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GRADUATE SCHOOL

A Tool for Constructing and Visualizing Tree Augmented Bayesian Networks for Survey Data

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Abstract

Bayesian learning is an effective method to learn the structure of data in variety of applications. In this thesis, we use the Construct-TAN algorithm [Friedman et al, 1997], an algorithm that learns a Bayesian network, to create a tool that learns the structure of epidemiological datasets and visualizes their structure effectively. To test our methods, we identify interesting relations between cardiovascular disease risk factors and mental health status variables, from the BTH 2000 dataset. In comparing the accuracy of our system with a naive Bayes learner, we find that the accuracy of our system is very high. Our interface allows a user to visually inspect and manipulate the resulting Bayesian network to better understand interactions in the dataset. We believe that our work brings new insights to relationships between cardiovascular diseases and mental health status problems. It may also provide a platform for developing more visually intensive tools that can improve visualization of survey data.

Chapter 1: Introduction

To better understand the overall health of the United States, there has been a significant growth in the collection of data with regards to people's health in the form of surveys. Several government organizations as well as non-government organizations conduct surveys and collect information regarding various aspects of a person's lifestyle related to health. This data can prove very useful in giving information about various diseases. In this thesis we use Bayesian learning techniques on an epidemiological survey dataset, to identify useful relationships between the variables that form the dataset and, in particular, examine relationships between cardiovascular disease risk factors and mental health status variables.

Heart disease and stroke, one of the main components of cardiovascular disease, are the first and third leading causes of death for both men and women in the United States, accounting for almost 40% of all deaths [NCCDPH, 2004]. Another staggering statistic is that 64 million Americans (almost one-fourth of the population) live with cardiovascular disease and over 6 million hospitalizations each year are due to cardiovascular disease [NCCDPH, 2004]. According to the Surgeon General's 1999 report [SGR, 1999] almost 54 million Americans suffer from some kind of mental illness. Depression and anxiety disorders — the two most common mental illnesses — each affect 19 million American adults annually [NMHA, 2001]. Also, this is important as depression greatly increases the risk of developing heart disease. People with depression are four times more likely to have a heart attack than those with no history of depression [NMHA, 2001]. In this thesis we present a Bayesian toolbox which we have used to explore relationships between variables pertaining to cardiovascular health and mental health in a regional population.

1.1 Machine Learning and Bayesian Theory

Machine Learning involves the development of methods that will allow machines to imitate the process of human learning. According to Dietterich [1999],

> *Machine learning is said to occur in a program that can modify some aspect of itself, often referred to as its state, so that on a subsequent execution with the same input, a different output is produced.*

Unsupervised learning, supervised learning, neural networks, decision trees and Bayesian learning are a few of the sub-fields of Machine Learning.

Bayesian theory is an important part of machine learning. This area of machine learning has become highly researched and Bayesian theory has been used in fields such as diagnosis [Rodrigues et al, 2000], expert systems [Stephen and Steven, 1986] and planning learning [Stavrulaki et al, 2003]. In this thesis we use Bayes nets to find probabilistic models to explain relationships in health survey data. There are several reasons why we focus on Bayesian methods. Bayesian methods provide various structure learning algorithms. They use probability theory as a foundation and can handle uncertainty. Finally, Bayesian networks provide a way to visualize results. We want to find the relationship amongst various variables in our data, and Bayesian methods provide a very good way of doing that.

1.2 Thesis Statement

In this thesis we use Bayesian learning techniques to find useful structures in a survey dataset. We built a toolbox of methods which lets the user create a Bayesian network, learn its structure and allow him/her to understand the relationship between different variables which are a part of the network. One of the main aims of this thesis is to show how the tool can be used to find relationships between cardiovascular disease variables and the mental health status variables in our dataset.

1.3 Thesis Outline

This thesis is organized as follows. Chapter 2 reviews the basics of Bayesian networks and how to learn from them. Chapter 3 introduces the Bridge to Health Survey dataset which is used to find relationships between cardiovascular disease risk factors and mental health status variables and also other features in the dataset. Chapter 4 outlines how Bayesian networks can be used for classification and structure learning. In the same section, we discuss the Construct-TAN algorithm [Friedman et al, 1997], which is the basis of the design of our toolbox. In Chapter 5 we describe the toolbox with regards to its representation and functionality. Chapter 6 describes our experiments to verify the effectiveness of our tool. Chapter 7 discusses related work in development of Bayesian networks. Chapter 8 discusses the future work that could follow the current research. Chapter 9 concludes the thesis.

Chapter 2: Background

In this chapter, we present the background for this work. We will first provide a brief introduction to Bayes theorem and some preliminary definitions. We then talk about the Bayesian optimal classification and the naive Bayes classifier. Finally we talk about Bayesian networks in detail.

2.1 Bayes Theorem

Bayes theorem is a mathematical formula used for calculating conditional probabilities. Bayes theorem provides a method to calculate the probability of a hypothesis *h* based on its prior probability, the probabilities of observing various data given the hypothesis, and the observed data itself. Bayes theorem is

$$P(h/D)=\frac{P(D/h)P(h)}{P(D)}$$

where

P(h) = the *prior probability* of hypothesis *h*, which is the probability of hypothesis *h* without knowing the training data *D*

P(D) = the prior probability of the training data *D*, which is the probability of the training data *D* depending on the data distribution of all the instances in the data

P(D/h) = the probability of observing data *D* given that hypothesis *h* holds, also called the *likelihood* of data *D* given *h*

P(h/D) = the probability that hypothsis *h* holds given data *D*, also called the *posterior probability* of *h* given *D*

The posterior probability *P(h/D)* reflects the influence of the training data *D* on the hypothesis *h*, in contrast to the prior probability *P(h)*, which is independent of *D*. Bayes theorem is the basis of Bayesian learning methods because it provides a way to calculate the posterior probability of a classification from the prior probability, *P(D)* and *P(D/h)*. Thus we observe that *P(h/D)* increases with *P(h)* and with *P(D/h)* and decreases as *P(D)* increases, because the more probable it is that *D* will be observed independent of *h*, the less evidence *D* provides in support of *h*.

Consider an example to illustrate Bayes theorem. Assume that a doctor knows that a particular kind of throat cancer causes the patient to have a severe sore throat 40% of the time. A doctor also knows that the prior probability that the patient has throat cancer is 0.001%, and the prior probability that any patient has severe sore throat is 5%. Let ***t*** be a proposition that the patient has throat cancer and ***s*** be a proposition that the patient has sore throat, then

$$P(s / t) = 40/100 = 0.4$$
$$P(t) = 1/10{,}000 = 0.00001$$
$$P(s) = 1/20 = 0.05$$

$$\begin{aligned} P(t / s) &= P(s / t)\, P(t) \;/\; P(s) \\ &= 0.4 * 0.0001 / 0.05 \\ &= 0.00008 \end{aligned}$$

This means that a doctor can expect that 1 in 12500 patients with a sore throat to have throat cancer. Even though throat cancer is strongly associated with sore throat, the probability of throat cancer in the patient remains small. The reason behind this is that the prior probability of having a sore throat is much higher than that of having throat cancer.

The *maximum a posteriori* (MAP) hypothesis h_{MAP} is any hypothesis $h \in H$ that is most probable from a given set of hypotheses *H* given the training data *D*. This maximally probable hypothesis can be determined using Bayes theorem by calculating the posterior probability of each candidate hypothesis as

$$h_{MAP} = argmax_{h \in H} P(h/D)$$

$$h_{MAP} = argmax_{h \in H} \frac{P(D/h)P(h)}{P(D)} \qquad (2.1)$$

$$h_{MAP} = argmax_{h \in H} P(D/h)P(h) \qquad (2.2)$$

Note that *P(D)* is dropped in Equation (2.2) as the prior*, P(D)* will be same for all the hypotheses and can be ignored.

The *maximum likelihood* (ML) hypothesis h_{ML} is any hypothesis $h \in H$ that maximizes the likelihood of the training data *D*. The assumption here is that every hypothesis in *H* is equally probable, that is, $P(h_i) = P(h_j)$ *for all* $h_i, h_j \in H$*.*

$$h_{ML} = argmax_{h \in H} P(D/h)P(h) \qquad (2.3)$$

$$h_{ML} \simeq argmax\, P(D/h) \qquad (2.4)$$

The MAP hypothesis h_{MAP} and the ML hypothesis h_{ML} are the same when the prior probability *P(h)* is distributed uniformly over all hypotheses in *H*. If the prior probability of *h* is uniformly distributed, the MAP hypothesis is the one with lower error rate on instance(s) of the evaluation data. The ML hypothesis has a lower error rate if one assumes the future instance(s) of the evaluation data follows the same distribution as the training data *D.*

2.2 The Bayes Optimal Classifier

Consider this problem. There are four possible hypotheses h_1, h_2, h_3, h_4 with probabilities given a dataset *D* as,

$P(h_1 / D)$ = 0.2	$P(h_2 / D)$ = 0.4
$P(h_3 / D)$ = 0.3	$P(h_4 / D)$ = 0.1

Given a new instance x,

$h_1(x) = neg$	$h_2(x) = pos$
$h_3(x) = neg$	$h_4(x) = neg$

We can then ask the question, what is the most probable classification of *x*?

Obviously $h_{MAP} = h_2$ which will classify the instance *x* as positive. However the probability of *x* being classified negative taking into account all of the hypotheses is 0.6, which is higher than the most probable classification probability 0.4, which classifies the instance *x* to be positive. This indicates that we could improve the overall classification by calculating the most probable classification of the new instance by combining the probabilities of all hypotheses and weighting them by their posterior probabilites.

$$P(v_j/D) = \sum_{h \in H} P(v_j/h) P(h/D)$$

$P(v_j/D)$ is the probability that correct classification of the new instance is v_j where v_j is some class from a set of class values V [Mitchell, 1997].

The Bayes optimal classification calculates the class probability in this type of case as

$$argmax_{v_j \in V} P(v_j/D)$$
$$argmax_{v_j \in V} \sum_{h_i \in H} P(v_j/h_i) P(h_i/D)$$

Revisiting the same problem,

$P(h_1/ D) = 0.2$	$P(neg / h_1) = 1$	$P(pos / h_1) = 0$
$P(h_2/ D) = 0.4$	$P(neg / h_2) = 0$	$P(pos / h_2) = 1$
$P(h_3/ D) = 0.3$	$P(neg / h_3) = 1$	$P(pos / h_3) = 0$
$P(h_4/ D) = 0.1$	$P(neg / h_4) = 1$	$P(pos / h_4) = 0$

therefore

$$\sum_{h_i \in H} P(\text{pos}/h_i) P(h_i/D) = 0.4$$

$$\sum_{h_i \in H} P(\text{neg}/h_i) P(h_i/D) = 0.6$$

and so

$$argmax_{v_j \in V} \sum_{h_i \in H} P(v_j/h_i) P(h_i/D) = \text{neg}$$

where V = { pos, neg}.

However Bayes optimal classification is generally impossible and in restricted cases computationally expensive because we cannot generate all possible classifiers in effiecient manner.

2.3 The Naive Bayes Classifier

Classification is an important task in data analysis and pattern recognition. The naive Bayes classifier [Domingos and Pazzani, 1997] and its variants are among the most successful known algorithms for learning to classify text documents [Kim et al, 2003], filtering email [Sahami et al, 1998], galaxy classification [Bazell and Aha, 2001] and even emotion recognition [Sebe et al, 2002]. Despite its simplicity and robust nature, its performance is comparable to that of state-of-the art classifiers like neural networks and decision tree learning. It has also exhibited high accuracy and speed when applied to large databases.

The naive Bayes classifier assigns the most likely class label C to instances described by a set of attribute values $A_1 ... A_n$**.** The naive Bayes classifier is based on an assumption that all the attributes A_i are conditionally independent given the class label C. Hence the probability of observing the conjunction $A_1 \ldots A_n$ is just the product of

Table 2.1: Training Examples used in our example of naive Bayes classification. The three attributes are *Smoker*, *Hypertensive* and *Weight* and are used to predict the class variable, *Heart disease.*

Patient no.	*Smoker*	*Hypertensive*	*Weight*	***Heart disease***
1	Chain-Smoker	No	Above 150 Lb.	Yes
2	Chain-Smoker	No	Above 150 Lb.	No
3	Chain-Smoker	No	Above 150 Lb.	Yes
4	Non-Smoker	No	Above 150 Lb.	No
5	Non-Smoker	No	Below 150 Lb.	Yes
6	Non-Smoker	Yes	Below 150 Lb.	No
7	Non-Smoker	Yes	Below 150 Lb.	Yes
8	Non-Smoker	Yes	Above 150 Lb.	No
9	Chain-Smoker	Yes	Below 150 Lb.	No
10	Chain-Smoker	No	Below 150 Lb.	Yes

probabilities for the individual attributes, which are calculated from the training data.

$$P(C/A)=P(C)\prod_i P(A_i/C)$$

$$C_{NB}=argmax\,P(C)\prod_i P(A_i/C)$$

Thus the naive Bayes learning method involves a learning step in which the various *P(C)* and *P(A$_i$/C)* terms are estimated, based on their frequencies over the training data. There is no explicit search through the space of possible hypothesis. The hypothesis is formed by counting the frequency of various combinations within the training examples.

