東　　海　　大　　學

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碩士論文

貝氏網路之醫療品質指標網之研究
—以急性照護指標為例

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A BN-Based Healthcare Quality Indicator Network
—An Application in Acute Care Indicators

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Abstract

In recent years, healthcare quality in Taiwan has become an increasingly important issue for the government, for the hospitals, and for the public. In order to survey and ultimately improve healthcare quality, the Taiwan Joint Commission on Hospital Accreditation (TJCHA) has imported, from the Maryland Hospital Association (MHA) in the United States, the *Quality Indicator Project* (QIP). TJCHA has re-named the Maryland QIP the *Taiwan Quality Indicator Project* (TQIP), and has been devoted to implementing the TQIP program in domestic hospitals.

At present, the TQIP is comprised of multiple sets of performance indicators for measuring four different pattern care settings of the hospital system: Acute Care, Psychiatric Care, Long-term Care, and Home Care. Each care setting uses numerous TQIP indicators for measuring quality. Among hospitals, statistical profiling is a generally accepted method for assessing healthcare quality. Statistical profiling allows hospitals to predict certain outcomes of the healthcare process and to thus survey the various causes that affect quality performance. However, the data from these indicators cannot be used, independent of an appropriate analysis method, to determine relationships among healthcare quality settings. TQIP indicators merely provide data for various settings within the healthcare system. Therefore, this study proposes a method for analyzing the relevance and uncertainty among data gathered from TQIP indicators. In addition, we devise a feasible mechanism, involving Bayesian Networks, to solve problems of structure and parameter requirements for the TQIP indicators. We provide hospitals with an objective auxiliary-assessment for indicator-data analysis and check whether it implies certain probability relationships among these TQIP indicators.

Keywords: Healthcare Quality, the Taiwan Quality Indicator Project, Bayesian Networks

貝氏網路之醫療品質指標網之研究
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中文摘要

近年來，無論政府、各醫院及社會大眾，醫療品質已逐漸成為一項重要關心的議題。為了加以監控及改善醫療品質，財團法人醫院評鑑暨醫療品質策進會（簡稱醫策會）引進美國馬里蘭醫院協會所主導的「醫療品質指標計畫」(Quality Indicator Project，簡稱 QIP)，以「台灣醫療品質指標改善計畫」(Taiwan Quality Indicator Project,簡稱 TQIP)，在國內致力於醫療品質指標計畫之推動。

目前，台灣醫療品質指標改善計畫已引進的照護指標群，計有急性照護、長期照護、精神照護及居家照護等，各群組下有不同的指標。對醫院而言，使用統計輪廓 (Statistical Profiling)來評估醫療品質是常用的方式，在統計管制下，醫院可以預測判斷流程上影響及品質造成的原因變異來檢視對品質的影響。然而，這些指標並非獨立使用卻透過衡量結果反映出不同醫療照護層面的醫療品質現況。因此，本研究由急性照護 TQIP 醫療指標群以貝氏網路來分析機制來衡量指標間相關程度及不確定性，並找出 TQIP 指標的非線性網路架構來協助醫院監控醫療品質且是否有隱含指標間機率性關係存在，同時，協助醫院在操作 TQIP 指標有客觀的衡量依據。

關鍵字：醫療品質、台灣醫療品質指標改善計畫、貝氏網路

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轉眼間，已經是碩士生涯的最後時刻，竟是要道別的時候，剎時一股莫名的感覺湧上心頭，不知是喜、是悲，亦或是不捨，這兩年的回憶如放映機上的影片般，不停地在播放這兩年在這裡的所有回憶。

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智慧型系統研究室 ISRG

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CHAPTER 1 INTRODUCTION

1.1 Research Background

Healthcare Quality

With the implementation of the “Bureau of National Health Insurance, BNHI” in 1995, the public has obtained comprehensive medical care (disease prevention, clinical care, hospitalization, residential care, and social rehabilitation) via insurance pooling. Among participating hospitals, the resources available for patients seeking medical service have been increased substantially. Nevertheless, for the NHI (National Health Care) program, the substantial volume of ambulatory care and contracted inpatient claims has resulted in a waste of medical resources and an increase in insurance fees. Furthermore, for each level of hospitals, since the startup of NHI program, those hospitals have had to face the pressure of competition among themselves. Recently, as the BNHI has been committed to establishing a suitable management-style for the National Health Insurance part II, healthcare quality remains an important issue as do controlling insurance payments. The importance of establishing and maintaining quality of healthcare has been a constant point of contention among hospitals, legislatures and the public.

Prior to 1990 [3], several medical establishments, such as National Taiwan University Hospital (NTUH) and Veterans General Hospital (VGH), in response to requests from hospital management, adopted and began to implement the “JCAHO (Joint Commission of Accreditation on Healthcare Organization) Ten Steps” of Quality Assurance from the United States. By 1992, Chang-Hua Christian Hospital (CCH) first imported the “Total Quality Management, TQM” from the U.S., which is comprised of some very important paradigm shifts. As a result, focusing on the patients and customer-oriented, high-quality medical services have become the standards for competition among medical service providers.

