GeNIeRate: An Interactive Generator of Diagnostic Bayesian Network Models

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Abstract

We propose a methodology to simplify and speed up the design of very large Bayesian network models. The models produced using our methodology are based on two simplifying assumptions: (1) the structure of the model has three layers of variables and (2) the interaction among the variables can be modeled by canonical models such as the Noisy-MAX gate. The methodology is implemented in an application named GeNIeRate, which aims at supporting construction of diagnostic Bayesian network models consisting of hundreds or even thousands of variables. Preliminary qualitative evaluation of GeNIeRate shows great promise. We conducted an experiment comparing our approach to traditional techniques for building Bayesian network models by rebuilding a Bayesian network model for diagnosis of liver disorders, HEPAR-II. We found that the performance of the model created with GeNIeRate is comparable to the performance of the original HEPAR-II.

1 Introduction

Bayesian Networks (BNs) [Pearl, 1988] are acyclic directed graphs with each node representing a variable and each arc representing a direct probabilistic influence between two variables. Although exact and approximate inference in Bayesian networks are both worst-case NP-hard [Cooper, 1990; Dagum and Luby, 1997], they still perform well, in our experience, for practical diagnostic models consisting of several hundred or even thousand nodes.

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A BN consists of a qualitative and a quantitative part. The qualitative part is an acyclic directed graph reflecting typically the causal structure of the domain, the quantitative part represents the joint probability distribution over its variables. Every variable is equipped with a conditional probability table (CPT) representing the probabilities of each state given the state of the parent variable. If a variable does not have any parent variables in the graph, the CPT represents the prior probability distribution over the variable. A BN is able to calculate the posterior probability distribution over an uncertain variable given some evidence obtained from related variables. This property and the intuitive way BNs model complex relationships among uncertain variables makes it a very suitable technique for building diagnostic models. Diagnosis is quite likely the most successful practical application of BNs.

While the existing diagnostic BN models perform very well, the technique is still not widely used and accepted. One of the main reasons for this is that building a BN model is a laborious and time consuming task. During the model building process, both the qualitative and quantitative parts of the BN have to be created. This can be done in three different ways: (1) both structure and parameters can be learned from data without human interaction, (2) a domain expert can be consulted to design the structure and the parameters, or (3) learning from data and consulting a domain expert can be combined. In order to learn successful diagnostic BN models from data one would need a very large data set, which is rarely available for diagnostic models. It is never available for new devices or devices that are designed for high reliability (such as, for example, airplanes). So building a diagnostic BN model will most of the time come down to an interaction of a knowledge engineer and a domain expert. They will consult technical manuals, test procedures, and repair databases to define the variables in that domain, determine the interactions among them, and to elicit the parameters. To give an idea of the time used

to design a diagnostic BN model: the construction of the HEPAR-II model [Oniśko *et al.*, 2001] used to diagnose liver disorders took approximately 300 hours of which roughly 50 hours were spent with domain experts. The final version of the model consisted of 73 variables. Its numerical parameters were learned from a data set of patient cases.

One of the first large diagnostic systems that used Bayesian networks was the QMR-DT system [Shwe *et al.*, 1991; Middleton *et al.*, 1991]. This system was a probabilistic reformulation of the Quick Medical Reference (QMR), a rule-based system based on the INTERNIST-1 knowledge base developed at the University of Pittsburgh [Miller *et al.*, 1982]. The QMR-DT system contained approximately 5,000 variables. The authors made several simplifying assumptions to deal with the complexity of constructing this network. The system was a BN with only two layers of nodes representing two different types of variables: *diseases* and *findings*. The structure was such that the *disease* variables influenced the *finding* variables. While this structure was simple, its performance was close to that of the original QMR. But since the the independence assumptions were made explicitly, the inconsistencies of QMR-DT could easily be explained.

Inspired by the QMR-DT system, we propose in this paper a methodology to build diagnostic BN models in an intuitive and fast way for users who are not necessarily experts in Bayesian networks. Using our methodology, a domain expert will be able to build a model without any interaction with a knowledge engineer. Skaanning [2000] addresses the same problem applied in an application called *BATS Author*. The BATS Author is domain specific, hides the causality of the models from the user, and is build around the single fault assumption. Our methodology can be applied in any domain, shows the causal structure of the graph, and supports multiple faults. We believe that showing the causality of the model helps the model builder in understanding the model building process better.