Table 2.1 considers the case for training examples for the class label Heart Disease.We want to predict whether a new patient who is a chain-smoker, hypertensive and above

150 Lb., has heart disease or not. The calculated conditional probabilities are shown below.

P(Chain-Smoker/Has heart Disease) = # of patients who are Chain-Smokers and have
heart Disease/# of patients who have Heart Disease
= 3/5
= 0.6

P(Chain-Smoker/Has Heart Disease) = 0.6	P(Chain-Smoker/No Heart Disease) = 0.4
P(Hypertensive/Has Heart Disease) = 0.2	P(Hypertensive/No Heart Disease) = 0.6
P (Above 150 Lb/Has Heart Disease) = 0.4	P (Above 150 Lb/No Heart Disease) = 0.6
P(Has Heart Disease) = 0.5	P(No Heart Disease) = 0.5

Our task is to predict whether our new patient {Smoker = *chain-smoker*, hypertensive = *yes* , weight = *above 150 Lb*} has Heart Disease or not.

$$C_{NB} = argmax_{C_j \in (yes,no)} P(C) \prod_i P(A_i/C_j)$$

$$C_{NB} = argmax_{C_j \in (yes,no)} P(chain-smoker/C_j) * P(hypertensive/C_j) * P(above\,150\,Lb./C_j)$$

P(chain-smoker & hypertensive & above 150 Lb. & has heart disease) =
P(chain-smoker/has heart disease) * P(hypertensive/has hearth disease) *
P(above150 Lb./has heart disease) * P(has heart disease) = 0.6 * 0.2 * 0.4 * 0.5 = 0.024

P(chain-smoker & hypertensive & above 150 Lb. & no heart disease) =
P(chain-smoker/no heart disease) * P(hypertensive/no hearth disease) *
P(above150 Lb/no heart disease) * P(no heart disease) = 0.4 * 0.6 * 0.6 * 0.5 = **0.072**

Thus the naive Bayes classifier classifies the given instance with class label Heart disease = ***no***, based on the probability calculations learned from the training data.

2.4 Bayesian Networks

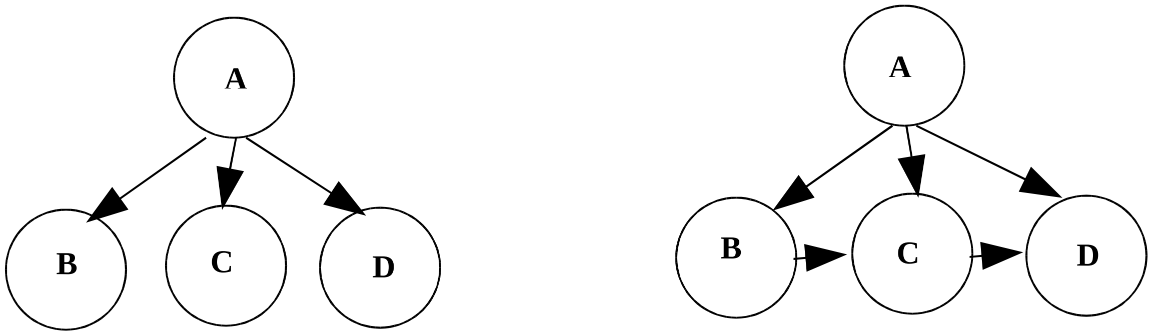
The naive Bayes classifier makes a strong assumption about independence of attributes, given the class label C. This assumption simplifies the calculations and reduces the complexity of classifier but it is overly restrictive. Also if we think intuitively about the conditional independence, we cannot ignore that there may exist correlations among attributes which should be accounted for. Relaxing the assumption of conditional independence could lead to more accurate classification.

Bayesian Networks (BNs), also referred as Bayes Nets or Belief Networks, are popular in Machine Learning beacuse they can handle incomplete datasets for predictions. Also they allow one to learn about causal relationships amongst attributes. Further, they facilitate the combination of domain knowledge and data and offer an efficient and principled approach to avoiding the overfitting of data in combination with Bayesian statistical techniques [Heckerman 1995].

Figure 2.1(a) shows a typical naive Bayes network while Figure 2.1(b) shows a typical Bayesian network. The naive Bayes network has the strong assumption of conditional independence amongst the attributes B, C and D as there are no edges among them. This means that the likelihood of occurence of attribute B given A is independent of the likelihood of occurence of attribute C given A. All the attributes are dependent on class variable A as there is an edge from A to them. This conditional independence assumptions amongst the attributes are relaxed in case of Bayesian network (see Figure 2.1(b)). This means that the likelihood of occurence of C given A is also dependent on the liklihood of occurence of B given A.

2.4.1 Concept of Conditional Independence

Two discrete random variables *X* and *Y* are said to be independent if $P(X) = P(X / Y)$. It can be alternatively stated as $P(X, Y) = P(X) P(Y)$. In the case of



(a) (b)

Figure 2.1(a) An example of naive Bayes classifier with strong independence assumption amongst nodes B, C and D with no edges and Figure 2.1(b) shows simple Bayesian network with relaxed independence assumptions amongst nodes B, C and D as there are edges from B to C and C to D.

three discrete random variables *X*, *Y*, and *Z* we can say that *X* and *Y* are conditionally independent given the value of *Z* if the probability distribution of *X* is independent of the value of *Y* given a value of *Z*, that is *P (X / Y, Z) = P(X / Z).* Extending this definition for the sets of variables, we can say that $X_{1.}..X_m$ is conditionally independent of $Y_{1.}..Y_n$ given the set of variables $Z_{1.}..Z_p$ if

$$P(X_1...X_m/Y_{1.}..Y_n,Z_1...Z_p)=P(X_1...X_m/Z_1...Z_p)$$

Consider Figure 2.2. In this network, nodes *B* and *C* are both dependent however *B* is independent of *C* *g*iven *A* that is $P(C/B,A)=P(C/A)$. Consider Figure 2.3. In this network, nodes *A* and *B* are both independent however *A* is dependent on *B* given *C.*

2.4.2 Representation

Figure 2.5 shows an example of a Bayesian network structure *S* and local probability distributions *P* of all nodes in the form of conditional probability tables.

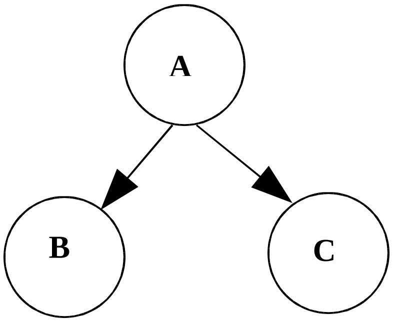


Figure 2.2 General network 1 with three nodes A, B and C with directed edges from A to both B and C.

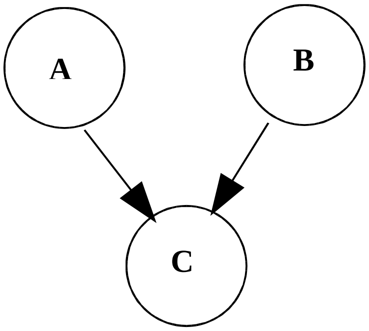


Figure 2.3 General network 2 with three nodes A, B and C with directed edges from A and B to C.

A Bayesian network describes the probability distribution governing a set of variables by specifying a set of conditional independence assumptions along with a set of conditional probabilities. It allows for the efficient and effective representation of the joint probability distributions over a set of random variables [Friedman et al, 1997].

A Bayesian network for a set of variables $X = \{X_{1.}..X_n\}$ consists of (1) a network structure S that encodes a set of conditional independence assertions about variables in X**,** and (2) a set P of local probability distributions associated with each variable

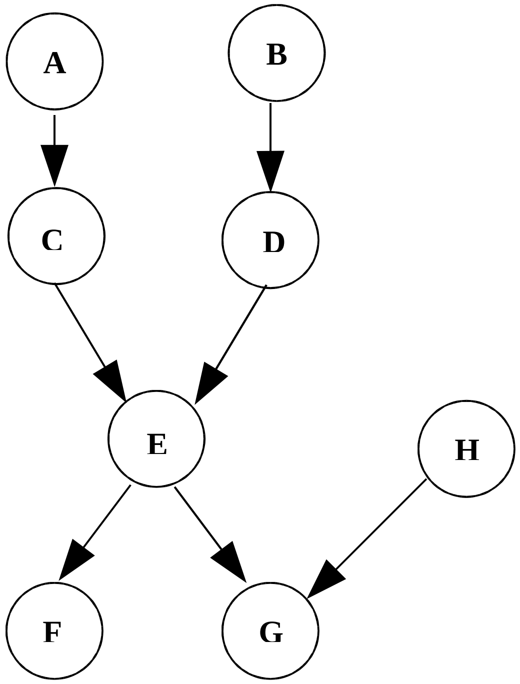


Figure 2.4 A Bayesian network with eight nodes A, B, C, D, E, F, G and H. With respect to node E, nodes A and B are non descendants, nodes C and D are parents while nodes F and G are descendants. Node H is a parent of node G.

[Heckerman, 1995]. These two are the components of the joint probability distribution for *X*.

Each vertex in *S* is a random variable from *X*, and each edge represents a correlation between the variables. The lack of an edge between two nodes encodes conditional independence between the two nodes. This network structure *S* is essentially an acyclic graph whose vertices correspond to variables in *X*. The local probability distributions *P* are represented as a table for each variable given its parents known as conditional probability table.

A Bayesian network encodes the *Markov Assumption*. Any variable X_i is conditionally independent of its non descendants, given its parents. $P(X_1 ... X_n) = \prod_{i=1}^{n} P(X_i / Parents(X_i))$, where $Parents(X_i)$ is set of parents of X_i.

Consider Figure 2.4. For node *E*, nodes *A* and *B* are non descendants while nodes *C* and *D* are parents and nodes *F* and *G* are descendants. Node *E* is independent of *A*, *B* given *C*, *D*.

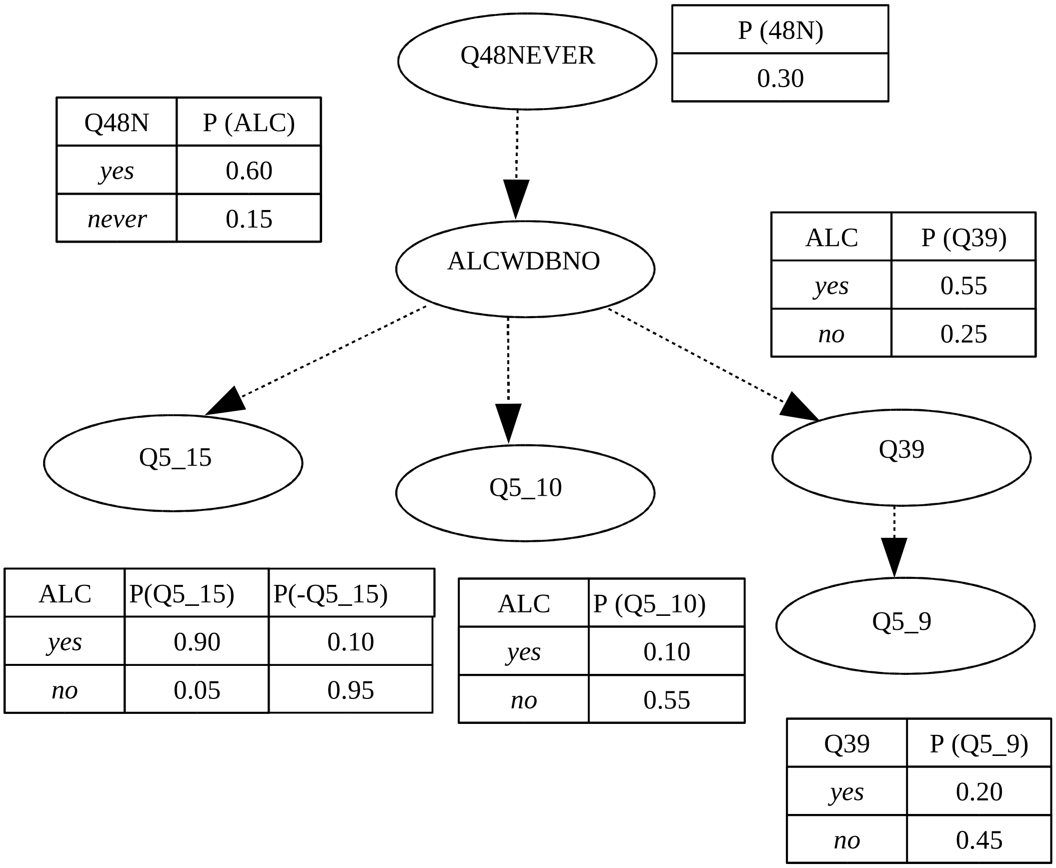
In general, a *Markov blanket* of some node *X* is a minimal set of variables that make the variable *X* independent from all the other variables in the network. It is a union of three sets – the parents of *X*, the children of *X* and the parents of the children of *X*.

Figure 2.5 shows a more complete Bayesian network for our test problem. Before explaining the Bayesian network in Figure 2.6, we will explain the variables denoted by nodes in the figure.

Q48NEVER	Had Blood Pressure Checked? {*never*, *yes*}
ALCWDBNO	Accomplished less, careless work, and felt downhearted and blue without being depressed or anxious {*yes*, *no*}
Q5_15	Diagnosed Depression {*yes*, *no*}
Q5_10	Diagnosed Stroke Related Problem {*yes*, *no*}
Q39	Limited in the kind of work {*yes*, *no*}
Q5_9	Diagnosed Heart Trouble {*yes*, *no*}

Q48NEVER directly affects the probability of ALCWDBNO. The value of Q5_15 to be *yes* or the value of Q39 to be *yes* for limited in the kind of work depends only on the state of ALCWDBNO as both the variables Q5_15 and Q39 are in the Markov blanket of ALCWDBNO.

The table associated with each of the nodes is called a Conditional Probability



P (48N)
0.30

Q48N	P (ALC)
yes	0.60
never	0.15

ALC	P (Q39)
yes	0.55
no	0.25

ALC	P(Q5_15)	P(-Q5_15)
yes	0.90	0.10
no	0.05	0.95

ALC	P (Q5_10)
yes	0.10
no	0.55

Q39	P (Q5_9)
yes	0.20
no	0.45

Figure 2.5 An example of typical Bayesian structure and local probability distributions in the form of Conditional Probability Tables for each node.