Measurements imply management and improvement. Nowadays, with ever more attention being paid to increasing the quality of healthcare, the objective measurement of clinical service and healthcare quality is indispensable. The medical quality indicators have been generally acknowledged as an effective

tool with high credibility for the increase of healthcare quality via objective data. Quality indicators can be seen as guidelines of assessment for the outcome and management of patient's healthcare. The goal is to provide standardized measurements of clinical efficiency and cost-effectiveness in healthcare [6]. For this reason, Taiwan Joint Commission on Hospital Accreditation (TJCHA) imported Quality Indicator Project (QIP) from Maryland Hospital Association (MHA) in U.S. as of 1999. Now named the Taiwan Quality Indicator Project (TQIP), it is a system devoted to achieving increases in healthcare quality. At present, QIP has compiled four sets of performance indicators for different care settings: acute care, psychiatric care, long-term care, and home care. Each indicator set has numerous measurements for which a facility can submit data and receive comparative feedback [27]. For example, the Acute Care indicator-set includes inpatient, outpatient and emergency ratings and totals 310 criteria by which the care setting can be assessed.

Using statistical profiling to assess healthcare quality has become an accepted methodology. Continuous and long-term measurements can reveal to monitor the performance of timely procedures such as early warnings for unusual tendency that depend on statistical process control (SPC) methods. Using statistical control methods, hospitals can analyze various processes and quality factors to identify potential causes affecting quality performance [13]. However, these methodologies focus mainly on surveying cause variances of only one indicator. These indicators reflect different levels of the healthcare system via the measurement data. Our research intends to, by using the artificial intelligence applications such as Bayesian Approach (see below), to analyze the relativity and uncertainty among these indicators. We are trying to discover the nonlinear network structure for TQIP indicators and to help hospitals survey the quality performance and best utilize the relationships among these indicators.

Bayesian Approach

In this study, the main stress falls on learning relationships among the observations of TQIP indicators and compiling them into a consistent mesh that can reveal the current state of healthcare quality, or an appropriate abstraction. Such meshes or networks of cause-effect relationships may be called causal models. The Bayesian Network (BN), a graphical model of these meshes, is able to more clearly represent cause-effect relationships and analyze criteria-based causal relationships. Discovering and analyzing multiple criteria-based causal

relationships of the healthcare system is our research goal.

A Bayesian network is a graphical model which encodes probabilistic relationships among a set of variables. Over the last decade, the Bayesian network has become a popular representation for encoding uncertain expert knowledge in expert systems [23]. More recently, many methods for learning Bayesian networks from data have been developed. These techniques have proven remarkably effective for some data-analysis problems.

Bayesian networks and Bayesian methods can offer at least four advantages over other techniques for data analysis [22]. One, Bayesian networks can easily handle incomplete data sets. When one of the inputs is not observed or missed, for example, most models will produce an inaccurate prediction. Bayesian networks offer a natural way to encode such dependencies. Two, Bayesian networks allow one to learn about causal relationships. The use of BN helps to gain understanding about a problem domain and answer certain questions even when no experiment about the effects of increased exposure to any incomplete data is available. Three, Bayesian networks, used in conjunction with Bayesian statistical techniques, can facilitate the combination of domain knowledge and data. Four, Bayesian methods provide an efficient and principled solution for over-fitting of data. That is, Bayesian methods naturally integrate all the available data in the BN.

1.2 Research Method and Goals

Healthcare quality is an important issue for hospitals, and TQIP indicators are effective tools for assessing and monitoring the quality performance of hospitals. At present, linear analytical methods, such as statistical process control applications, are widely adopted by hospitals. Hospitals want to realize where, if anywhere, the cause variances exist. These observations show that hospitals are analyzing and monitoring their process variances, but just for one certain indicator.

This study hopes to use the nonlinear analytical method of the Bayesian approach to analyze multiple indicators simultaneously. First, we focus on the acute care indicators of TQIP and the level of medical centers. Second, we construct a learning mechanism to learn the Bayesian network by combining the domain knowledge and data. Third, we construct an inference mechanism to

realize the causal relationships among these indicators. Finally, interested hospitals are provided the network structure as a whole for analyzing TQIP indicators. There are four issues to be tackled in this study.

1. Assess the feasibility for applying the Bayesian approach to TQIP analysis.
2. Understand if these indicators, when adopted by hospitals, can determine the present level of quality by using Bayesian networks.
3. Identify any previously unknown variables between the relationships of these indicators.
4. Monitor the quality of hospital-based healthcare as a whole.

