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Exploiting causal functional relationships in Bayesian network modelling for personalised healthcare

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ABSTRACT

Bridging the gap between the theory of Bayesian networks and solving an actual problem is still a big challenge and this is in particular true for medical problems, where such a gap is clearly evident. We argue that Bayesian networks offer appropriate technology for the successful modelling of medical problems, including the personalisation of healthcare. Personalisation is an important aspect of remote disease management systems. It involves the forecasting of progression of a disease based on the interpretation of patient data by a disease model. A natural foundation for disease models is physiological knowledge, as such knowledge facilitates building clinically understandable models. This paper proposes ways to represent such knowledge as part of engineering principles employed in building clinically practical probabilistic models. The methodology has been used to construct a temporal Bayesian network model for preeclampsia – a pregnancy-related disorder. The model is the first of its kind and an integral part of a mobile home-monitoring system intended for use in daily pregnancy care. We conducted an evaluation study with actual patient data to obtain insight into the model's performance and suitability. The results obtained are encouraging and show the potential of exploiting physiological knowledge for personalised decision-support systems.

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1. Introduction

As making decisions in medicine is fraught with difficulty because of the significant uncertainties involved, researchers have tried to represent that uncertainty explicitly. In particular Bayesian networks appear to offer a natural and intuitive formal foundation for uncertainty models that are part of clinical decision-support systems [20]. However, despite the progress made in the research, there are still very few systems based on Bayesian networks that are actually used in daily clinical practice. A possible explanation for this is that medical doctors are reluctant to adopt new technology unless its advantages are crystal clear. One new area that meets such requirement is the *personalisation* of healthcare. Personalisation is understood as involving the forecasting of the progression of a disease based on the interpretation of patient data by a probabilistic model. Without intelligent systems that are able to fuse information coming from different sources, with much of this information being uncertain, personalisation will not be possible. Bayesian networks in particular appear to offer the right capabilities to represent and manipulate this uncertain knowledge for personalisation. The predictions obtained in this way inform the patient and doctor on whether or not the disease is under control. Forecasting concerns reasoning about the state of a system that evolves over time, and therefore temporal data and knowledge are of interest here.

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It is often the case with a severe disorder in medicine that the number of patients with this disorder is limited, whereas the whole group of patients under surveillance for the disorder is much larger. Under such conditions it is hard to develop a probabilistic model based on data alone. Exploiting biological knowledge about the way the relevant organ systems function, i.e. *physiological* knowledge, if available, may then guide the modelling process.

In contrast to earlier work exploiting such knowledge, in our research we are aiming at the development of a generic Bayesian network methodology for building probabilistic clinical models to predict disease progression. As the resulting models must be suitable for daily clinical use, employing sound engineering principles is of crucial importance. A novel contribution is that the introduced principles support finding the right balance between incorporating simple, easy-to-collect measurements and risk factors, on the one hand, and physiological knowledge to structure these measurements, on the other hand. The resulting models are also suitable for personalisation of disease management.

Thus, modelling organ functioning at a certain level of abstraction is taken as the principle that integrates the interactions between disease outcome, observables, such as signs, symptoms and lab tests, actions or treatments, and risk factors. This choice has been motivated by the way clinical knowledge is presented in medical textbooks and in clinical education. The method was used in developing a Bayesian network for predicting the development of a hypertension-related pregnancy syndrome, called *preeclampsia*, with personalisation of the associated treatment as a goal. The model built is the first of its kind and an integral part of a smart home-monitoring system for pregnancy care that provides decision support to the patient and the caregiver with the aim to offer timely management of the life-threatening complication of preeclampsia.

The paper is organised as follows. In Section 2 we review related research in the area of modelling within the medical domain with an emphasis on the development of patient-specific models. Basic Bayesian network theory and the proposed methodology for modelling disease progression – the main scientific contribution of this research – are described in Section 3. In the same section we also discuss issues concerning evaluation of the methodology and propose a number of criteria for that. The application of the methodology to the development of a mobile system for pregnancy care is described in Section 4. What we have achieved in this research is brought in perspective in Section 5.

2. Related work

Early work mostly focused on using Bayesian network as aids for the diagnosis of disease. Well-known examples include the MUNIN [2] and Pathfinder [12,11] models. Special diagnostic reasoning methods for test selection in medicine have also been developed [1,45]. Various approaches for simplifying the network structure and the specification of probability distributions when building diagnostic models are discussed in [25]. In [31] the authors propose techniques for automatic construction of dynamic influence diagrams from a set of causal rules in a knowledge base, with an application to diagnosis of acute abdominal pain.

Later more emphasis was placed on treatment selection and making a prognosis, e.g. [8,17–19]. Markov decision processes and dynamic influence diagrams are examples of temporal probabilistic models that have been used in [35] for selection of treatment strategies. In [36] a noisy-threshold model has been proposed including 11 attributes measured at admission and playing the role of causes for predicting carcinoid heart disease; the model has been learned and trained on a small dataset of 54 patients. The use of dynamic Bayesian networks as the basis for the construction of prognostic models has been explored in [34] with the particular application to prognosis of low-grade carcinoid tumours; evaluation results regarding three patients were also presented. Another Bayesian-network-based decision-support system, called TREAT, aiming at predicting bacteremia in patients is described in [28]. A randomised clinical trial showed improvement in the percentage of appropriate empirical antibiotic treatments when using the system [29]. A study that dealt with the problem of predicting the susceptibility to future antibiotic treatments using a Bayesian network is presented in [47], which also discusses the potential of including the method in a larger decision-support system. To facilitate explaining the optimal policies of decision-making problems solved by means of influence diagrams, a method based on parsimonious lists of alternative decisions is proposed in [5]; the practical usefulness of the method is investigated with respect to the treatment of non-Hodgkin lymphoma of the stomach. A construction method of a prognostic Bayesian network model using clinical data and supervised learning models, such as decision trees, is proposed in [42]. An application to the domain of cardiac surgery, where hospital mortality is used as outcome variable, illustrates the use of the methodology. Anther recent paper that studied the use of probability theory in the context of rule-based computer-assisted diagnosis is presented [6].

There is some other, earlier, work on exploiting physiological knowledge in building Bayesian networks [26,4,32,16]. Other investigations have focused on the development of patient-specific models based not only on probabilistic graphical models [33], but also on causal hierarchical structures representing physiological knowledge [27], fuzzy cognitive maps for modelling cause-effect relationships in the medical domain [21] and probabilistic soft logic specifying medical domain knowledge [3].

Despite the large body of research, only a very small number of applications have successfully made the step towards clinical deployment. With the emerging trend towards provision of personalised healthcare, there is a clear need for the development of novel approaches to the construction of patient-specific models that can cope with the often limited availability of clinical data, capture physiological causal relationships in a systematic manner and allow easy deployment. The methodology presented next is a step in this direction.

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