Table (CPT). The CPT of the variables Q5_15, Q5_10 and Q39 have two rows each. Each of the row corresponds to a value of the variable ALCWDBNO. Each column of the CPT corresponds to the particular variables value. For example, if we look at the first row of the CPT of Q5_15, the probability of Q5_15 = *yes* when ALCWDBNO = *yes* is 0.9 and the probability of Q5_15 to have value *no* when ALCWDBNO= *yes* is 0.1. Again, in the second row, the probability of Q5_15 = *yes* when ALCWDBNO is *no* is 0.05 and the probability of Q5_15 to have value *no* when ALCWDBNO = *no* is 0.95. As we can see, each row of the CPT must add up to 1. Each row in CPT contains the conditional probability of each node value for the conditioning case. A conditioning case is just a possible combination of values for the parent node. All the root nodes (like

Q48NEVER), with no parents are represented with prior probabilities of each possible value of that variable.

2.4.3 Inference

After a Bayesian network is created from the data and prior knowledge about the variables, we need to determine various probabilities of our interest from this network which may not be available directly from the net. Thus we need to compute this probability distribution for any subset of variables of interest given the values of any subset of remaining variables.

There are several variants of probabilistic inference algorithms developed for Bayesian networks. Overall they all can be categorized in two main kinds of inference: (1) exact, and (2) approximate.

Exact inference of probabilities for an *arbitrary* Bayesian network is NP hard [Mitchell, 1997]. Exact inference is possible when all nodes of Bayesian network have linear Gaussian distributions [Mitchell, 1997]. There are two main types of exact inference algorithms, those that work only on directed acyclic graph (DAG) models and those that work on both directed and undirected graphs.

The DAG-only inference algorithms exploit the chain-rule decomposition of the joint probability,

$$P(X)=P(X_1)P(X_2/X_1)P(X_3/X_1,X_2)...$$

and the “push sums inside products” approach to remove the irrelevant nodes. This kind of algorithm is called the variable elimination algorithm. This results in a single marginal probability $P(X_i/X_j)$.

Algorithms that work on both undirected and directed graphs are generally defined in terms of message passing on a tree. The tree can be directed or undirected and the messages can be passed sequentially or in parallel. One of the advantages of message passing algorithms is that they use dynamic programming to avoid redundant computations used by variable elimination algorithms when computing all the marginal probabilities simultaneously. A few good examples of message passing algorithms are Pearl's algorithm [1988] and the Hugin/JLO algorithm [Jensen et al, 1990]

There are a couple of reasons why it is difficult to use exact inference in all cases. In cases when exact inference is mathematically possible, the computation time to get the exact solution is often very long. There are also cases when there is no possible closed-form solution. In both such cases, approximate inference is often employed. There are few different types of approximate inference algorithms that are used.

Sampling Methods are one of the techniques that are used to perform approximate inference. Importance sampling is one the simplest kinds of these methods. In importance sampling random samples are drawn from prior probabilities [Cheng and Druzdzel, 2000]. One of the most popular approximation approaches is the Markov Chain Monte Carlo (MCMC) method, in which the random samples are drawn from the posterior probabilities. Other methods include Gibbs sampling [MacKay, 1998] and the Metropolis-Hasting algorithm [Neal, 1993].

Another kind of approximation methods are the variation methods. One example of these is the mean-field approximation method [Jordan et al, 1998]. This method exploits the law of large numbers to approximate large sums of random variables by their means. The mean-field algorithm produces a lower bound on the likelihood of the approximations.

Belief Propagation algorithms [Berrou et al, 1993] apply the message passing algorithm to the original graph even if it has loops. These algorithms are closely related to the variation methods and have been used to do approximate Bayesian inference in algorithms like the Expectation Propagation algorithm.

2.4.4 Learning Bayesian Network Structure

Why do we need to learn Bayesian networks? Sometimes we do not know the structure of a network or only know parts of the structure. Also, the graph structure provides us a method to gather new knowledge by providing an insight into the domain of our problem.

There are two main kinds of learning: parameter learning and structure learning. In parameter learning, there can be two cases: one in which the network structure is known and there are no hidden/missing variables and another in which the network structure is known but there are hidden/missing variables.

In the first case, where the network structure is known in advance and all the variables are fully observable, the task of parameter learning is to estimate the conditional probability table entries. This is a simple task. There have been various algorithms that have been proposed for such a case. If the network structure is a directed acyclic graph, the problem decomposes fully, since we can construct the conditional probability tables independently of each other. When the network is undirected, methods like Iterative Proportional Fitting (IPF) and the generalized iterative scaling algorithm [Darrech and Ratcliff, 1972] can be used.

In the case where the network structure is known but not all of the variables' values are observable (missing and/or hidden values in dataset), learning is more difficult. In this case, a locally optimal solution is preferred. Algorithms such as the Expectation Maximization (EM) algorithm [Lauritzer, 1995] can be used to find such a locally optimal solution. There are other methods that can also be used, such as the “bound and collapse” method [Ramoni and Sebastini, 1997] and gradient based methods [Koller et al, 1997]. However, the EM algorithm is generally preferred over these because of its simplicity and the fact that it deals with constraints automatically. The EM algorithm can be sped up by combining it with gradient methods [Jamshidian and Jennrich, 1993].

When the underlying structure of data *D* is not known, we must perform Structure Learning. The Structure Learning task can be informally stated as: Given a training dataset *D*, find a network *B* that best matches *D*, where *D* is a set of independent instances. There are two different approaches to graphical probabilistic model learning (structure learning) from data [Cheng et al, 1997]: (1) dependency-analysis-based methods, and (2) search and score methods.

A dependency-analysis-based methods depend on the assumption that the underlying network which is studied has many dependencies amongst the nodes. Algorithms based on this approach try to discover the relevant set of these dependencies and independences in the network from the training data and use them to infer the structure of network. Dependency relationships are calculated using some form of Conditional Independence (CI) tests. This is also called the constraint based approach. A few algorithms based on this approach are the Boundary DAG algorithm [Pearl, 1988], the Wermuth-Lauritzen Algorithm [Wermuth and Lauritzen, 1983], the Constructor algorithm [Fung and Crawford, 1990], the SRA algorithm [Srinivas et al, 1990], and the SGS algorithm [Sprites et al, 1990].

Although the dependency-based method has advantages, such as being more efficient for sparse networks and often finding the correct structure when the probability distribution of data satisfies certain assumption, it can be unreliable when the CI tests have large condition sets (number of different conditions in data). Moreover, this approach often requires an exponential number of CI tests.

The more popular approach is the search and score method. This approach attempts to find the structure that can fit the data best using a search process. All the search and score methods attempt to *search* a graph that maximizes the selected *scoring* function. Algorithms falling in this category generally start with a simple graph without any edges and then use some search method to add/delete edges recursively. The score method is used to measure the goodness of each explored graph from the space of feasible solutions. This process continues until they do not get a candidate which defines the data in a better way. Thus each algorithm is characterized by a specific search procedure and scoring function. The scoring function is based on different criteria such as the *Bayesian scoring method* [Cooper and Herskovits, 1992; Heckerman et al, 1995; Ramoni and Sebastini, 1997], the entropy based method [Herskovits and Cooper, 1990], the minimum description length (MDL) method [Suzuki 1996; Friedman and Goldszmidt, 1996; Lam and Bacchus, 1994] and the minimum message length method [Wallace et al, 1996]. We discuss a few of these algorithms briefly below.

The *Chow-Liu Tree Construction Algorithm* [Chow and Liu, 1968] is used to do structure learning and is a variant of the [Friedman and Goldszmidt, 1996] algorithm. This algorithm uses two different kinds of scores to learn a Bayesian network. It used both the minimum description length (MDL) score and the Bayesian score. It is effective algorithm since it learns the Bayesian network and the local structure of the conditional probability tables at the same time. When we add a new edge using this algorithm, it chooses the direction which gives the better score as the direction for the edge.

The *K2 Algorithm* [Cooper and Herskovits, 1992] was the first serious attempt at learning a Bayesian belief network. It is one of the first search and scoring based algorithms for learning a Bayesian belief network. The working of this algorithm is very simple in that it takes as input a dataset and a node order, and constructs a belief network structure as the output. This algorithm uses a Bayesian scoring method and computes the conditional probabilities by the brute force method.

The *MDL length method* [Suzuki 1996] addressed the issue of learning Bayes networks using the minimum description length (MDL) principle. The MDL principle basically selects a rule that takes both simplicity and fit to the data into account and achieves the best results. This algorithm uses a formula for description length and applies a branch and bound technique to find the network structure. The branch and bound technique thus developed determines whether a branch needs to be searched more by calculating a lower bound after adding an arc to the structure. This algorithm is very different from other search and score algorithms in that it does not use a heuristic and it also guarantees that we find an optimal structure.

The *Construct-TAN algorithm [Friedman et al, 1997]* that we use to do our structure learning is a variant of the tree augmented naive Bayes [Friedman and Goldszmidt, 1996] algorithm. It uses both the minimum description length (MDL) score and the Bayesian score to learn the network. It is also a good algorithm since it learns the Bayesian network and the local structure of the conditional probability tables at the same time [Friedman et al, 1997]. When we add a new edge using this algorithm, it chooses the direction which gives the better score as the direction for the edge. The toolbox we have implemented is based on this algorithm. The Construct-TAN algorithm is explained in detail in Chapter 4.

Chapter 3: The Bridge to Health Dataset

This chapter is organized as follows. Section 3.1 introduces the Bridge to Health survey data, followed by Section 3.2 which explains in detail the method by which data was collected. Section 3.3 describes the statistical weighting of data. The next subsection describes the data, while the last section, 3.5, lists variables of interest, cardiovascular disease risk factors and mental health status variables.

3.1 The Bridge to Health Survey Dataset

The Bridge to Health survey was a regional health status assessment carried out between November 1999 and February 2000. This population-based survey was mainly conducted to gather information on health indicators. The Bridge to Health Survey dataset is a local (county level) survey data of more than 6200 adult residents in a sixteen-county region in Northeastern Minnesota and Northwestern Wisconsin [Block et al, 2000].

3.2 Data Collection

The Bridge to Health 2000 survey (BTH 2000) data was collected through 6251 computer-aided telephone interviews by the Survey Research Center of Division Health Services Research and Policy located in the School of Public Health at the University of Minnesota for Bridge to Health Collaborative. One adult (above the age of 18) from each sampled household was selected to participate in the survey. Out of 8559 eligible households contacted by phone between November 1999 and February 2000, 6251 interviews were completed with the response rate of over 74% [Block et al, 2000].

The BTH 2000 collected data on lifestyle behaviors, health care access, disease prevalence, preventive health practices, injury prevention and violence, preventive screening and tobacco-alcohol use. The BTH 2000 Questionnaire had 101 questions for which the responses of the interviewees were recorded. The questions were designed to gather information about the general health of an individual as perceived by himself and as diagnosed by a doctor.

Most of the questions had a choice of response as YES/NO. An example question is

In the last year, have you had a flue shot?

- *Yes*
- *No*

But some questions were more descriptive, with the choices as in

How much of the time during the past four weeks, have you felt downhearted and blue?

- *All the time*
- *Most of the time*
- *A good bit of the time*
- *Some of the time*
- *A little of the time*
- *None of the time*
- *Refused*
- *Don't know*

3.3 Statistical Weighting of Data

The BTH 2000 dataset was required to be weighted because of the differences in household size, differences in the size of the population in each of the 18 strata (counties), and differences in response rates between men and women and people of different ages [Block et al, 2000]. The statistical weighting was already done by [Block et al, 2000] before we used the data for our research. However the process of weighting the data is crucial and so I would like to mention it here. The first step involved weighing the data by the inverse of the selection probability within the household (that is, the number of adults age 18 and older living in the household). The next step was to weigh the data by the actual size of the adult population in each of the strata divided by the number of respondents from each stratum. The third step was to post-stratify the data based on the 1998 U.S. Census estimates of the age and gender distributions for adults with each of the strata. The last step was to divide the weights by a numeric constant, which forced the weighted total sample size to be equal to the total number of respondents in the sample.

3.4 Data Description

BTH 2000 has 6251 records, each one representing the response of an interviewee. Each record has 334 features.

These features are either the direct responses of the interviewees, new/recoded variables or maintenance variables. The new or recoded variables were added to facilitate research of the dataset. These variables are calculated from the direct responses either to make them more specific or more general. Some of the continuous variables were made discrete. The various features can be categorized as follows:

1. General information such as the sex, age, education, height, weight or marital status of a person.
2. Physical health status variables such as chronic conditions, overweight issues and person suffering from particular diseases.
3. Mental health status variables such as anxiety, panic attacks, depression and accomplished less due to mental health.
4. Diagnosed diseases such as allergies, asthma, back problems, cancer, diabetes, digestive disorder, high blood pressure and high cholesterol.

Table 3.1 Mental health status variables used as class variables to create tree augmented networks using Construct-TAN algorithm.

Variable name	***Description***	***Response***
Q15NEW2	Diagnosed depression	1: Yes 10: No
Q16NEW2	Diagnosed anxiety	2: Yes 20: No
DEPRANX2	Diagnosed depression and anxiety	2: Yes 5: No
ALDPANX2	Accomplished less without depression or anxiety	31: Yes 33: No
CWDPANX2	Careless work without depression or anxiety	31: Yes 34; No
DBDPANX2	Feel downhearted or blue without depression or anxiety	31; Yes 35: No

5. Preventive care such as consumption of fruits and vegetables, avoidance of certain food due to toothache and flu vaccination.
6. Preventive screening such as mammogram, pap-smear test, prostate examination and colon screening.
7. Injury prevention and violence such as seat-belt use, safety equipment in home and victims of violence or crime against property.
8. Tobacco-Alcohol use such as cigarette smoking, smoking in the home, attitudes towards smoking regulations and alcohol consumption patterns.
9. Health care access such as health insurance coverage and failure to receive medical care.
10. Recoded variables such as combination/recalculation of direct responses.
11. Data maintenance variables.