This study plans to use TQIP indicators to build up an analytical "Warning System" for hospital care which is based on Bayesian networks. Moreover, we aim to devise and construct a feasible and rational Bayesian network and mechanism for parameter modification of TQIP indicators.

1.3 Research Scope and Constraints

The following comes within the scope and constraints of this study:

1. The main objects are "Acute Care Indicators" that give priority to inpatient, emergency, and outpatient departments.
2. These indicators range from January 1, 2000 to December 31, 2004.
3. We take the complete dataset into consideration.
4. Although the value of each indicator item is recorded monthly, time is not a variable for the Bayesian Learner.

1.4 Research Significance

Bayesian Application

Bayesian networking, as a knowledge representation tool, can demonstrate and apply our ideas for evaluating a situation. With the probabilistic properties and learning capability of Bayesian networks, one can more easily deal with the uncertainty and dynamics of certain domain problems. This study attempts to apply the Bayesian approach to the probing of correlative dependencies among TQIP indicators. Then, this study hopes to find a learning mechanism for applying Bayesian networks to TQIP networks

under appropriate assumptions beyond the function of time. Moreover, depending on the indicators' framework, we can attempt a cross-referencing to find the causal relationships among them as well.

For hospitals

Healthcare quality is gradually becoming a big issue for hospitals no matter in rising patient expectations or the government regulations. Hospitals are having to pay increasingly more attention to quality-care surveillance, whether it be clinical, inpatient, or ambulatory. Hospital are required to be increasingly aware of what affects quality of care by using statistical profiling methods to analyze the cause variance behind indicators. This study provides hospitals with a nonlinear analytical methodology, the Bayesian approach, adopted from artificial intelligence applications. We hope and expect that the advantages of Bayesian networking, applied to the TQIP indicators, will provide hospitals with a more comprehensive method for analyzing healthcare quality and correlatives.

1.5 Thesis Framework

There are five chapters in this study, shown in Figure 1.1. Chapter I illustrates the reason for applying the Bayesian approach to healthcare indicators. Chapter II surveys related literatures with special emphasis on medical-care circumstances and the Bayesian approach. Chapter III presents a BN-based model for which we elaborate on the procedures for implementation in the healthcare system. Chapter IV applies the BN-based model to TQIP indicators and proposes a performance measure. Chapter V illustrates the conclusions and future research.

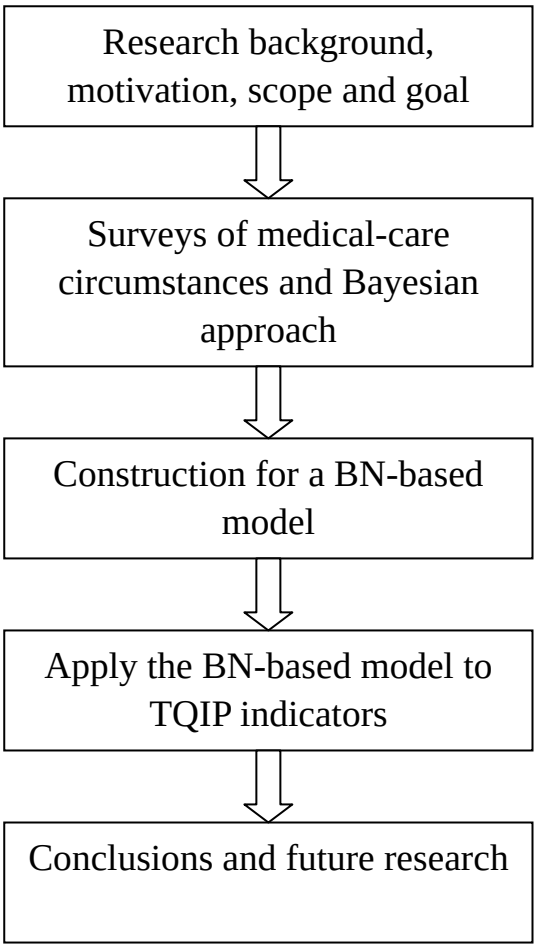

Figure 1.1 The thesis framework.

CHAPTER 2 LITERATURE REVIEW

2.1 Healthcare Quality and Assessment

Healthcare quality can be defined as a social service that, after accounting for the risk, benefit and cost for medical treatment, achieves a maximum benefit for the patient while maintaining minimal risk and cost. Han [9] considered quality healthcare, for patients and hospitals, to include both the evaluation of a patient's health by a doctor, and the evaluation of a treatment's effects for achieving patient satisfaction for which hospitals strive. The healthcare system (institutions, work-force, facilities, execution, etc.) is charged with the responsibility of alleviating rational health burdens of patients and society.