To make the model building easy for the user, our methodology is based on two simplifying assumptions. The first assumption is in the qualitative part of the model. The structure is such that it can only consist of three layers of variables. The top layer represents *context* variables, the middle layer represents the *fault* variables and the bottom layer represents *evidence*, which are observable effects of *faults*. Relations are only allowed in a top-down way: from *contexts* to *faults* and from *faults* to *evidences*. The second simplification is in the quantitative part. All the variables are modeled using canonical probabilistic interaction models currently the Noisy-MAX gate. The Noisy-MAX gate is a generalization of the Noisy-OR gate for multi-valued variables. The goal of using the Noisy-MAX gate is to reduce the size of the CPTs of the variables. It implies that the number of parameters that have to be elicited by the user decreases from exponential to linear in the number of parents of that variable. Research shows that many interactions in practical models can be approximated by the Noisy-MAX gates [Zagorecki and Druzdzel, 2004b]. With these simplifications we sacrifice some theoretical modeling power and precision. However, we found, after having tested this in practice, that the resulting models are not significantly less accurate while being much easier to build.

The remainder of this paper is structured as follows. Section 2 gives an introduction to Bayesian networks. Section 3 discusses our proposed three layer structure of diagnostic BN models. Section 4 explains the Noisy-MAX gate. Section 5 gives a complete description of GeNIeRate our implementation of the methodology. Finally, Section 6 discusses an experiment comparing GeNIeRate to traditional model building techniques.

2 Bayesian Networks

Bayesian networks are acyclic directed graphs in which nodes represent random variables and arcs represent direct probabilistic dependencies among them. A Bayesian network encodes the joint probability distribution over a set of variables $\{X_1, \ldots, X_n\}$, where n is finite, and decomposes it into a product of conditional probability distributions over each variable given its parents in the graph. In case of nodes with no parents, prior probability is used. The joint probability distribution over $\{X_1, \ldots, X_n\}$ can be obtained by taking the product of all of these prior and conditional probability distributions:

$$\Pr(x_1, \ldots, x_n) = \prod_{i=1}^{n} \Pr(x_i | Pa(x_i)) \; . \qquad (1)$$

Figure 1 shows a highly simplified example Bayesian network modeling causes of a car engine failing to start. The variables in this model are: *Age* of the car (A), dead *Battery* (B), dirty *Connectors* (C), *Engine* does not start (E) and *Warning* lights on your dashboard (W). For the sake of simplicity, we assumed that each of these variables is binary. For example, W has two outcomes, denoted w and $\overline{w}$, representing "Warning lights are present" and "Warning lights are absent," respectively.

A directed arc between B and E denotes the fact that whether or not the battery is dead will impact the likelihood of the engine failing to start. Similarly, an arc

from A to B denotes that the age of the car influences the likelihood of having a dead battery.

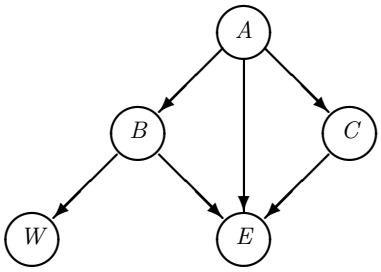

Figure 1: An example Bayesian network for engine problem

Lack of directed arcs is also a way of expressing knowledge, notably assertions of (conditional) independence. For instance, lack of a directed arc between A and W encodes the knowledge that the age of the car does not influence the chance of the car having warning lights at the dashboard, only indirectly through the variable dead battery B. These causal assertions can be translated into statements of conditional independence: W is independent of A given B. In mathematical notation,

$$\Pr(W|B) = \Pr(W|B, A) \ .$$

Similarly, the absence of arc $B \rightarrow C$ means that whether or not the battery is dead will not influence the chance of having dirty connectors.