3.5 Class Variables: Features of Interest

In this research, we are interested in finding the correlations between the variables given a particular (class) variable and analyzing the structure created by the Construct-TAN algorithm (explained in Chapter 5). Table 3.1 lists all the cardiovascular disease risk factors and Table 3.2 lists all the mental health status variables used as class variables for structure learning.

Table 3.2 Cardiovascular disease risk factors used as class variables to create tree augmented networks using Construct-TAN algorithm.

Variable name	*Description*	*Response*
Q5_11	Diagnosed high blood pressure	1: Yes 2: No
Q5_12	Diagnosed elevated cholesterol	1: Yes 2: No
Q48REC	Blood Pressure checked in last 2 years	1: Within past 2 years 2: Not within past 2 years
Q49REC2	Cholesterol checked in last 2 years	1: Within past 2 years 2: Not within past 2 years
OVERWGT2	Overweight or not overweight based on BMI	0: Not overweight 1: Overweight
BMICUTS	Normal weight, overweight, obese based on BMI	0: Not overweight 1: Overweight 2: Obese
EXCERREC	Moderate or vigorous exercise 3X per week	1: Exercise less than 3 times per week 2: Exercise more than 3 times per week
Q69A	Current smoker	1: Yes 2: No

Variable name	***Description***	***Response***
CHRONIC	60+ drinks per month	0: Less than 60 drinks per month 1: 60+ drinks in the past month
URRURNEW	Urban or rural residence	1: Urban 2: Rural

Chapter 4: The Construct-TAN algorithm [Friedman et al, 1997]

In this chapter we present the algorithm that we used to create our Bayesian networks. The tool we describe in Chapter 5 is based on the Construct-TAN [Friedman et al, 1997] algorithm.

4.1 Using Bayesian Networks for Classification

As we have already seen in the background section, a naive Bayes classifier learns from training data *D* the conditional probability of each attribute A_i given the class variable *C* (note that all variables in training data *D* except *C* are called attributes). Classification is then done by applying Bayes rule to compute the probability of *C* given the particular instance of $A_1 ... A_n$ and then predicting the class with the highest posterior probability.

But in general, the strong assumption of conditional independence between the attributes given the class variable *C* is not realistic for real world datasets. The classification using naive Bayes could be skewed (and yet good) because of the fact that it neglects the correlation between attributes in highly interrelated network.

In our classifier, we start with the connections from the class variable *C* to every attribute A_i**.** This gives the class variable a special status in the network. The connection from *C* to each A_i ensures that, in the learned network, the probability $P(C/ A_1 ... A_n)$ will take all attributes in account [Friedman et al, 1997]. Thus we start with a naive Bayes network and change it by adding edges amongst the attributes maintaining the acyclic nature of the graph. These additional edges signify a correlation amongst variables in the structure. Thus the newly created classifier is called as *augmented naive Bayes classifier.*

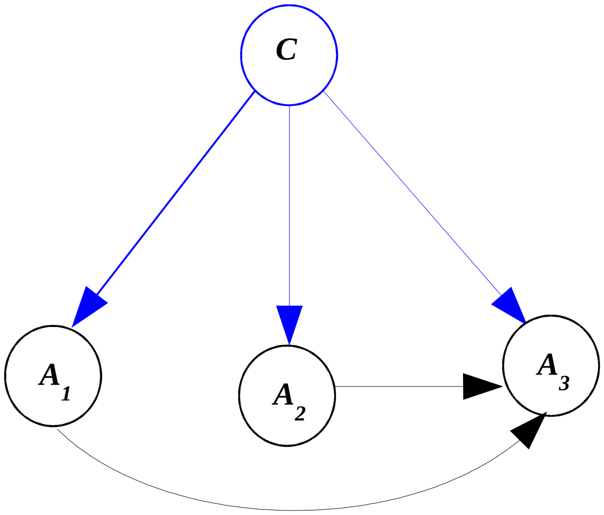


Figure 4.1 shows an augmented naive Bayesian classifier with class variable *C* and three attributes *A_1*, *A_2* and *A_3*. *C* is connected to all the attributes (naive Bayes connections). There are also additional edges from *A_1* to *A_3* and *A_2* to *A_3*.

Such an augmented naive Bayesian classifier network is shown in Figure 4.1. Observe that the class variable C has an edge to all the attributes A_1, A_2 and A_3. Also there are few edges from one attribute to another depending on necessity. For example, there is an edge from A_1 to A_3 and also from A_2 to A_3. The interpretation of these edges could be made as follows. The influence of A_3 for predicting the value of the class variable C also depends on the value of A_1. Similar logic extends to the edge from A_2 to A_3.

As one observes in Figure 4.1, construction of an augmented naive Bayesian classifier is equivalent to finding a good Bayesian network with the class variable C as root. However finding the best Bayesian network from among in all the possible super exponential number of networks is a computationally intensive problem. An efficient solution of finding a useful set of edges amongst variables can be learned in polynomial

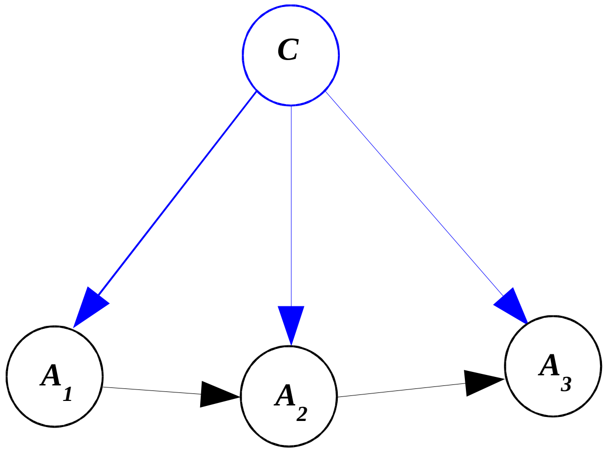


Figure 4.2 A Tree Augmented Network (TAN) with class variable *C* and three attributes nodes *A_1*, *A_2* and *A_3*. *C* is connected to all the attributes. There are also directed edges from *A_1* to *A_2* and *A_2* to *A_3*.

time by imposing restrictions on allowable interactions amongst the variables. This results in a new network called a *Tree Augmented Network* or TAN.

In a TAN, the network is restricted in that the class variable has no parents and each attribute has as parents the class variable *C* and at most one other attribute. The edges in a TAN are called augmented edges. One should notice that each attribute in TAN can have one augmented edge pointing to it.

Figure 4.2 shows a tree augmented network where class variable *C* is connected to all the attributes A_1, A_2 and A_3**.** Also there are edges from one attribute to another depending on necessity. For example, there is an edge from A_1 to A_2 and also from A_2 to A_3. Note that the TAN cannot have any attribute node with more that one attribute as its parent. In Figure 4.2, both A_1 and A_2 have only one attribute as parent. However an augmented naive Bayesian network can have nodes with more than one attribute as their parents. In Figure 4.1, A_3 has two parents A_1 and A_2. This is where an augmented naive Bayesian network differs from a TAN.

4.2 The Construct-TAN algorithm

Chow and Liu [1968] developed a procedure (shown in Table 4.1) for constructing of TAN (learning the appropriate set of edges in the network). This procedure reduces the problem of building a Bayesian network to finding a maximal weighted spanning tree in a graph. This means the problem of finding such a tree is to select a subset of arcs from a graph such that the selected arcs constitute a tree and the sum of weights attached to the selected arcs is maximized [Friedman et al, 1997].

Table 4.1: The Construct-tree procedure of CL [Chow and Liu, 1968]

1. Compute $I_P(X_i\ ;X_j)$ between each pair of variables, *i* is not equal to *j*
2. Build a complete undirected graph in which the vertices are the variables in ***X***. Annotate the weight of an edge connecting $\boldsymbol{X_i}$ to $\boldsymbol{X_j}$ by $\boldsymbol{I_P(X_i\ ;X_j)}$
3. Build a maximum weighted spanning tree
4. Transform the resulting undirected tree to a directed tree one by choosing a root variable and setting the direction of all edges to be outward from it

$$I_p(X;Y)=\sum_{x\in X,y\in Y} P(x,y)\log\frac{P(x,y)}{P(x)P(y)} \tag{4.1}$$

The function $\boldsymbol{I_P(X_i\ ;X_j)}$ is called the *mutual information* (MI) function and is shown in equation (4.1). This function characterizes the mutual information between the two variables *X* and *Y*. The MI between two variables *X* and *Y* can tell us whether the two variables are dependent or not and if they are, then how close the relationship is. If MI has a smaller value than a particular threshold *t*, then the two variables are called conditionally independent. The time complexity of this procedure is $O(f^2 * n)$, where *f* is the total number of variables in the data *D*.

The Construct-TAN [Friedman et al, 1997] algorithm, shown in Table 4.2, on which my tool is designed, is based on the procedure Construct-tree [Chow and Liu, 1968], with a slight modification. The Construct-TAN algorithm is a five step procedure to build a tree augmented network for a given class node *C*. The first step determines the weight of each edge between two nodes of the network. The weighting function is called conditional mutual information function as shown in equation (4.2). This function calculates the mutual information between two attributes given the value of class variable *C*. The CMI between the two variables *X* and *Y* can tell us whether the two variables are dependent or not, given the value of another variable *C* . The dependency of the variables *X* and *Y* is determined with respect to the value of *C*. If CMI has a smaller value than a particular threshold *t,* then the two variables are conditionally independent given *C*. The next step constructs a undirected graph with all attributes (all nodes other than the class node) and the weights are assigned to all the edges. The next step builds a maximum-weighted spanning tree. In the toolbox, we have implemented Prim's algorithm [Tenenbaum et al, 1995] for building the spanning tree. The fourth step converts the undirected graph to directed one.

$$I_P(X;Y/C) = \sum_{x \in X, y \in Y, c \in C} P(x,y,c) \log \frac{P(x,y/c)}{P(x/c)P(y/c)} \qquad (4.2)$$

Table 4.2: The Construct-TAN procedure explained from [Friedman et al, 1997]

1. Compute $I_P(A_i \,; A_j / C)$ between each pair of variables, where i is not equal to j

2. Build a complete undirected graph in which the vertices are the attributes A_1 ,..., A_n. Annotate the weight of an edge connecting A_i to A_j by $\boldsymbol{I_P(A_i \,; A_j / C)}$.

3. Build a maximum weighted spanning tree.

4. Transform the resulting undirected tree to a directed one by choosing a root variable and setting the direction of all edges to be outward from it.

5. Construct a TAN model by adding a vertex labeled by C and adding an arc from C to each A_i.

Our implementation of this step selects the variable next to class variable in the comma separated data file as the root node. The last step adds the class node to the graph. The time complexity of this procedure is also $O(f^2 * n)$ where f is the total number of variables in the data D.

The two methods, Construct-tree and Construct-TAN, although they appear similar, have a few differences as follows.

- Construct-tree is a four step method to build a general tree of all the variables in the data while Construct-TAN is a five step algorithm to build a specialized tree with a class node as parent of all the remaining nodes.

- A tree built by the Construct-tree method has one node (root node) with no parents and all the other nodes with only one parent. On the other hand, the network built by

Construct-TAN has one node with no parent (class node), one node with only one parent (root node with class node as parent) and all the other nodes with two parents (class node and some other node in the tree).

Chapter 5: Our Bayesian Toolbox

This chapter describes the toolbox that we developed using the Construct-TAN algorithm. In this section, first we will discuss the motivation to create such a tool for our survey data. Then we will discuss the representation used while creating this toolbox, the interface design of the tool. In the next section, we will demonstrate the working of the tool with an example TAN. Finally we enumerate the capabilities of the tool.

5.1 Motivation

There are various machine learning techniques that can be used to discover various kinds of relationships amongst features in our data. However we wanted a technique that would be: (1) accurate, (2) able to learn Bayesian network structures, (3) efficient, and (4) effective for visualization.

We want to do *structure learning* using the Construct-TAN algorithm as it gives a probable network by doing heuristic search over the space of network structures. The structure that is created using our tool should describe the data very closely. There should be a measure by which this structure can be validated. We use cross validation technique to test the *accuracy* of the network created.

The tool thus developed should not only learn the structure of data but also displays as a network of nodes and edges efficiently thus making *speed* an important factor in the design of the tool. The algorithm used to develop the network is very efficient and learns the data fast. Last but not the least, the tool should provide an *effective* way to *visualize* the network and. The tool thus incorporated what was desired.

5.2 Design of the Tool

This section discusses the design of the tool. It explains how the structure learning and inference methods are implemented in the tool, the representation of the network built by the tool and software issues related to the tool.

5.2.1 Representation of the Network

The network is in the form of a DAG, more specifically a tree augmented network. The structure created by the tool has a class node which is connected to all the other nodes in the graph. However the number of attributes in our dataset is very large (over 100) and to show the edges (directed from the class node to the attributes) would make the network crowded and unreadable. Hence we do not show all of these edges in the resulting network.

5.2.2 Structure Learning

The Construct-TAN algorithm constructs the network. As preprocessing of data handles the elimination of missing values in the data and discretization of data, the structure learning algorithm is implemented on data which is fully observed with no hidden, no missing value variables. The input to the tool is an ordinary database table in the comma separated variable file format. The first field of the data is treated as a class variable, the next as the root variable. Each record is a complete instantiation of all the variables in the domain. The conditional mutual information of variables is computed using the relative frequencies from the database. The Construct-TAN algorithm, as described in Chapter 4, is applied to the data and its structure is determined. The resulting network is then displayed in a JAVA applet.