Donabedian [20] submitted the earliest and most cited definition of healthcare quality: use minimal risk and cost to achieve the most appropriate health condition, and analyze the structure of medical quality via the framework of structure, process and outcome. On the whole, healthcare quality includes the medical specialties as well as patients' satisfaction and can be divided into technical and service areas. Hence, in assessing healthcare quality, we must take into consideration the viewpoint of both doctors and patients as operating within the framework of structure, process, and outcome. In other words, our evaluation of healthcare quality must include both the technical aspects of medical science and the doctor-patient relationship that develops in the course of treatment. Only after such a comprehensive evaluation, can we hope to meet patients' expectations and requirements and increase medical efficiency.

Consulting on healthcare quality is based primarily on the structure-process-outcome framework and the patient's individual circumstances. These are important factors affecting treatment results. The purpose for assessing healthcare quality is to ascertain whether treatment goals have been met. The purpose for controlling healthcare quality is to proceed with continuous surveillance. For these purposes, measuring and manipulating quality assessment must be based on specialized standards and criteria. Therefore, Joint Commission of Accreditation on Healthcare Organization (JCAHO) has submitted the "Identification Indicators" method for monitoring and assessing healthcare quality. These "Indicators" are measurable standards

that are related to the system structure, execution processes, and treatment outcomes [29].

Ni [6] considered integration of related apparatuses into the healthcare system, using current medical knowledge and resources, necessary to increasing the quality of the structure-process-outcome framework. This reasoning hopes to promote widely accepted and efficient standards of care within the healthcare profession for patients, and to decrease the chances of ineffective or inappropriate care.

Domestic hospital-survey programs depend mostly on indicators of a structural type (i.e., hospital scale, hospital level, teaching conditions, number of medical practitioners and staff) to assess quality. Few indicators are process and outcome oriented (patient history, mortality, etc). Recently, as healthcare quality is being increasingly valued, the field of assessing healthcare quality has been expanded to include healthcare process and outcome. Indicators of process and outcome will need to play an increasingly larger role in assessing healthcare quality.

2.2 Indicators for Healthcare Quality

Healthcare quality utilizes objective evidences for quantification and standardization. Before proceeding with improvements, one must measure clinical services in process and healthcare quality in outcome. The quality and clinical indicators, as defined by JCAHO, are quantified measurements of healthcare. Those indicators can be viewed as the foundation for detecting, assessing, and improving the quality and appropriation of healthcare [5] [7]. However, indicators alone are unable to measure the medical quality directly, but act more like a screen that monitor healthcare organizations. In order to provide a foundation for improving the healthcare quality, the indicators must still be evaluated [28].

Quality Indicator Project (QIP) led by Maryland Hospitals Association in U.S. has defined the healthcare quality indicators that can be used as a tool for constructing standards and reference points. They have also presented a quality trend and events' timeline of patients' medical care by performing statistical analysis with the indicator data in relation to time [1].

Indicator itself doesn't provide the judgment of performance but simply

presents the outcome of clinical manifestation [7]. Gagel [23] considered that the key to improve the accurate measures of healthcare quality is the quality-indicator information system, like Health Care Quality Improvement Program (HCQIP) provided to Health Care Financing Administration (HCFA), which is a multi-indicator system for enhancing the quality, effectiveness, and efficiency of healthcare services.

Indicators are used as screens and flags for monitoring situations that might require further analysis within the healthcare system [35]. However, indicators are not the final step in assessing quality performance. Knowledge of long-term trends should be developed to provide a basis for deeper investigation and understanding of healthcare. Such a knowledge-base might also increase the efficiency of patient evaluation by decreasing the time needed for surveying numerous patient histories [4].

2.3 Taiwan Quality Indicator Project

Taiwan Quality Indicator Project (TQIP), enacted in August 1999, was imported by Taiwan Joint Commission on Hospital Accreditation (TJCHA) from Quality Indicator Project (QIP) directed by Maryland Hospital Association (MHA).

At present, QIP has developed care-indicator groups including Acute Care Indicators, Long-term Care Indicators, Psychiatric Care Indicators and Home Care Indicators. Each group has different detail indicators. In 1999, TQIP introduced the general Acute Care Indicators (shown in Table 2.1) that give advance priority to in-patient, emergency and outpatient services. In the third quarter of 2001, TQIP continued to introduce the Psychiatric Care Indicators (shown in Table 2.2) and Long-term Care Indicators (shown in Table 2.3). These indicators, shown in the Tables, are currently being executed in domestic medical centers, regional hospitals and district hospitals. The following are care-indicator groups [8].

Table 2.1 Acute Care Indicators.

