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Hybrid time Bayesian networks ☆

Manxia Liu [a,1], Arjen Hommersom [c,a,2], Maarten van der Heijden [a,2], Peter J.F. Lucas [a,b]

[a] Radboud University, ICIS, Nijmegen, The Netherlands
[b] Leiden University, LIACS, Leiden, The Netherlands
[c] Open University, MST, Heerlen, The Netherlands

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ABSTRACT

Capturing heterogeneous dynamic systems in a probabilistic model is a challenging problem. A single time granularity, such as employed by dynamic Bayesian networks, provides insufficient flexibility to capture the dynamics of many real-world processes. The alternative is to assume that time is continuous, giving rise to continuous time Bayesian networks. Here the problem is that the level of temporal detail is too precise to match available probabilistic knowledge. In this paper, we present a novel class of models, called hybrid time Bayesian networks, which combine discrete-time and continuous-time Bayesian networks. The new formalism allows us to more naturally model dynamic systems with regular and irregularly changing variables. We also present a mechanism to construct discrete-time versions of hybrid models and an EM-based algorithm to learn the parameters of the resulting BNs. Its usefulness is illustrated by means of a real-world medical problem.

1. Introduction

Many real-world systems exhibit complex and rich dynamic behavior. As a consequence, capturing these dynamics is an integral part of developing models of physical-world systems. Time granularity is an important parameter in characterizing dynamics as it determines the level of temporal detail in the model. In cases where one time granularity is coarser than another, dealing with multiple time granularities becomes significantly important, e.g., in the context of mining frequent patterns and temporal relationships in data streams and databases [2].

Bayesian networks (BNs) have been very successful in modeling complex situations involving uncertainty [3]. Dynamic Bayesian networks (DBNs) are part of the Bayesian network framework, supporting the modeling of dynamic probabilistic systems [4]. DBNs extend standard Bayesian networks by assuming that changes in a process can be captured by a sequence of states at discrete time points. Usually the assumption is made that the distribution of variables at a particular time point is conditional only on the state of the system at the previous time point. A problem occurs if temporal processes of a system are best described using different rates of change, e.g., one temporal part of the process changes much faster than another. In that case, the whole system has to be represented using the finest time granularity, which is undesirable from a

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E-mail addresses: m.liu@cs.ru.nl (M. Liu), arjenh@cs.ru.nl (A. Hommersom), m.vanderheijden@cs.ru.nl (M. van der Heijden), peterl@cs.ru.nl (P.J.F. Lucas).

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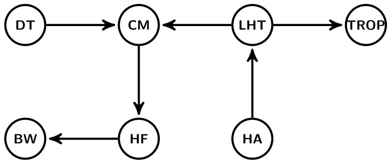

Fig. 1. Causal model for heart failure: CM = Contractility Myocardium, DT = Digitalis, LHT = Loss Heart Tissues, HA = Heart Attack, TROP = Troponin, HF = Heart Failure, BW = Body Weight.

modeling and learning perspective. In particular, if a variable is observed irregularly, much data on discrete-time points will be missing and conditional probabilities will be hard to estimate.

As an alternative to DBNs, temporal processes can be modeled as continuous time Bayesian networks (CTBNs), where time acts as a continuous parameter [5]. In these models, the time granularity is infinitely small by modeling transition rates rather than conditional probabilities. Thus, multiple time granularities, i.e., slow and fast transition rates, can easily be captured. A limitation from a modeling perspective is that all probabilistic knowledge, for example derived from expert knowledge, has to be mapped to transition rates which are hard to interpret. Moreover, it is assumed that the transition rates, governing the time until a transition occurs, are exponentially distributed, which may not always be appropriate.

In this paper, we propose a new formalism, which we call *hybrid time Bayesian networks* (HTBNs), inspired by discrete-time and continuous-time Bayesian networks. We develop the theoretical properties of HTBNs and show their practical use by means of a medical example. HTBNs facilitate modeling the dynamics of both irregularly-timed random variables and random variables whose evolution is naturally described by discrete time. As a result, the new formalism increases the modeling and analysis capabilities for dynamic systems.

In the next section we introduce the running, clinical example for the rest of this paper, followed by preliminaries on DBNs and CTBNs to fix the notation. Then, in Section 4, we define HTBNs with their associated factorization, followed by a construction that allows transforming an HTBN into an equivalent BN. Subsequently we return to our running example and demonstrate how the equivalent BN can be used to obtain a meaningful clinical simulation. The paper is concluded by a discussion.

2. Motivating example

To illustrate the usefulness of the proposed theory, we consider the medical problem of heart failure and, in particular, one possible cause of heart failure: heart attack (myocardial infarction). This usually occurs as the result of coronary artery disease giving rise to reduced blood supply to the heart muscle (myocardium). One consequence is that part of the heart muscle will die, which is revealed later in a blood sample analysis in the lab by an increased level of particular heart muscle proteins, in particular troponin. Loss of heart muscle will inevitably have an impact on the contractility of the myocardium, and thus heart function will be negatively affected. This is known as *heart failure*. In particular, the heart fails with respect to its function as a pump. This will enforce an increase in the amount of extracellular fluid (the patient is flooded with water), which can be measured quite simply by means of the body weight. With regard to treatment, digitalis is considered as one of the drugs to improve contractility. This causal knowledge is formalized as a directed graph in Fig. 1.

Heart attacks can occur repeatedly in patients, although after some interval of time, and this may negatively affect heart function. After administration of digitalis it will take some time before the drug has a diminishing effect on heart failure. Thus, the course of heart failure will likely depend on various factors, and how they interact. Of particular importance here is the dynamic over time of the probability distributions.

In modeling processes such as heart failure, it is essential to notice the existence of different time granularities. There are *discrete*, *regular* variables which are observed regularly such as a routine checkup for body weight and a regular intake of a drug. On the other hand, some variables are observed *irregularly*, such as the indicator troponin which is elevated after about half an hour after damage to the heart muscle is obtained; however its measurement is repeated with time intervals that increase after the patient's condition has been stabilized. Clearly, it is not possible to obtain a satisfactory representation of the clinical evolution of heart failure using only discrete time, regular or irregular, or continuous time. In the remainder of this paper we propose a method to deal with these heterogeneous time aspects.

3. Preliminaries

We start by introducing Bayesian networks, dynamic Bayesian networks and continuous time Bayesian networks. In the following, upper-case letters, e.g. X, Y, or upper-case strings, e.g. HA, denote random variables. We denote the values of a variable by lower-case letters, e.g. x, or by T or F, short for *true* and *false*. Note that all variables considered here have a finite domain of values. Continuous-time variables are variables that have a finite domain of values over infinite trajectories. For discrete-time variables time changes regularly, evenly, whereas continuous-time variables are irregularly spaced over time. In what follows we will make use of a successor function s, which is defined on a countable, linearly ordered set of numbers Z in which every element $z_i \in Z$ with index i is mapped to element $s(z_i) = z_{i+1} \in Z$ (with the potentially greater