5.2.3 Inference

Because all the variables in the dataset are discrete, inference is practically viable for implementation. Because of the simple approach of the algorithm, an inference algorithm could be implemented in terms of a product of potentials. A potential is an object variable which helps to execute the inference algorithm efficiently. In our case, the potential is represented as the conditional probability table of a node, given all possible states of its parents. The tree which is created by the tool is a spanning tree, and therefore for each node the number of parents is at most two. Inference in TAN can then be simplified as shown in equation (5.2). Equation (5.1) shows a generalized formula for inference learning.

$$P(C/X_1 \ldots X_n) = \prod_{i=1}^{n} P(X_i / Parents(X_i)) \qquad (5.1)$$

where $Parents(X_i)$ are the parents of node $X_{i.}$ There are only two parents of node *X* in TAN , the class node *C* and some other node *Y*.

$$P(C/X_1 \ldots X_n) = \prod_{i=1}^{n} P(X_i / Y, C) \qquad (5.2)$$

The inference algorithm is easy to implement and enables optimization at implementation level. In the case of inference, the inputs to the tool are the training data file which learns the structure of the data and the testing data file for inference.

5.2.4 Software Issues

The tool has been implemented in JAVA because of the various functions JAVA provides. JAVA has rich set of built-in data structures, facilities for drawing graphs and use of applets to display the network. The use of JAVA as a programming language makes the tool runnable on any JAVA-enabled browser.

5.3 Working of the Tool with an Example

Consider a training data file to develop a network for the class variable CHRONIC using our tool.

```
CHRONIC,SEX,Q36,Q37,Q38,Q39,Q40,Q41,Q44,Q45,Q46,Q48,...
0,2,3,100,2,2,2,2,5,2,5,1,...
0,2,3,100,2,2,2,2,2,3,6,1,...
0,1,3,100,2,2,2,2,1,3,6,1,...
0,1,3,100,2,2,2,2,2,3,6,1,...
0,2,1,1,2,2,100,100,2,100,5,1,...
0,2,3,100,2,2,2,2,2,4,5,1,...
...
```

The training data file has 3115 records and 54 variables including the class variable CHRONIC. The training data file and the testing data file are both comma separated files. The top row lists the variable names which are represented as nodes in the TAN. The first variable (CHRONIC) is considered as the class variable for which the structure is built. The next variable (SEX) is the root variable which has only one parent, the class variable. All the other rows (except the first one) contain the values of all the nodes. The network thus created by the tool is shown in Figure 5.1. It shows the tree augmented network for the class variable CHRONIC. All the variables other than the class variable are represented as nodes in the network. The edges are weighted by the conditional mutual information value (see equation 4.2). Our tool searches the space of all possible networks and builds a network which is a maximum-weighted spanning tree. The algorithm we implemented for building the spanning tree is Prim's algorithm. It is described below.

Table 5.1: Prims Algorithm

1. Create a tree *T* containing a single vertex *v*, chosen arbitrarily from the graph *G*. *v* is known as the root node.
2. Create a set *S* containing all the edges in *G*.

3. Remove from S an edge e with maximum weight that connects a vertex in the T with a vertex u in G. Add edge e and vertex u to the tree.
4. Repeat step 3 until every edge in S connects two vertices in T .

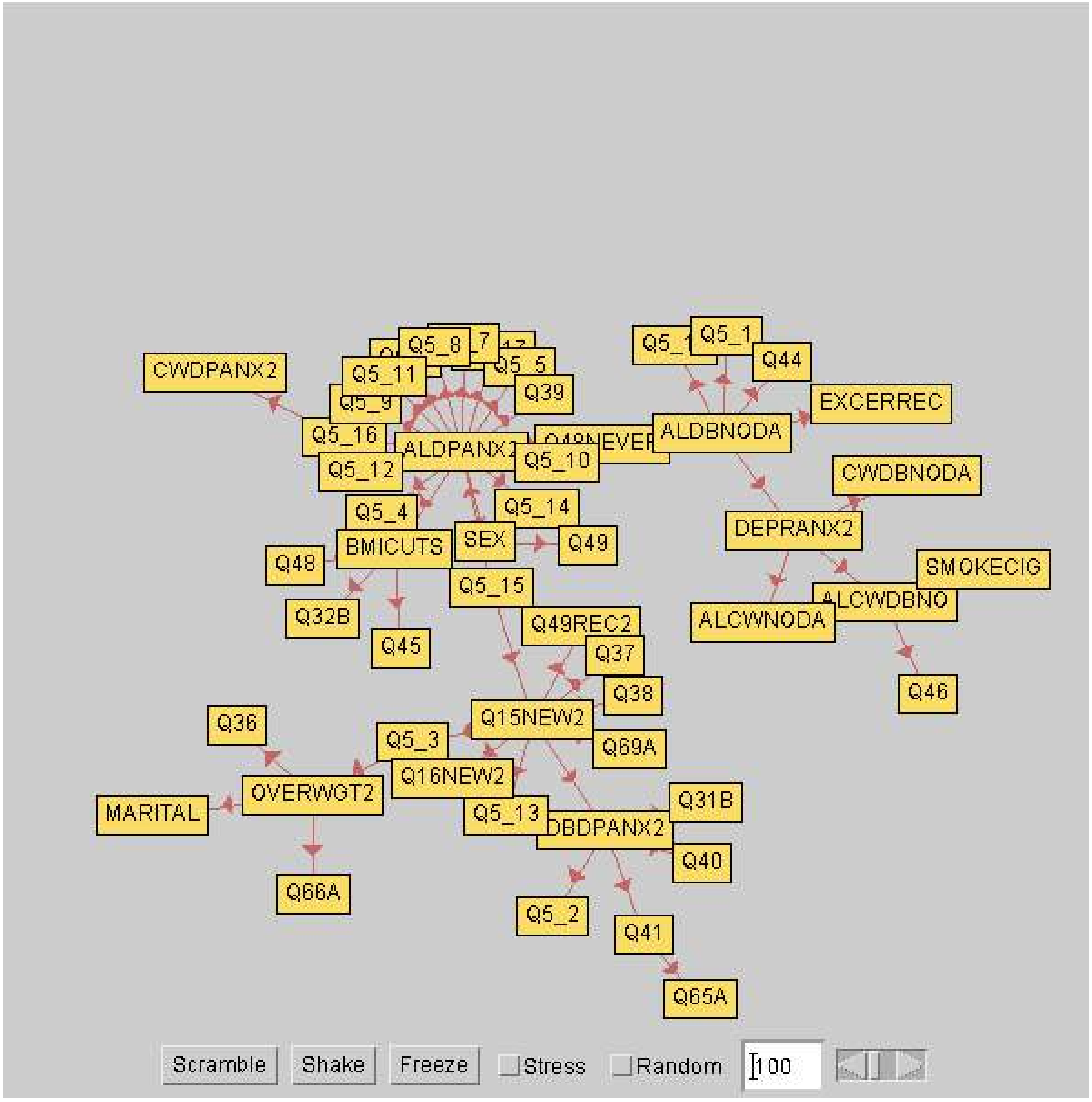


Figure 5.1 Tree augmented network for class variable CHRONIC

5.4 Features

The toolbox has various features incorporated into it right now. The tool builds a TAN with the following features: (1) it is web enabled, (2) time efficient, (3) the network spaces itself in given area, (4) the network can be frozen for examination, (5) nodes are distanced according to their association with each other, and (6) the user can choose a percentage of edges.

5.5 Discussion

Although there are many Bayes Network tools which are freely available that can provide some similar functionality to our tool, almost all of them had a restriction on the size of the dataset that one can use. We wanted to create a tool which did not put any restrictions on the dataset one can use.

Another drawback with many tools is that they use some kind of node ordering requirement. Node Ordering is a type of domain knowledge used by many Bayesian network learning algorithms that satisfies a causal or temporal order of the nodes of the graph. Most algorithms either assume that there is a node ordering requirement or they prefer to use it. We wanted to make a tool which did not necessarily have this requirement of node ordering. That is the reason we chose the Construct-TAN algorithm described earlier; it does not require any node ordering.

Most of the visual tools that are available online have a constraint on the number of nodes in the graph. We did not want any constraints on the number of nodes that are present in the graph. We wanted to visualize all variables in the dataset and then analyze from their structure using some measures.

Finally, there is a dearth of publicly available learning tools for real world data mining datasets and applications. Real world data mining datasets have hundreds of variables and thousands to millions of records in them. Most of the tools we found had restrictions on data size and hence were not really meant for any real world application. They ran on at most 40 features and 5000 records. I had a dataset that consisted of over 300 features and hence we wanted to create a tool that would handle this size of data efficiently.

Chapter 6: Experiments and Analysis

In this chapter, we present the experiments to verify the usefulness of the tool we constructed. In the first section, we describe how the data was preprocessed. The data preprocessing technique was carried out in two phases: (1) feature elimination, and (2) handling of missing values in the dataset. We compare the effectiveness of the network we create using the tool with the naive Bayes classifier in Section 6.2. Section 6.3 describes the results obtained from our tool for class variable *Q5_12: Diagnosed elevated cholesterol* in detail. Finally, in Section 6.4 we show several example TANs created by our tool and provide some analysis.

6.1 Data Preprocessing

The BTH 2000 dataset (presented in Chapter 3) is a large dataset with 6251 records and 334 variables. The focus of this thesis was to demonstrate that our tool could find relationships between the cardiovascular disease risk factors and mental health status variables and to analyze the kind of correlations that exist between the variables (see table 3.1 and 3.2) along with other variables. When the original dataset with 334 features was assessed, it was observed that there were many features which were irrelevant to our purpose. There are several variables like maintenance variables in the dataset used as sanity checks of data and to statistically weigh the data. For example variables like ID (the respondent's ID number), SRVYMODE (Mode of survey), STATEWT (sample weights for state level analysis) and COUNTYWT (sample weights for county level analysis) are maintenance variables. The original dataset also contained several recoded variables. BMICUTS (body mass index cuts) is a recoded variable of BMI (body mass index) with a new definition. There are several other variables which are recoded and suffixed with “new” or “rec”. For example variable Q48 (had blood pressure check?) is recoded as Q48REC (has blood pressure checked in last 2 years) and Q48NEVER (never had blood pressure checked). There were also some other variables which were categorized variables of another variable and thus conveyed similar information. For example Q92A1 (drink and drive: car or truck), Q92B1 (drink and drive: boat) , Q92C1 (drink and drive: snowmobile) and Q92D1 (drink and drive: other) were summarized by one variable Q96 (drink and drive). So there were several variables in BTH 2000 which conveyed very little or no information of the variables of our interest. Bayesian structure learning with all entire set of variables would have been computationally and memory-wise costly. Also the extracted structure would be overly crowded and hard to decipher. Hence a preprocessing of BTH 2000 dataset was necessary to make the Bayesian learning process efficient.

The data had to be converted from SPSS format to the format that we could be easily manipulate. The dataset was converted to a comma separated format as an input to our tool while it was converted to C4.5 format to test it against a naive Bayes classifier.

6.1.1 Feature Elimination

The purpose of the feature elimination process was to select an appropriate set of features that could predict the output variable (that is, either a cardiovascular disease risk factor or mental health status variable, see Tables 3.1 and 3.2). The feature elimination process tried to identify the contribution of each variable to predict the class variable and identify its rank compared to others. It recursively discarded those features which even when eliminated from the dataset would not affect the desired accuracy. We used C4.5 as the classification mechanism to predict the class variable. Each variable from the dataset was categorized as *probably irrelevant* or *very likely relevant* variable. A *probably irrelevant* variable is a variable which conveys little or no information about the class variable we are trying to predict. For example, YNGKIDS (number of young kids in the household), CRIMEREC (crime record of the interviewee) have no relevance to class variable Q5_11 (Diagnosed Hypertension). Also any variable which carry no extra information about the class variable was considered as *probably irrelevant.* For example, consider a class variable BMICUTS, variable BMI very much has the same information and so could be conveniently not considered. The inclusion of such variables might have created a bias in the learning algorithm as they will show high correlation between the class variable and hence overshadow the variables of interest. To classify the variables in each of the above classes, all the variables were dropped one at a time and the change in accuracy value of the classification of class variable was noted.

Out of the 334 variables in the BTH 2000 dataset, 76 variables were determined to have little potential bearing with class variables and removed as irrelevant, 86 were removed by feature elimination process. Sixty more variables (considered either irrelevant or recoded) from the remaining 172 variables were with the help of an domain expert, Dr. Timothy Van Wave [2004] who reviewed the dataset for us.

6.1.2 Handling Missing Values in Dataset

After the feature elimination process the dataset had 110 variables and 6251 records. 61,196 data points out of total 687,610 data points had missing value (represented as '$null$' in the dataset) meaning 8.9% of data was missing. While carrying out experiments to do inference learning as well as structure learning of this dataset, all the missing values were replaced with a unique value representing 'unknown'. Records with a missing value for the class variable however were removed from the data set before using the dataset. Thus the data after this process was cleaned for missing data points by simple substitution for null values.

6.1.3 Handling Continuous Values in Dataset

The initial set of experiments using the dataset with 110 variables made the learning process very slow due to the presence of a few continuous-valued variables (variables with more than 10 values). A further assessment of the dataset was then done to handle these variables. Four variables (Q7B, HHSIZE, PCS12 and MCS12) were discretized by range while three variables (DOLLARS, AGE, BMI) were dropped from the dataset. The complete preprocessing process was examined by our domain expert, Dr. Van Wave.

After the data preprocessing phase, there are a further assumptions that we have made about the data. They are: (1) all the variables of the dataset have discrete values, (2) all missing values for all the variables are handled, (3) the records occur independently given the underlying probabilistic distribution of the data, and (4) the volume of data is large enough.

6.2 Two-Fold Cross Validation Testing

N-fold cross validation is a well known technique for testing of dataset for a given method. In our experiments, we verify the effectiveness of the TAN created by the Construct-TAN algorithm against the naive Bayes classifier. The two-fold cross validation divides the data in two folds. The instances are randomly divided amongst the two folds. One of the two folds is then trained using the structure learning algorithm. Then the learned structure is then tested against the other fold and accuracy of the classifier is calculated using confusion matrix of the predicted values of the classifier against the actual values of the classifier. The same procedure is repeated considering the second fold to be the train data and the first fold to be the test data. Average accuracy is thus calculated. Table 6.3 and 6.4 show the two fold cross validation results for all the class variables from Tables 3.1 and 3.2 for both TAN and naive Bayes classifier.