AC Indicator 1a:	Device-Associated Infections in Intensive Care Units
AC Indicator 1b:	Device Use in Intensive Care Units
AC Indicator 2a:	Surgical Site Infections
AC Indicator 2b:	Prophylaxis for Surgical Procedures
AC Indicator 3:	Inpatient Mortality
AC Indicator 4:	Neonatal Mortality
AC Indicator 5:	Perioperative Mortality
AC Indicator 6:	Management of Labor
AC Indicator 7:	Unscheduled Readmission
AC Indicator 8:	Unscheduled Admission Following Ambulatory Procedures
AC Indicator 9:	Unscheduled Returns to Intensive Care Units
AC Indicator 10:	Unscheduled Returns to the Operation Room
AC Indicator 11:	Isolated CABG Perioperative Mortality
AC Indicator 12:	Physical Restraint Events
AC Indicator 13	Documented Falls
AC Indicator 14:	Complications following Sedation and Analgesia
AC Indicator 15:	Pressure Ulcers in Acute Inpatient Care
AC Indicator A-1:	Unscheduled Returns to the Emergency Department
AC Indicator A-2:	Length of Stay in the Emergency Department
AC Indicator A-3:	X-Ray Study Discrepancies in the Emergency Department Requiring a Change in Patient Management
AC Indicator A-4:	Patients Leaving the Emergency Department Before Treatment is complete
AC Indicator A-5:	Cancellation of Ambulatory Procedures

Table 2.2 Psychiatric Care Indicators.

PC Indicator 1:	Injurious Behavior
PC Indicator 2:	Unplanned Departures Resulting in Discharge
PC Indicator 3:	Adult Transfers to Acute Inpatient Care
PC Indicator 4:	Readmissions to Psychiatric Inpatient Care
PC Indicator 5:	Physical Restraint Events
PC Indicator 6:	Seclusion Events
PC Indicator 7:	Partial Hospitalization Programs
PC Indicator 8:	Documented Falls

Table 2.3 Long-term Care Indicators.

LTC Indicator 1:	Unplanned Weight Change
LTC Indicator 2:	Pressure Ulcers
LTC Indicator 3:	Documented Falls
LTC Indicator 4:	Unscheduled Transfers/Discharges to Inpatient Acute Care
LTC Indicator 5:	Nosocomial Infections
LTC Indicator 6:	Physical Restraint Use

TQIP is based mainly on clinical indicators. Hospitals address selected indicators, which represent the hospital performance with regards to select criteria. Furthermore, in order to best utilize hospital resources in pursuing the desired criterion, the main function of TQIP is to assist hospitals with internal improvement and is not to involve external comparison.

TQIP includes mainly process and outcome indicators. There are three main frames partitioned into TQIP indicators. The first is to monitor care status. The second is to monitor mortality. The third is to measure care process.

As of 2002 [3], a total of sixty-six district-level advanced hospitals have participated in the TQIP program. There are fifteen medical centers, forty-three regional hospitals and six district hospitals, all of which are shown in Table 2.4.

Table 2.4 Hospitals participate in TQIP program.

Hospital Level	Participation Number	Participation-level Rate
Medical Centers	15	82%
Regional Hospitals	43	62%
District Hospitals	6	14%

2.4 Bayesian Approach

A Bayesian network (BN) is a knowledge representation defined by probability distributions and graphical models. It consists of two properties:

1. The network structure is in the form of a directed acyclic graph (DAG).

2. A set of probability distributions of the random variables for each node (variable) and its parents.

A directed graph G [14] can be defined as that which consists of a finite set, V, of nodes and an adjacency relation E on V. The graph G is denoted as (V, E). For each $(x, y) \in E$, there is a directed edge from node x to node y. However, a directed acyclic graph (DAG) contains no directed cycles.

That is, a Bayesian network is defined as follows:

A network structure constructed as a Bayesian network (shown in Figure 2.1) represent alternative paths of causal relationships between certain variables in the BN. Let P be a joint probability distribution of the nodes in some set V, and G= (V, E) be a DAG, in which BN can be represented as (G, P).

where P is defined as follow:

$$P(X_1, X_2, \cdots, X_n) = \prod_{i=1}^{n} P(X_i \mid Pa(X_i)) \qquad (2.1)$$

where, $Pa(X_i)$ is the set containing the parents of X_i in the BN.

Thus, we can compute the joint probability of each feasible path by (2.1). An example of Bayesian networks together with the conditional probability tables is shown below:

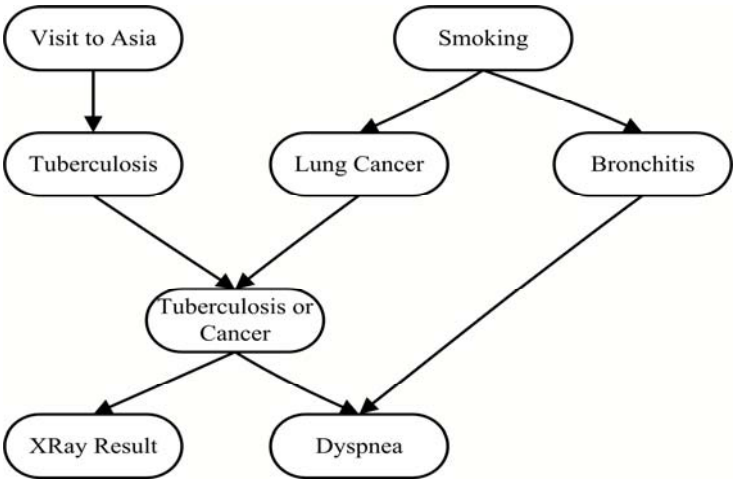

Figure 2.1 An example Bayesian network of Chest Clinic.