These independence properties imply that:

$$\Pr(a, b, c, w, e) = \\ \Pr(a)\ \Pr(b|a)\ \Pr(c|a)\ \Pr(w|b)\ \Pr(e|a, b, c) \ ,$$

i.e., that the joint probability distribution over the graph nodes can be factored into the product of the conditional probabilities of each node given its parents in the graph. Please note that this expression is just an instance of Equation 1.

The assignment of values to observed variables is usually called *evidence*. The most important type of reasoning in a probabilistic system based on Bayesian networks is known as *belief updating* or *evidence propagation*, which amounts to computing the probability distribution over the variables of interest given the evidence. This evidence propagation makes Bayesian networks very suitable for diagnosis. For example, in the model of Figure 1, the variables of interest for diagnosis could be B and C and the focus of computation could be the posterior probability distribution over B and C given the observed values of A, W, and E, i.e., $\Pr(b, c|a, w, e)$, often approximated in practice as marginal probability distributions, $\Pr(b|a, w, e)$ and $\Pr(c|a, w, e)$. Bayesian network software can be applied to calculate these posterior probabilities. Today's software is capable of very fast belief updating in models consisting of hundreds or even thousands of variables. After the belief updating, the software can make a decision or support the user in making a decision what actions to perform given that probability.

3 The BN3M model

We believe that there are three fundamental types of variables in diagnostic models. The first type (1) are variables representing the failures of the device or a specific part of the device. We will call these failure variables *Faults*. The second type (2) are variables which have an observable effect if the device is in some faulty state. Sometimes you cannot observe the effect of the given *fault* clearly, then you can perform a test which will give you information about the state of the device. These observation or test variables will be called *Evidence* variables. The last type of variables (3) are variables which indicate context properties of the device that may influence the risk of a *fault*. We will call these variables *Context* variables. Example *context* variables are the age of the device or the history of failures of the device.

In the QMR-DT model, mentioned in the introduction, the authors distinguish two types of binary variables: *diseases* and *findings*. These variables are graphically structured in two layers in which the *disease* variables influence the *findings*. This structure is based on strong independence assumptions. The first of these is *marginal independence of the diseases*, which amounts to no arcs among the disease variables. The second is *conditional independence of the findings*, which amounts to no arcs among *finding* variables. Figure 2 shows an example of the graphical structure used in the QMR-DT model.

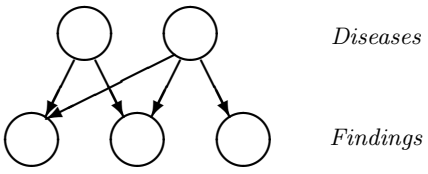

Figure 2: The two-layer QMR-DT model

The structure of the QMR-DT model was simple, yet the performance of the model was close to that of the original rule-based QMR system. This motivated us to design an extension of their structure to connect our three types of variables in a diagnostic BN model. The authors of the QMR-DT system already mention the

fact that assuming their two layer structure is not always very accurate. They state that it would be more accurate to model some of their *findings* representing, for example, historical findings as parent variables of the *diseases*. We decided to cover this inaccuracy in our model in making our *context* variables the parents of the *fault variables*. We also decided to support multi-valued variables instead of binary variables used in QMR-DT. This means that our structure becomes a three layer structure with the *context* variables on top, *fault* variables in the middle and the *evidence* variables at the bottom. We call this structure: 3-layer Bayesian network using Noisy-MAX gates (BN3M). An example of this structure is showed in Figure 3. We will discuss the Noisy-MAX gate in Section 4.

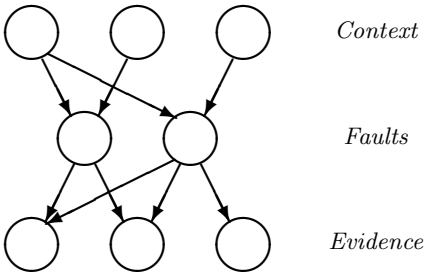

Figure 3: The BN3M model

As mentioned in the introduction, this structure sacrifices some modeling power and precision. For example, the arc between variables A and E of the example given in Figure 1 cannot be created in our methodology. We tested whether this theoretical imprecision has a big impact on the practical performance of models. We found that a model created by our methodology performs similarly to its original version, which is not a BN3M model. A large model that is theoretically very precise may turn out to be inferior in practice because elicitation of a huge number of parameters from a human expert may decrease their quality.

