right) Symptoms and signs of pneumonia.