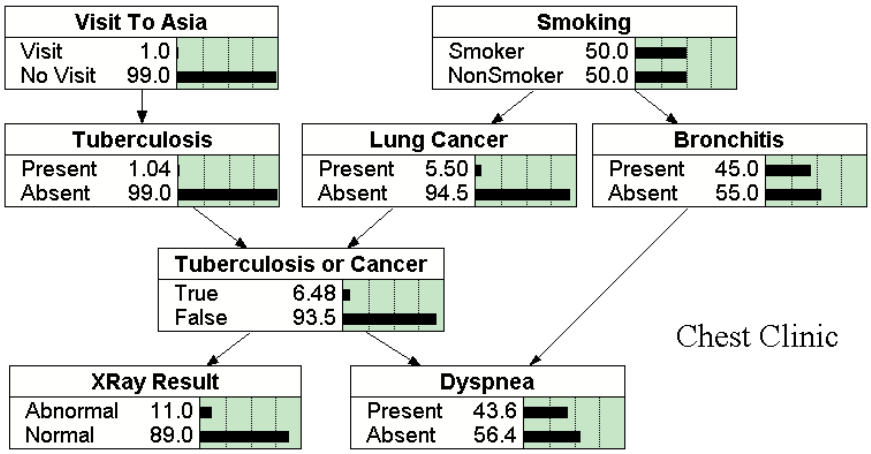

Figure 2.2 An example of Bayesian networks with probability tables [37].

A simplified network could be used to help in diagnosing patients arriving at a clinic. Each node in the network corresponds to two states and some conditions of the parents, for example, “Visit to Asia,” indicates whether the patient has recently visited Asia.

The links between any two nodes indicate that there are probability relationships that exist between the states of those two nodes. For example, smoking increases the chances of getting lung cancer and bronchitis. And so on.

Many learning techniques rely heavily on data. A Bayesian network, which is a knowledge representation, can allow us to learn new knowledge by combining expert domain knowledge and statistical data. Learning using Bayesian networks has two advantages [24]. One, we can easily encode expert knowledge in a Bayesian network and use this knowledge to increase the efficiency and accuracy of learning. Two, the nodes and arcs in learned Bayesian networks often correspond to recognizable distinctions and causal relationships. Consequently, we can more easily interpret and understand the knowledge encoded in the Bayesian network representation.

The conceptual map of Bayesian networks is shown below:

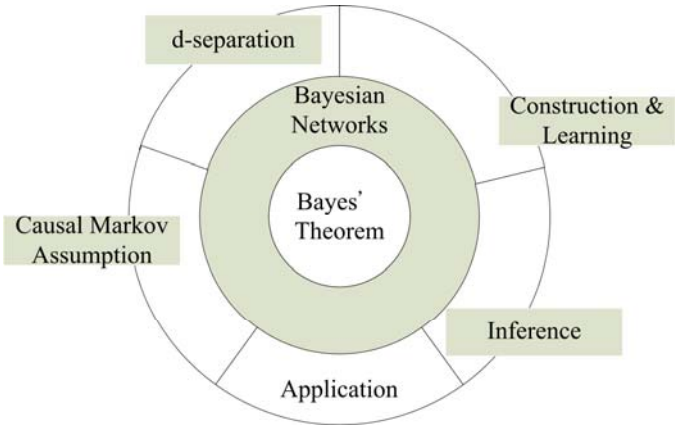

Figure 2.3 Bayesian network concept map.

Hence, Bayesian networks, based on the Bayes' theorem of applying probabilities, can be used to denote causal inferences. Moreover, the two properties of d-separation and Markov assumption [36] are conditions of BN.

2.4.1 Construction and Learning for Bayesian Networks

The process of constructing a BN structure will be called "Learning Bayesian networks". It can be divided into two parts: structure-learning and parameter-learning. Structure learning looks for the relationships between variables within networks of unknown structure. Parameter learning looks for the node probabilities within networks of known structure [21].

Structure learning of BN can be viewed as a causal discovery, which looks for the network structure between uncertain variables in domain knowledge [12]. When one variable is dependent on another, there will be an observable relationship. When relationships between nodes are independent of each other, there will be no observable relationship.