4 Canonical interaction models

In order to gain speed in designing the quantitative part of the model, the interaction among the variables in our structure is approximated by canonical interaction models that require fewer parameters. One type of canonical interaction, widely used in Bayesian networks, is known as the Noisy-OR gate. This gate was first introduced outside the BN domain by [Good, 1961]. Later it was applied in the context of BNs [Pearl, 1986], and it became very popular among BN model builders because it reduces the growth of a CPT of a variable within a BN from exponential to linear in the number of parents. An extension of the Noisy-OR gate for multi-valued variables is the Noisy-MAX gate [Henrion, 1989; Díez, 1993]. For the sake of simplicity, we will discuss the Noisy-OR gate in depth and give a short description of the extended Noisy-MAX gate later in this section.

4.1 Noisy-OR

The Noisy-OR gate models a non-deterministic interaction among n binary parent cause variables X and a binary effect variable Y. Every variable has two states: a distinguished state, which represents that the variable is in its normal working state. Commonly this is *absent* or *false* and a non-distinguished state: *truth* or *present*. The effect variable Y works as a deterministic OR gate. This means that if all the parent variables are *absent*, the child variable is also *absent*. However if a parent variable X_i is *present* and all other parent variables are *absent*, it has a probability p_i of causing the effect y. These probabilities p_i address the noisy property of the gate and have to be elicited by the model builder or can be learned from data. The probabilities are fairly easy to understand since they can be represented by questions like: *What is the probability that the effect y will occur, given that only one cause X_i is present and all other causes are absent?* In other words,

$$p_i = Pr(y|\overline{x}_1, \overline{x}_2, \ldots, x_i, \ldots, \overline{x}_{n-1}, \overline{x}_n) \; . \qquad (2)$$

The probability of an effect y occuring given a subset X of causes which are *present* is now formally given by:

$$p(y|X) = 1 - \prod_{i=1}^{n} (1 - p_i) \; . \qquad (3)$$

This formula is sufficient to derive the complete CPT of Y conditional on its predecessors $X_1, X_2, \ldots, X_n$.

Henrion [1989] proposed a direct extension of the Noisy-OR gate which models that an effect y can also occur if all the causes are *absent* and called it: *leaky Noisy-OR* gate. This can be modeled by introducing an additional parameter p_0, which is called the *leak probability*, formally given by:

$$p_0 = Pr(y|\overline{x}_1, \overline{x}_2, \ldots, \overline{x}_n) \; . \qquad (4)$$

The leak probability represents the phenomenon that an effect occurs spontaneously, i.e., in absence of any of the causes that are modeled explicitly.

In the leaky Noisy-OR gate, p_i $(i \neq 0)$ no longer represents the probability that X_i causes y given that all other parent variables are absent, but rather the probability that Y is present when X_i is present and every other explicit parent causes (all the X_j's such that $j \neq i$) are absent.

Let p'_i be the probability that Y will be true if X_i is present and every other parent of Y including unmodeled causes (the leak) are absent:

$$1 - p'_i = \frac{1 - p_i}{1 - p_0} \ . \tag{5}$$

From here we have

$$p_i = p'_i + (1 - p'_i)\, p_0 \ . \tag{6}$$

It follows that the probability of Y given a subset of parent variables X is given in the leaky Noisy-OR gate by the following formula:

$$p(y|X) = (1 - (1 - p_0)) \prod_{i=1}^{n} \frac{1 - p_i}{1 - p_0} \ . \tag{7}$$

An alternative way of eliciting the parameters of a leaky Noisy-OR gate is given in [Díez, 1993]. It amounts essentially to asking the expert for the parameters p'_i as defined by Equation 5. The difference between the two proposals has to do with the leak variable. While Henrion's parameters p_i assume that the expert's answer includes a combined influence of the parent cause in question and the leak, Díez's parameters p'_i explicitly refer to the mechanism between the parent cause in question and the effect with the leak absent. Conversion between the two parameters is straightforward using Equation 6. If the Noisy-OR parameters have to be elicited by an domain expert, Díez's definition is more convenient, since the question to be answered is more intuitive for the expert: *What is the probability that the effect y will occur when you know that all modeled and unmodeled causes X are absent?* It has been found both preferred by experts [Oniśko *et al.*, 2001] and results in higher elicitation accuracy [Zagorecki and Druzdzel, 2004a]. Henrion's definition will be more convenient if the parameters are learned from data.