Tables 6.1 and 6.2 show two-fold cross validation results for both mental health status variables and cardiovascular risk factors using Construct-TAN networks and naive Bayes networks. These results show that the Construct-TAN networks outperform the naive Bayes networks for all the mental health status variables, in some cases significantly, and for the cardiovascular risk factors the Construct-TAN networks either perform similarly to the naive Bayes networks or in some cases significantly outperform the naive Bayes networks. This is not entirely surprising as a Construct-TAN network is

Table 6.1 Two-fold cross-validation results for both TAN and naive Bayes for Mental Health Status variables.

Class Variable	*TAN*	*naive Bayes*
Q15NEW2	**99.01%**	96.65%
Q16NEW2	**98.86%**	92.92%
DEPRANX2	**99.60%**	96.52%
ALDPANX2	**99.94%**	97.21%
CWDPANX2	**98.81%**	97.04%
DBDPANX2	**99.77%**	99.47%

Table 6.2 Two fold cross-validation results for both TAN and naive Bayes for Cardiovascular Disease Risk factors.

Class Variable	*TAN*	*naive Bayes*
BMICUTS	92.81%	**93.23%**
EXCERREC	99.64%	**99.93%**
Q69A	**93.13%**	88.66%
CHRONIC	**88.90%**	81.68%
URRURNEW	99.77%	**99.90%**
Q5_11	86.85%	**87.51%**
Q5_12	86.77%	**87.95%**
Q48REC	**97.76%**	97.60%
Q49REC2	98.13%	**98.65%**
OVERWGT2	**99.61%**	97.86%

capable of taking into account the same probability estimates as a naive Bayes network, but it also shows that in many cases, the learned connections in the resulting TAN can significantly increase performance.

6.3 Bayesian Learning for Q5_12: Diagnosed elevated cholesterol

Q5_12, diagnosed elevated cholesterol, is a cardiovascular disease risk factor (see Table 3.1). In this section, the Bayesian learning for Q5_12 using our tool is discussed in detail. Bayesian learning for all the class variables from Tables 3.1 and 3.2 are discussed in brief in the next section.

The main goal of all the experiments conducted is to find the interesting subset of variables from the list of variables which have strong correlation amongst them as well as with the class variable Q5_12. We also intend to find the meaningful links between the variables of interest and analyze them.

6.3.1 Bayesian Network Structure

The tree augmented network created by the tool is shown in the Figure 6.1. The TAN created has 106 nodes and 105 edges. In TAN, the class variable (Q5_12) is connected to all the other nodes in the network. These edges indicate that the class node is a parent of all the nodes. But these edges are not weighted. Our TAN has more than one hundred nodes in the graph and so if we would have shown edges from the class node to all the nodes, it would have made the network crowded. Also it would have made observing meaningful links between the other nodes difficult, and so the network we display does not show the class node.

6.3.2 Top Ten Associations Amongst Variables

The TAN was also analyzed to find interesting links between the variables of our interest. Using the slider in the toolbox, we varied the percentage of links we want to concentrate on. Figure 6.2 shows the top 10% of the links. The mental health status variables which appeared in the diagram are highlighted with red color while cardiovascular disease risk factors are highlighted using blue color. Various randomly selected datasets with at least 3000 records were trained and the structures were studied to find the top links amongst the variables. The top 20 associations between the variables of all networks were compared and the common associations were ranked according to their occurrences in all the networks. The most common top ten associations for predicting the value of Q5_12 are listed in Table 6.3.

Table 6.3 List of top 10 associations to predict the class Q5_12.

Parent	***Child***
STATE	Q5_5
Q56	OVERWGT2
Q56	BMICUTS
CHRONIC	Q52REC
STATE	Q5_6
CHRONIC	Q51REC
STATE	Q5_8
OVERWGT2	Q66A
OVERWGT2	Q65A
CHRONIC	POVEREC

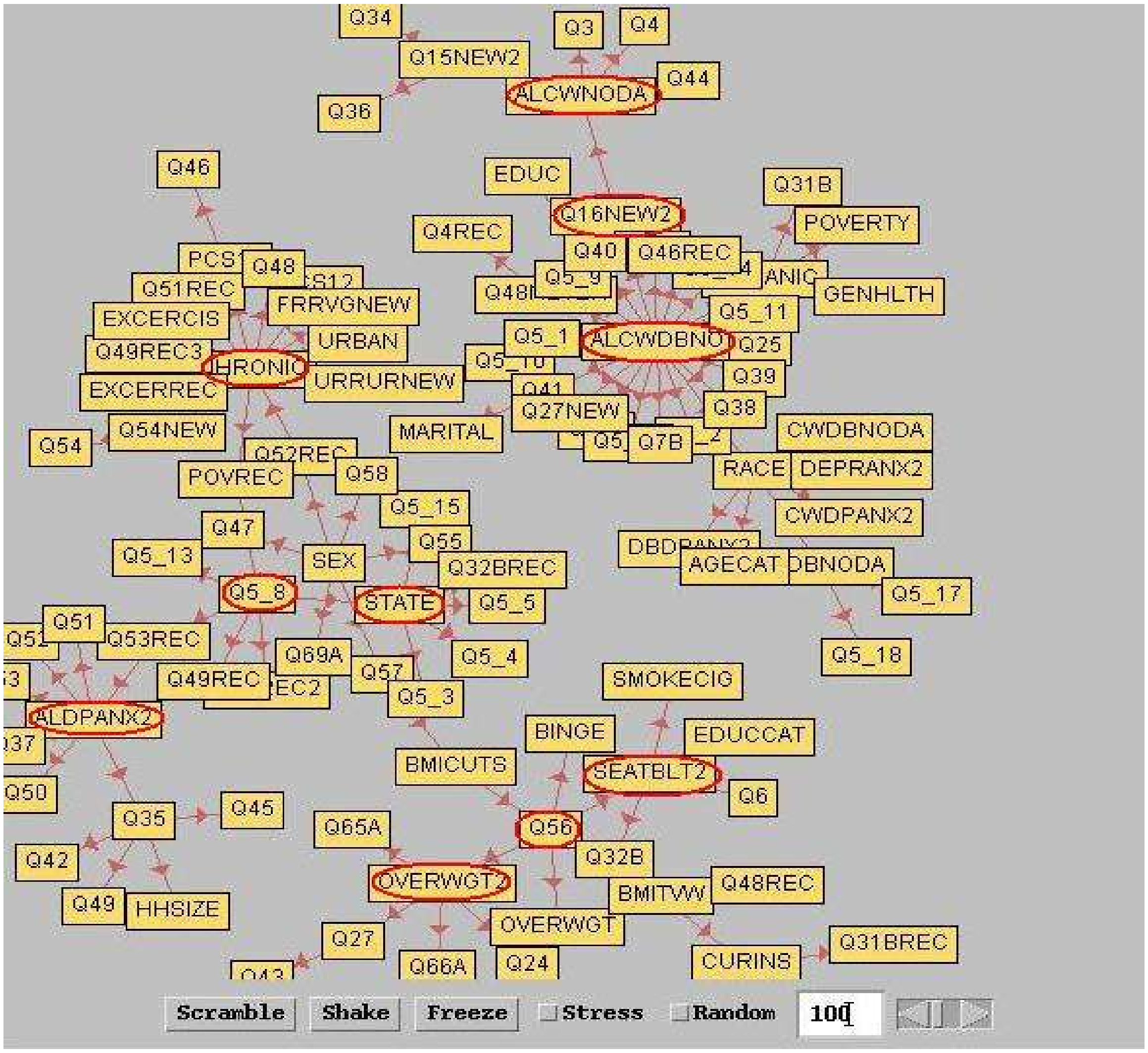


Figure 6.1 TAN for structure learning of class variable Q5_12: Diagnosed elevated Cholesterol.

6.3.3 Top Ten Parent Nodes

We use the same datasets to find the variables which are associated with a larger number of other variables. If any node in the network has a parent node, it means that the value of that child node used to predict the value of class variable is influenced by the value of its parent node and taken into account while classifying the class variable. So we

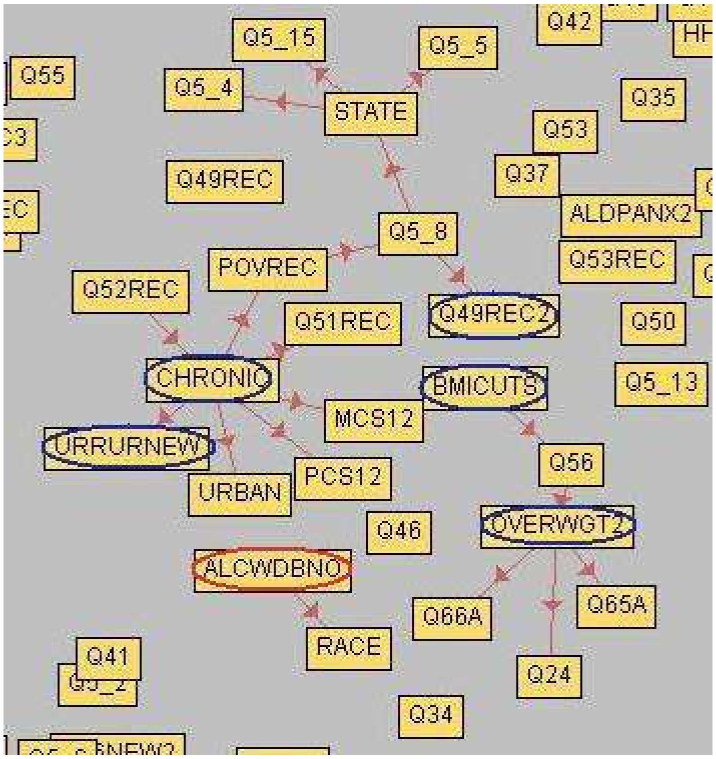


Figure 6.2 Top 10% links for the class variable Q5_12.

can intuitively think that if a node is a parent of many other nodes in the network, its contribution in prediction of the class variable is significant. If we are interested in finding the links between two variables, the parents of both the variables also play a crucial part. An example of this is Figure 6.1. Table 6.2 lists the top 10% of the nodes which are parents of another nodes in the structure. Another use of identifying such parent nodes is to find the nodes at the top of the spanning tree. The nodes from Table 6.2 are highlighted in Figure 6.1. Table 6.2 shows that many nodes of interest like ALCWDBNO, CHRONIC and ALDPANX2 appear in the list of top parent nodes.

6.3.4 Bayesian Multinets

The TAN shown in Figure 6.1 shows the relationship between all the nodes to be the same for all the different values of the class variable Q5_12. The two values (responses, see Table 3.1) of the class variable Q5_12 are 1 (*yes*) and 2 (*no*). Different

Table 6.4 List of top 10 parents to predict Q5_12

PARENT NODE	*NOTES*
ALCWDBNO	Accomplished less and careless work without depression and anxiety. (Mental health status recoded variable)
CHRONIC	Chronic drinker. (Cardiovascular risk factor)
SEATBLT2	Seatbelt used
ALDPANX2	Accomplished less without depression and anxiety. (Mental health status variable)
Q56	Have in home; smoke detector.
STATE	Minnesota/Wisconsin
OVERWGT2	Overweight according to new BMI definition. (Cardiovascular risk factor)
Q16NEW2	Diagnosed Anxiety (Mental health status variable)
Q5_8	Diagnosed heart trouble
ALDBNODA	Accomplished less without downhearted blues and without depression and anxiety. (Mental health status variable)

values of a class variable could have a different structure and hence a different set of augmenting edges. The collection of all the networks with a different value of class variable is called a multinet. We created multinets by partitioning the data according to the values of the class variable.

Figure 6.3 shows a local network for Q5_12 having the value 1. The figure shows cardiovascular disease risk factors like OVERWGT2 and BMICUTS. Since Q5_12 means whether a patient is diagnosed with elevated cholesterol, we can see in the network that general health variables like Q48NEVER (BP never checked) , GENHLTH (general health of a person) and Q4REC (general health compared to others) appear in the top ten percent of meaningful edges. Also we observe an interesting relationship between Q41 (careless work due to emotional problems), Q46REC (felt downhearted and blue – recoded) and Q5_17 (diagnosed with other mental problems). The top parent node for this network is Q35 (moderate activity because of health).

Figure 6.4 shows a local network for those values in which Q5_12: *diagnosed elevated cholesterol* has the value *no*. This network does not give us much information about other interesting variables related to the class variable because not being diagnosed with high cholesterol does not really tell us about other health problems that the person may have. However, the network does confirm directed links between BMICUTS, Q56 and OVERWGT2 which appear in all the networks for Q5_12.

6.4 Bayesian Learning for other variables

There were many class variables that we experimented our tool with. We varied the parameters like the value of class variable and percentage of edges. In this section we present some of the interesting results that we got and their analysis.

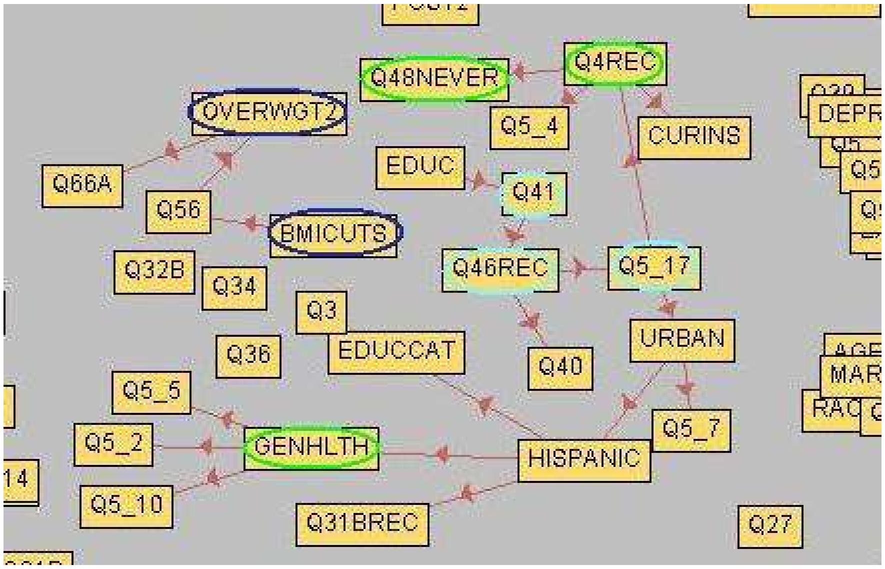


Figure 6.3 shows the local TAN network with top 10% edges of *Q5_12: diagnosed elevated cholesterol* being diagnosed with having elevated cholesterol.