The structure of relationships between nodes can be constructed by domain personnel or by the statistic data collected from the domain knowledge. However, to acquire the experts' domain knowledge is not easy, because they are too busy to get assistances, or they can't illustrate the hidden relations. Furthermore, numerous variables will make experts hard to describe all relations exactly. Hence, to construct the network using data is an essential method. In addition, Heckerman *et al* [25] describe a method for learning Bayesian networks from a combination of prior knowledge and statistical data.

In their learning algorithm, a user specifies his prior knowledge about the problem by constructing a prior network, and by assessing his confidence in this network which uses a database of cases generated from the network.

In general terms, there are five different methods of learning probabilistic network structures from data. The first three methods are [42]: 1) the first is based on linearity and normality assumptions; 2) the second is based on the testing of independent relationships; 3) the third is based on the Bayesian approach. The other two methods of learning Bayesian network are partitioned into: 1) constraint-based algorithms; 2) Bayesian methods [15] [19].

Bayesian methods utilize heuristic methods to search the space of DAGs which are evaluated by scoring functions. There are many variations on Bayesian methods. Most researches have focused on the application of heuristics searching, such as *K2* algorithm [17]. Others introduced to search scoring functions which are used to evaluate each network for maximizing Bayesian scores, such as *BDe* method [26] and *Minimum Description Length Principle* [31].

Constraint-based methods identify the dependencies between the two associated nodes by using Conditional Independence (CI) test [43]. *PC* algorithm [43] is one of the notable constraint-based algorithms. One of most advantages is that constraint-based algorithms are relatively fast and possess the ability to deal with latent variables. However, it takes time while computing CI test. The most significant drawback to Bayesian methods is that they are relatively slow [19], and they may not find the best structure due to heuristic methods.

Friedman *et al* [21] discovered four rules for utilizing Learning-Bayesian Networks (LBN). These rules revolve around recognizing whether data and structure for the LBN are known or unknown: 1) Learn the parameters for applying known data within a known structure; 2) Learn the parameters for incomplete data within a known structure; 3) Learn the parameters for complete data within an unknown structure; 4) Learn the parameters for incomplete data and unknown structure.

First, learning parameters for a complete data set and a known structure is a simple method in which *Beta-distribution* and *Dirichlet-distribution* are often used [24].

Second, applying partial or hidden variables with missing data to a known learning-structure will result in permutated combinations, especially and exponentially when time is a factor. In this case, an approximation method, such as the *Gradient Ascent* method [21] [40], may be used.

Third, if complete data is applied to an unknown structure, such algorithms for solving structures generally fall into two groups: 1) constraint-based algorithms; and 2) Bayesian-method algorithms [15].

Fourth, using an incomplete data set to define a previously unknown structure can be achieved by using the *Structural EM* algorithm [22].

2.4.2 Inference

Once a Bayesian network has been constructed from the complete or incomplete prior knowledge, data, or a combination, various probabilities need to be determined from the model. In general, the calculation of a probability for a given model is known as Probabilistic Inference (PI). PI can be adopted either by exact inference or approximate inference. For example, we can examine the following Bayesian network that has been devised to detect credit-card fraud [24]:

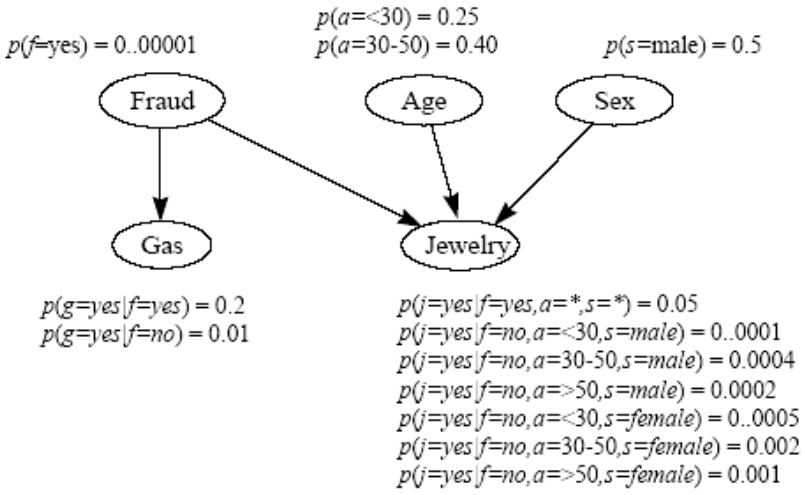

Figure 2.4 A Bayesian network for detecting credit-card fraud.

We can apply the conditional independencies encoded in the BN to exploit the probability of fraud given the other variables, which can be computed as

follows:

$$P(f \mid a,s,g,j) = \frac{P(f,a,s,g,j)}{P(a,s,g,j)} = \frac{P(f,a,s,g,j)}{\sum P(f',a,s,g,j)} \tag{2.3}$$

where $P(f')$ denotes the prior probability of fraud.