4.2 Noisy-MAX

The Noisy-OR gate can be generalized if it is used for multi-valued variables. These variables are allowed to have more than two states. However, these variables still contain a distinguished state. The difference is that the CPT of the effect variable Y is the deterministic MAX function instead of the deterministic OR function. Therefore it is called Noisy-MAX gate or, if the leak probability is included, leaky Noisy-MAX gate.

In our proposed methodology we set the leak probability distribution of an effect variable $p_0(Y)$ by default to 0 for the non-distinguished states $y_i, \ldots, y_{n-1}$ and 1 for the distinguished state $\overline{y}$:

$$p_0(Y) = \begin{cases} 1 & \text{if } Y = \overline{y} \\ 0 & \text{otherwise} \end{cases} \ . \tag{8}$$

In this way, the interaction among variables is by default Noisy-MAX, it becomes leaky Noisy-MAX if an user defines a specific leak probability distribution for the effect variable.

To give an example of the reduction of the number of parameters that have to be elicited by the user we define the number of states of a parent variable X_i as n_{X_i} and the number of states of an effect variable y as n_y. The total number of parameters N that have to be elicited by the model builder using leaky Noisy-MAX becomes:

$$N = \sum_{i=1}^{n} (n_{X_i} - 1)(n_y - 1) + (n_y - 1) \ , \tag{9}$$

compared to the exponential number of parameters using CPT:

$$N = (n_y - 1) \prod_{i=1}^{n} (n_{X_i} - 1) \ . \tag{10}$$

If $n_i = 3$ and $n = 10$, we have 2,048 parameters with CPT compared to 42 parameters using Noisy-MAX. Every additional parent of y increases this number by multiplying the current number of parameters by 2 in CPT compared to adding 4 in Noisy-MAX.

Using Noisy-OR and Noisy-MAX gates for some of the conditional distributions in the HEPAR-II model [Oniśko *et al.*, 2001] not only reduced the number of parameters that had to be elicited from 3,714 to 1,488 but also improved the diagnostic performance of the model.

5 GeNIeRate

We embedded the ideas presented in Sections 3 and 4 in an interactive environment for generation of diagnostic BN models that we call GeNIeRate. GeNIeRate is a member of the family of software developed at the Decision Systems Laboratory (DSL) of the University of Pittsburgh. This software is developed for the purpose of probabilistic modeling with special extensions for diagnostic inference, such as rank ordering, tests, and case management. The main part of this family is SMILE (Structural Modeling Reasoning, and Learning Engine) which is a library of C++ classes implementing graphical probabilistic and decision-theoretic models. In order to use SMILE in other programming languages some wrappers are developed: jSMILE for Java, SMILE.NET for a Microsoft .NET environment and pocketSMILE for the

Pocket PC. Next to the libraries, there are some applications with a Graphical User Interface (GUI) using these libraries. GeNIe is the main application, it is a development environment for building graphical decision models. Other applications are ImaGeNIe which is a general purpose model building interface and GeNIeRate which is discussed in this paper. GeNIeRate is developed in Java therefore it uses jSMILE as its modeling library. All the software can be downloaded at: `http://www.sis.pitt.edu/~genie`.

The main goal of GeNIeRate is to support a user in building the simplified diagnostic BN3M models in a fast and intuitive way. In order to keep the model building process simple, GeNIeRate contains three different screens, representing three steps for building a BN3M model: (1) add General information, (2) add the Variables, and (3) add the Relations and the probabilities (G-V-R). We will discuss these three steps in this section and support our description with different screen-shots of GeNIeRate.