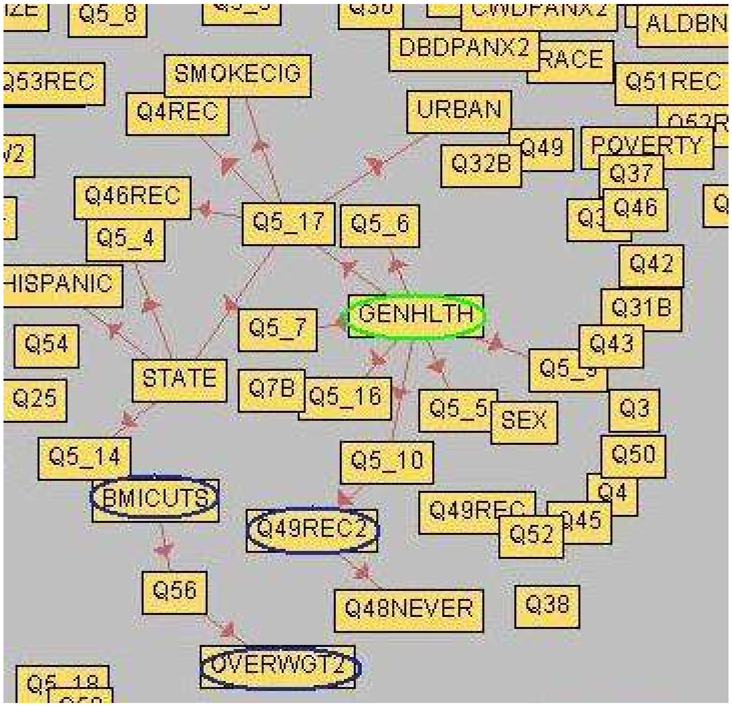


Figure 6.4 shows the local TAN network with top 10% edges of *Q5_12: diagnosed elevated cholesterol* being diagnosed with not having elevated cholesterol.

6.4.1 Bayesian Learning for *Q15NEW2: diagnosed depression*

Figure 6.5 shows a part of the TAN created for class variable Q15NEW2 with class value *'yes'*. The variable OVERWGT2 is connected to Q5_15 (Diagnosed depression). Q5_15 is the parent of the maximum number of variables in this structure and hence influences the classification of the class variable significantly. Q5_15 is shown to be correlated to Q16NEW2 and OVERWGT2.

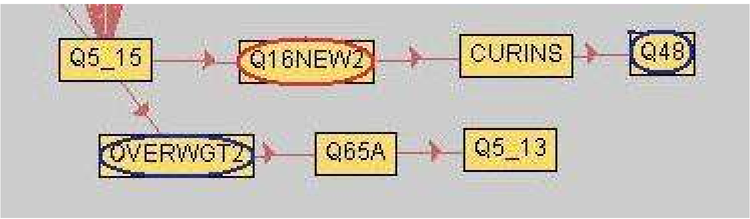


Figure 6.5 shows a part of the structure for Q15NEW2 with class value *'yes'* . The nodes having interesting connections are circled with red and blue.

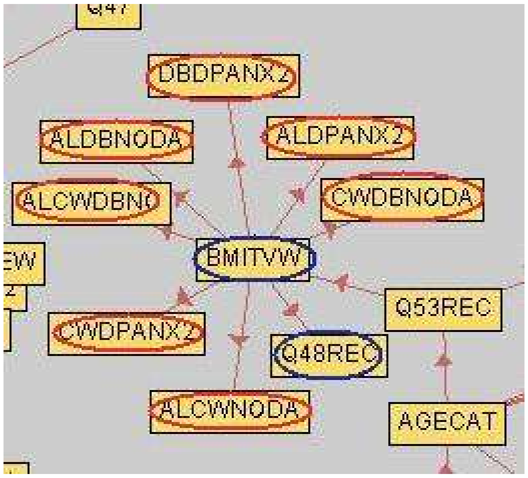


Figure 6.6 shows a part of the structure for Q15NEW2 with class '*yes*'. The nodes having interesting connections are circled with red and blue.

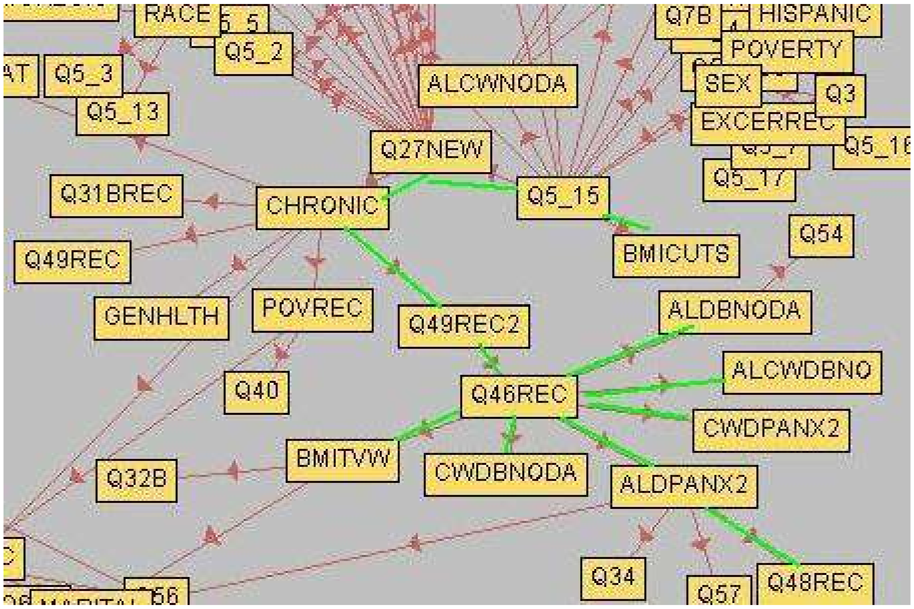


Figure 6.7 shows a part of the structure created for the class variable DBDPANX2 with class value '*yes*'.

Figure 6.6 shows that BMITVW (obese or not) is highly correlated to many mental health status variables like CWDPANX2, ALDPANX2 and DBDPANX2. The same variable is also connected to heart disease related recoded variable Q48REC (Blood Pressure checked in last two years).

6.4.2 Bayesian Learning for DBDPANX2 with Class Value *'yes'*

Figure 6.7 shows correlation amongst several mental health status variables and cardiovascular risk factors. Both Q27NEW and Q5_15 are top ranking parent nodes and are connected to various variables of interest. Q46REC (felt downhearted and blue) is a self assessed mental health status variables and variables like CWDPANX2, ALDPANX2 are recoded using this variable. The link between Q46REC and Q49REC2 shows association between self assessed mental health status variable and risk factor for heart diseases.

6.4.3 Bayesian Learning for Q69A with class value *'yes'*

Figure 6.9 shows the top 10% connections in the network build for the class variable having value 1. The variable SMOKECIG (Cigarette smoking status) show high correlation with variables ALDBNODA and CWDBNODA (recoded mental health status variables). In a fully connected network, as shown in figure 6.8, SMOKECIG shows connections with CHRONIC and EXCERREC as well.

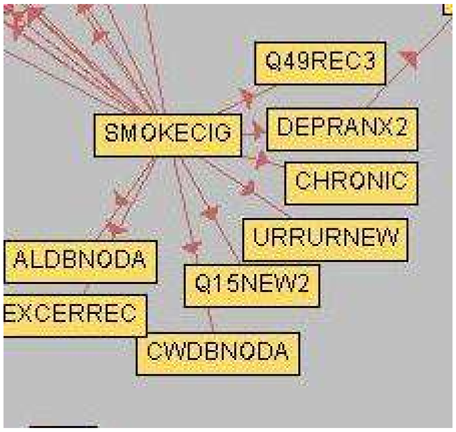


Figure 6.8 shows a part of network build for Q69A (Current smoker) with class value *'yes'*. The network shows variable SMOKECIG connected to various other mental health status variables in the system

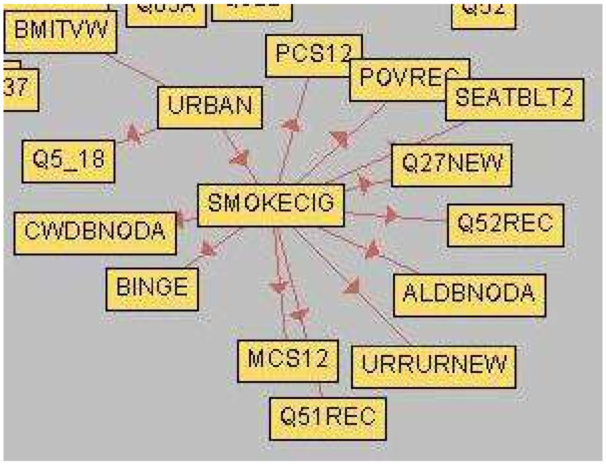


Figure 6.9 shows a part of network build for Q69A (Current smoker) with class value *'yes'*. The network shows the top 10% connections amongst variables in the network.

Chapter 7: Related Work

In this chapter, we discuss other research that is related to what we present in this thesis and discuss how our research differs. Section 7.1 discusses a technique which classifies survey data using Bayesian modeling. Section 7.2 presents an example of the usage of the TAN algorithm for classification of gene expression data. Finally we discuss a similar Bayesian network toolbox in section 7.3. The last section discusses other related work.

7.1 Survey Data using Bayesian Modeling

Sebastiani and Ramoni [2001] use Bayesian modeling techniques to analyze a data set extracted from a British General Household survey. They believe that instead of presenting the statistical findings via contingency tables relating two or three variables at a time, building a model to show association between large numbers of variables would give a better picture of data. Their approach, the K2 algorithm as proposed by Cooper and Herskovitz [1992], searches for a model within a subset of networks (rather than all possible networks) in which there would be significant directed associations. The modeling of the data was carried out with the program Bayesware Discoverer [BD, 2004] which implements the model search approach described earlier. Bayesian modeling was done on thirteen variables indicative of the composition of British households. The dataset used for Bayesian modeling was limited to only thirteen variables. In our analysis of data, we have included all the features from the dataset (over a hundred) which could be potentially useful.

7.2 TAN algorithm for Classification

Mittal et al, [2004] in their work use TANs as a classification method to classify a protein into different structural and fold classes. Their implementation framework is called BAYESPROT, in which they have incorporated two methods, feature discretization and a Mean Probability Voting (MPV) scheme, in addition to the TAN classifier. The preprocessing of data is done by extracting attributes from the dataset and converting them into features of six different categories, and then a feature discretization method is used to discretize the values of features. Frequency discretization is applied to two significant categories, namely Composition and Secondary Structure, separately while all the other categories discretized together. The TAN Bayes classifier routine is then applied to each set of features separately and then finally MVP scheme is used to predict the Structure class and Fold class value individually. In their work, the TAN was used mainly for classification. However our thesis exploits the structural information extracted from the TAN algorithm as well.

7.3 Bayes Net Toolbox

The Bayes net toolbox (BNT) is an open source package implemented in MATLAB for probabilistic models [Murphy 2003]. Major features of the BNT include support for exact and approximate inference, support for both dynamic and static Bayesian networks, parameter learning and structure learning. It also supports various types of conditional probability distributions. The visualization aspect of BNT is limited to MATLAB graphs and some plotting routines. The support is too basic for the size of data we are representing in our tool.

7.4 Other Related Work

Dr. Van Wave [2004] in his secondary analysis of the BTH 2000 dataset suggests that significant associations exist between self-assessed and physician-diagnosed mental health status variables and heart disease risk factors. In his research, two-way contingency table analysis was used to evaluate the statistical relationship between the mental health status variables and cardiovascular risk factors. Pearson's Chi-Square and Odds ratios were used to estimate the independence between the above mentioned variables. He suggests that early intervention addressing poor mental health status and recognized heart disease risk factors may work together to reduce heart disease risk more effectively. His work is significant to our thesis in many ways. His analysis of the BTH 2000 dataset with promising results inspired us to identify the association between the above mentioned variables in broader perspective, considering all the other variables of the dataset. In this work we focus on analyzing the BTH 2000 dataset using the Bayesian methods.

Takale [2004] in his thesis has developed a predictive model to identify the predictors of mental health status (MHS) variables and cardiovascular disease risk factors (CRF). In his thesis, he has built a genetic algorithm based system employing decision trees to identify good, small subsets of features having high classification accuracy. The predictive model also establishes relationships within the data, especially between MHS and CRF. The predictive model identifies a subset of the dataset with high accuracy to classify the class variable whereas our thesis identifies dependencies between all the variables in the dataset.

Chapter 8: Future Work

In this chapter we discuss future enhancements that could be made to our current work. In the first section we talk about the work that can be done with regards to the tool that we created. We then talk about the changes that can be made to the theoretical aspects of the algorithm that we employ.

8.1 Practical Aspects

In this section we talk about possible enhancements that can be made to the toolbox that we created. The following are the suggested enhancements that can be made to the tool: (1) support for various data formats, (2) support for continuous variables and missing values, (3) make more interactive, (4) provide more visualization, (5) incorporate various inference algorithms, and (6) make an API available.

There are various different data formats available online. A few examples of data formats are BIF, BNET and HUGIN. We can add facilities to read the data in these formats. Another feature that can be added is to save the results that we get in a user chosen format.