5.1 General information

In the first tab, the user can define general model information: name, identifier, and description of the model. Since not all designed models will contain *context* variables, these variables can be switched on or off. Furthermore, feedback can be enabled which amounts to verbal feedback given by GeNIeRate for each action of the user. If the user is not a BN expert, this feedback will help with natural language dialogs to get familiar with this technique and give the user some insight about the causality of the graphical structure of his model. Figure 4 shows a part of this first tabbed screen.

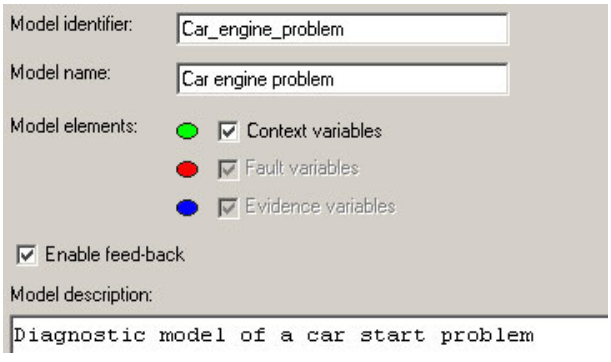

Figure 4: Part of the model info panel

5.2 Adding variables

In the second tab, the variables of the model can be added, edited or deleted. For each type of variable (*context*, *fault*, and *evidence*) there is a tree structure representing the variables of that type added to the model. Figure 5 shows a part of this screen containing different tree structures.

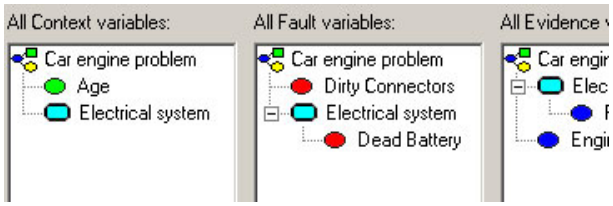

Figure 5: Part of the model variables panel

GeNIeRate uses the concept of a *system* to divide large diagnostic models into manageable parts. A system is typically a module of a device that, while interconnected with other modules, can be thought of in separation from the rest of the device. Typically devices, whether natural or artificial, are composed hierarchically and have clearly identifiable modules, for example electrical system, power train, break, or steering system in an automobile. Systems are the largest entities through which the user can interact with a model, i.e., the users can view a system's variables after selecting that system and add variables to it or remove variables from it. This supports working on a specific part of the model, ignoring the rest of the model and, since humans can only focus on a small number of things at a time, limiting the amount of information presented to the user.

Furthermore, documentation can be added to the variables and the states of the variables. This documentation can be a treatment for each non-distinguished state of a *fault* variable or a question for each *context* or *evidence* variable. The documented questions and treatments can later be used when the model is applied in diagnostic software. Answers to these questions can be used as evidence for the belief updating (Section 2) to calculate the most probable *fault(s)*. After this calculation, the documented treatment of that fault can be presented to help the user make a decision how to fix his problem.

5.3 Adding relations

The last screen allows for creation of relations among the variables. When, for example, a *fault* variable is selected, *context* variables can be added as parents or *evidence* variables as children of that *fault*. After relations are created, the graph at the right side of the screen shows the relevant part of the graph (see Figure 6).

A *system* can be selected to show only the relations

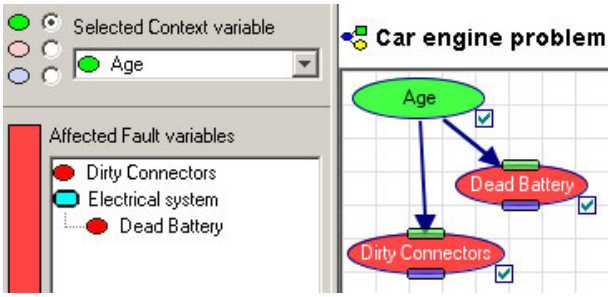

Figure 6: Part of the model relations panel

of the selected variable with the variables within that system. Navigating the graph can be done by clicking on the top or the bottom of a node to show the parents or children of that node respectively.

All the parameters can be defined by double-clicking on a node or an arc in the graph. If a node has parents, the leak-probability distribution for that variable can be defined, otherwise the prior probability distribution can be defined. If an arc in the graph is selected the Noisy-MAX parameters for the relation represented by that arc can be defined.

After the diagnostic BN model has been created, it can be saved and used for applying diagnosis. This can be done after loading the network into GeNIe, which contains a tool for diagnosis. The network could also be loaded in user applications using (j)SMILE or other BN building software (Figure 7).

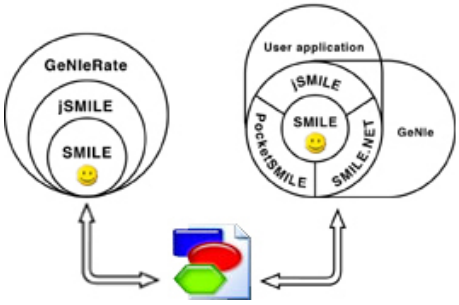

Figure 7: GeNIeRate architecture and interaction with other DSL software

6 Empirical Evaluation

A qualitative evaluation of our methodology and GeNIeRate was performed by Mr. M. D. Campbell, a professional consultant with 5 years of practical experience in building diagnostic BN models. GeNIeRate was received warmly and Mr. Campbell estimated that this methodology will be of great help especially in building large diagnostic models. He mentioned that a domain expert usually spends 90% of the time in analyzing and understanding his diagnostic problem as a probabilistic model. However, his estimate was that our approach will reduce the model building time by 20-30% for an inexperienced Bayesian network model builder.

We also performed an empirical study evaluating the performance of our methodology by rebuilding the HEPAR-II model mentioned in the introduction. We rebuilt the structure of the model from scratch using GeNIeRate, which took approximately 8 hours. We will refer to this new structure as HEPAR-II-BN3M. Because the original 300 hours spent on building HEPAR-II included learning, interaction with experts and literature study, comparing it to the 8 hours that took us to develop HEPAR-II-BN3M is not fair. However, we are primarily interested in the performance of the new model compared to the original. The CPTs of the HEPAR-II model were learned from a data set of patient cases. This data set was created in 1990 and thoroughly maintained since then. It contains approximately 700 patient cases and it is still growing. In order to use the same learning algorithm to get a fair comparison, we had to transform the variables of HEPAR-II-BN3M from noisy-MAX to normal CPTs. After learning we were interested whether, after setting some evidence in the model, the most probable diagnosis (fault) given by the model is indeed the correct diagnosis. Furthermore we were also interested whether the set of k most probable diagnoses contains the correct diagnosis for small values of k (we chose a "window" of k=1, 2, 3, and 4). Results were 64% (compared to 59% for the original HEPAR-II model), 75% (72%), 82% (79%), and 87% (85%) for k=1, 2, 3, and 4 respectively. Figure 8 shows the results graphically.

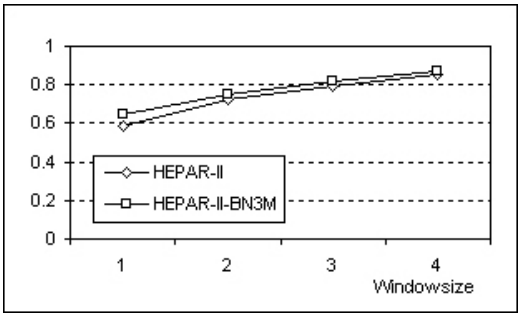

Figure 8: Diagnostic accuracy as a function of different window sizes

We did not expect that the new HEPAR-II-BN3M model would show a better diagnostic performance. The most plausible explanation of this surprising results is that the original HEPAR-II models con-

tained erroneous conditional independence assumptions. However, we believe that GeNIeRate should take some credit for facilitating building a better quality model. We expect that results like this will not always be observed in other models.

7 Concluding remarks

This paper has presented a methodology for building large diagnostic Bayesian networks. An implementation of the methodology was received well by a professional consultant in building diagnostic Bayesian networks. His estimate is that using this methodology for building large diagnostic BN models will reduce the model building time with approximately 20-30%.

An empirical study comparing our methodology to traditional model building techniques shows that the diagnostic performance of the model created by traditional model building techniques is close to the performance of the same model created by our methodology. It seems that a model that can be build significantly faster does not necessarily suffer in terms of its performance.

Acknowledgments

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