Currently we do not use continuous variables in our data. Future enhancements can incorporate the use of such variables. Also, we could handle missing values better, instead of just replacing them with a fixed value like we do now.

The toolbox could be made more interactive. We could add features like displaying the conditional probability tables related to each node when a user clicks on the node. We can also provide other information such as the data distribution for a particular node. We can provide the option of zooming on a particular area of the network. These enhancements can make the tool more interactive and produce more effective visualization.

Another aspect which we can improve is the way we do inference. We can let the user choose which inference algorithm he/she wants to use to do inference. We would need to implement more inference algorithms in our code to provide such a functionality.

Finally we can make the API of our code available online so that other users that are creating applications similar to ours can interface their code with ours.

8.2 Theoretical Aspects

In this section we will talk about what changes could be made to the algorithm that we used to create our tool. The following are the suggested enhancements that can be made to the current system: incorporate other algorithms to do structure learning and learn model with hidden variables.

One possible future enhancement to the current system could be to incorporate other structure learning algorithms or even create some hybrid algorithm that uses both our current algorithm and some other algorithm to learn the structure.

We assume that the survey dataset is fully observable, that is there are no hidden variables in the system other than those in the dataset. So Bayesian learning is done to find the structure of the data. However there could be some hidden variables which are not represented in the structure. Sometimes it is convenient to introduce hidden variables in the system. If these variables are identified, they could represent the structure of the data more compactly, improve structure accuracies, and also save some computation time. Parameter learning methods for networks with hidden variables have been developed [Russell et al, 1995]. Any future work can involve considering hidden variables while creating the network.

We can embed an algorithm for estimating statistical confidence like the one suggested by Friedman [2000]. Currently, the tool has a choice of viewing the given percentage of Markov related features. However, if we are able to determine the order of confidence relations amongst the features, we can incorporate this structure into our tool.

Chapter 9: Conclusions

Bayesian learning is an effective method to learn the structure of data in a variety of applications. We used Bayesian learning to learn the structure of the BTH 2000 dataset, given a class variable from the features of interest, and to identify meaningful links in the data. The same dataset was also used to find such links in the data using statistical methods like Pearson's Chi Square and odds ratio by Dr. Van Wave [2004]. Our approach of using the Bayesian learning is an extension to the simple statistical methods.

We implemented the Construct-TAN algorithm in our tool and displayed the resulting Bayesian structure and added simple features to our tool to visualize the structures effectively. We also implemented inference learning to verify the effectiveness of our tool.

Experiments with our toolbox showed that the accuracy of the TAN built by our tool was comparable to that of a naive Bayesian network created using the same dataset. We observed that the accuracy of TAN is generally well above 80%. Various structures with different parameters were studied to identify links in the dataset between the features of interest, and the results were discussed with the domain expert, Dr. Tim Van Wave, who found them to be meaningful.

The tool seems to be a good direction to incorporate Bayesian theory to not only learn the structure of data but also to visualize it effectively. Such tools find applications to learn from large survey dataset available. This work can be considered as the starting point for other works which can incorporate more features like visualization of a subset of data, facility of changing (fixed value) the value of class variable and seeing the structure formed at runtime. We also believe that this tool will help in understanding the relationship between cardiovascular and mental health diseases. It will help the concerned authorities to identify various risk factors related to both kinds of diseases and try and reduce such cases.

Bibliography

[Bazell and Aha, 2001] Bazell D. and Aha D. 2001. Ensembles of Classifiers for Morphological Galaxy Classification, *Astrophysical Journal,* 548, 219-223.

[BD, 2004] http://www.bayesware.com/products/discoverer/student.html 2004. *Bayesware Discoverer.*

[Berrou et al, 1993] Berrou, C., Glavieux, A. and Thitimajashima, P. 1993. Near Shannon Limit Error-Correcting Coding and Decoding: Turbo Codes. *Proceedings of the IEEE International Communication Conference.*

[Block et al, 2000] Block, D., Kinney, A., Sundberg, L., Peterson, J., Kelly, G. and Bridge To Health Collaborative. 2000. Bridge to Health Survey 2000: Northeastern Minnesota and Northwestern Wisconsin Regional Health Status Survey. *Available from Community Health Department,* St. Mary's/Duluth Clinic Health System, 407 E Third Street, Duluth.

[Cheng and Druzdzel, 2000] Cheng J. and Druzdzel M. 2000. AIS-BN: An Adaptive Importance Sampling Algorithm for Evidential Reasoning in Large Bayesian networks. *Journal of AI Research,* 13:155-188.

[Cheng et al, 1997] Cheng, J., Bell, D., Liu, W. 1997. Learning Bayesian Networks from Data: An Efficient Approach Based on Information Theory. *In proceedings of ACM CIKM'97.*

[Chow and Liu, 1968] Chow, C. and Liu, C. 1968. Approximating Discrete Probability Distributions with Dependence Trees. *IEEE Transactions on Information Theory,* Vol. 14, Pg 462-467.

[Cooper and Herskovits, 1992] Cooper, G. and Herskovits, E. 1992. A Bayesian Method for the Induction of Probabilistic Networks from Data. *Machine Learning*, 9, 309-347.

[Darrech and Ratcliff, 1972] Darrech J. and Ratcliff D., 1972. Iterative Scaling for Log Linear Models. *Annals of Mathematical Statistics*, 43[5]: 1470-1480.

[Dietterich, 1999] Dietterich, T. 1999. Machine Learning. In Rob Wilson and Frank Keil (Eds.) *The MIT Encyclopedia of the Cognitive Sciences*, MIT Press.

[Domingos and Pazzani, 1997] Domingos, P. and Pazzani, M. 1997. Beyond Independence: Conditions for the Optimality of the Simple Bayesian Classifier. *Machine Learning,* 29, 103-130.

[Friedman and Goldszmidt, 1996] Friedman, N. and Goldszmidt, M. 1996. Building Classifiers Using Bayesian Networks, *Thirteenth National Conference on Artificial Intelligence.*

[Friedman et al, 1997] Friedman, N., Geiger, D. and Goldszmidt, M. 1997 Bayesian Network Classifiers. *Machine Learning*, 29:131-163.

[Friedman et al, 2000] Friedman, N., Linial, M., Nachman, I., and Pe'er, D. 2000. Using Bayesian networks to analyze expression data. *J. Comput Biol*, vol 7, 601-620.

[Fung and Crawford, 1990] Fung, R.M. and Crawford, S.L., 1990. Constructor: A System for the Induction of Probabilistic Models, *Proceedings of the Seventh National Conference on Artificial Intelligence.*

[Heckerman 1995] Heckerman D., 1995. A Tutorial on Learning with Bayesian Networks. MSR-TR-95-06, *Microsoft Research.*

[Heckerman et al, 1995] Heckerman, D., Geiger, D. and Chickering, D. 1995. Learning Bayesian Networks: The Combination of Knowledge and Statistical Data. *Machine*

Learning, 20, 197-243.

[Herskovits and Cooper, 1990] Herskovits, E. and Cooper, G. 1990. Kutató: An Entropy Driven System for the Construction of Probabilistic Expert Systems from Databases. *In Proceedings of the Sixth Conference on Uncertainty in Artificial Intelligence*.

[Jamshidian and Jennrich, 1993] Jamshidian M. and Jennrich R. 1993. Conjugate Gradient Acceleration of the EM Algorithm. *JASA*, 88[421]:221-228.

[Jensen et al, 1990] Jensen F., Lauritzen S. and Olesen K. 1990. Bayesian Updating in Causal Probabilistic Networks by Local Computations. *Computation Statistics Quarterly,* 4:269-282.

[Jordan et al, 1998] Jordan, M., Ghahramani, Z., Jaakkola, T. and Saul,L. 1998. An Introduction to Variational Methods for Graphical Models. *Learning in Graphical Models.* MIT Press.

[Kim et al, 2002] Kim S., Seo H. and Rim H. 2003. Poisson Naive Bayes for Text Classification with Feature Weighting. *International Workshop on Information Retrieval with Asian Languages.*

[Koller et al, 1997] Koller, D., Binder, J., Russell, S., and Kanazawa, K., 1997. Adaptive Probabilistic Networks with Hidden Variables. *Machine Learning*, 29:213-244.

[Lam and Bacchus, 1994] Lam, W. and Bacchus, F. 1994. Learning Bayesian Belief Networks. An Approach Based on the MDL Principle. *Computational Intelligence*, 10, 269-293.

[Lauritzer, 1995] Lauritzer, S. 1995. The EM Algorithm for Graphical Association Models with Missing Data. *Computational Statistics and Data Analysis,* 19:191-201.

[MacKay, 1998] MacKay, D. 1998. Introduction to Mote-Carlo Methods. *Learning in Graphical Models*. MIT Press.

[Mittal et al, 2004] Mittal, A., Chinaswamy, A. and Sung, W. 2004. Protein Structure and Fold Prediction Using Tree-Augmented Bayesian Classifier. *In Pacific Symposium on Biocomputing*.

[Mitchell, 1997] Mitchell, T. 1997. *Machine Learning,* McGraw Hill.

[Murphy, 2001] Murphy, K. 2001. The Bayes Net Toolbox for MATLAB. *Computing Science and Statistics*, vol 33.

[Murphy, 2003] Murphy, K. 2003. *Bayes Net Toolbox v5 for MATLAB.*

[NCCDPH, 2004] www.cdc.gov. 2004. *National Center for Chronic Disease Prevention and Health Promotion.*

[Neal, 1993] Neal, R. 1993. Probabilistic Inference Using Markov Chain Monte Carlo Methods. *Technical Report, University of Toronto.*

[NMHA, 2001] http://www.nmha.org/infoctr/factsheets/15.cfm 2001. *National Mental Health Association.* Mental Illness and the Family: Mental Health Statistics.

[Pearl 1988] Pearl J., 1988. Probabilistic Reasoning in Intelligent Systems: Networks of Plausible Inference, *Morgan Kaufmann.*

[Ramoni and Sebastini, 1997] Ramoni, M. and Sebastini, P. 1997. Learning Bayesian Networks from Incomplete Databases. *UAI.*

[Rodrigues et al , 2000] Rodrigues, M., Liu, Y., Bottaci, L. and Rigas, D. 2000. Learning and Diagnosis in Manufacturing Processes Through an Executable Bayesian

Network. *13th International Conference on Industrial and Engineering Applications of Artificial Intelligence and Expert Systems IEA/AIE-2000.*

[Rusell et al, 1995] Rusell, S., Binder, J., Koller, D., and Kanazawa, K. 1995. Local Learning in Probabilistic Networks with Hidden Variables. *In Proceedings of the Fifteenth International Joint Conference on Artificial Intelligence*, pp. 1146-1152 Montreal, Canada.

[Sahami et al, 1998] Sahami M., Dumais S., Heckerman, D. and Horvitz E. 1998. A Bayesian Approach to Filtering Junk E-Mail. *In Learning for Text Categorization, Papers from the 1998 Workshop. AAAI Technical Report* WS-98-05.

[Sebastiani and Ramoni, 2001] Sebastiani, P. and Ramoni, M. 2001. On the Use of Bayesian Networks to Analyze Survey Data. *Research in Official Statistics*, 4(1), 53-64.

[Sebe et al, 2002] Sebe N., Lew M., Cohen I., Gary A. and Huang T. 2002. Emotion Recognition Using Cauchy Naive Bayes Classifier. *International Conference on Pattern Recognition*, Volume 1.

[SGR, 1999] http://www.surgeongeneral.gov/library/mentalhealth/home.html 1999.
Mental Health: A Report of the Surgeon General.

[Spirtes et al, 1990] Spirtes, P., Glymour, C. and Scheines, R. 1990. Causality from Probability. *Proceedings of Advanced Computing for the Social Sciences*, Williamsburg, VA.

[Srinivas et al, 1990] Srinivas, S., Russell, S. and Agogino, A. 1990. Automated Construction of Sparse Bayesian Networks from Unstructured Probabilistic Models and Domain Information. *In Henrion, M., Shachter. R.D., Kanal, L.N. and Lemmer, J.F. [Eds], Uncerta.*

[Stavrulaki et al, 2003] Stavrulaki, E., Fong D. and Lin D. 2003. Two-Resource Stochastic Capacity Planning Employing a Bayesian Methodology. *Journal of the Operational Research Society*. pp. 1198-1208.

[Stephen and Steven, 1986] Stephen, B. and Steven, N. 1986. Knowledge Engineering Within a Generalized Bayesian Framework. *Proceedings of the 2nd Annual Conference on Uncertainty in Artificial Intelligence (UAI-86).*

[Suzuki, 1996] Suzuki, J. 1996. Learning Bayesian Belief Networks Based on the Minimum Description Length Principle: An Efficient Algorithm Using the B&B Technique. *In Proceedings of the Thirteenth International Conference on Machine Learning,* 462-470.

[Takale, 2004] Takale, A. 2004. Constructing Predictive Models to Assess the Importance of Variables in Epidemiological Data Using A Genetic Algorithm System employing Decision Trees. *Submitted as Master's Thesis*, Computer Science Department ,University of Minnesota, Duluth.

[Tenenbaum et al, 1995] Tenenbaum, A., Langsam Y. and Augustein, M. 1995. Data Structures Using C and C++. Second Edition. *Prentice Hall.*

[Van Wave, 2004] Van Wave, T. 2004. Secondary Analysis of Bridge to Health Survey 2000 Dataset Using Statistical Methods. Unpublished Work. *Department of Family Medicine, University of Minnesota Dulut*h.

[Wallace et al, 1996] Wallace, C., Korb, K. and Dai H. 1996. Causal Discovery via MML. *Proceedings of the Thirteenth International Conference on Machine Learning ICML'96*, pp. 516-524.

[Wermuth and Lauritzen, 1983] Wermuth, N. and Lauritzen, S. 1983. Graphical and Recursive Models for Contingency Tables. *Biometrika,* 72, 537-552.