Several probabilistic inference algorithms have been developed for Bayesian networks with discrete variables that exploit conditional independence. Pearl [38] developed a message-passing scheme of *Polytree* that updates the probability distributions for each variable in a BN, which responses to other observations of variables.

Methods that encode *Multivariable-Gaussian* or *Gaussian-mixture* distributions for exact inference in Bayesian networks have been developed [32] [41].

Methods of approximation for other distributions such as a generalized linear-regression model for inference in BN have also been developed [24]. Other methods use stochastic simulation such as *Logic-sampling* method and *Likelihood-weighting* method [24].

Although conditional independence can be used to simplify probabilistic inference, exact inference in a BN for discrete variables is NP-hard [16]. Even approximate inference, such as *Monte-Carlo* method, is NP-hard [18].

2.4.3 d-separation and Markov Assumption

The rules of d-separation can be used to realize independencies in the domain when given the structure of a BN. These rules can resemble graph connectivity with some important dependency on variables. For example, conditioning on a variable may block or unblock a dependent path between two variables, depending on the direction of traversal of that variable along that path. According to d-separation, Z is blocked if an undirected path p traverses along the following directions:

1. If coming from a child of Z.
2. If coming from a parent of Z and existing from a child of Z.

According to the rules of d-separation, we can simplify a large scale

Bayesian network into several small scale structures without losing the knowledge representative properties of the model.

The formal definition of d-separation is as follows [39]:

Definition (d-separation): Let **S**, **T**, and **V** be three disjointed subsets of nodes in a DAG, and let p be any path between a node in **S** and a node in **T**, where by a path we mean any succession of arcs, regardless of their directions. Then **V** is said to block p if there is a node Z on p satisfying one of the following two conditions:

1. Z has converging arrows along p and neither Z nor any of its descendants are in **V**.
2. Z does not have converging arrows along p and Z is in **V**.

That is, **V** is said to d-separate **S** from **T**, if **V** blocks every path from a node in **S** to a node in **T**. Below are some examples of d-separations:

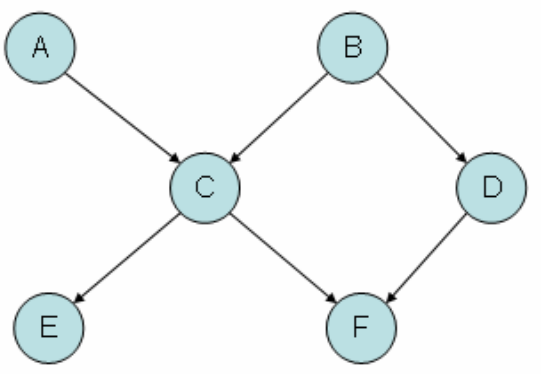

Figure 2.5 A Bayesian network example.

1. $A \perp D$ when both paths between A and D are blocked: path A—C—B—D is blocked while C is instantiated and path A—C—F—D is also blocked while F is instantiated.
2. $E \perp D \mid B$, while B is instantiated.

As we know, A Bayesian network encodes a set of independencies that exist in the domain. If we want to learn the structure using conditional independencies, here are the assumptions that should be followed [34]:

1. Markov Assumption: Given a Bayesian network model B, any variable is independent of all its non-descendents in B, given its parents.

2. Faithfulness Assumption: A BN graph G and a probability distribution P are faithful to one another if each and all independence relations valid in P are those entailed by the Markov assumption on G.

The Markov assumption expresses independence relations, which exist between every node and its non-descendants given a Bayesian network model. Hence, given Markov assumption, we can learn the BN structure from data by testing the conditional independence of every node in the model.

2.5 Partitioned Clustering

The Clustering method is used to explore a data set in which the goal is to separate the sample into groups or to provide understanding about the underlying structure or nature of the data. In the partitioned clustering, the data is distributed in a multidimensional space within the clusters. The centroid of each cluster is first selected, and then the clusters are generated by repeatedly re-calculating the centroid repeatedly using a measure of dissimilarity between cluster points.

The goal of partitioned clustering is to partition a data set into groups such that the observations in one group are dissimilar to those in other groups. Here, one of the ways to measure the dissimilarity is the *Euclidean distance*, given by

$$d_{rs}=\sqrt{\left(\mathrm{x}_r-\mathrm{x}_s\right)^T\left(\mathrm{x}_r-\mathrm{x}_s\right)} \tag{2.4}$$

where x_r is a column vector representing one observation.

K-means clustering (MacQueen 1967) can best be described as a partitioning method. That is, K-means partitions the observations of any chosen data into K mutually exclusive clusters, and returns a vector of indices indicating to which of the k clusters it has assigned each observation. In addition, K-means uses an iterative algorithm that minimizes the sum of distances from each object to its cluster centroid, over all the clusters.

Fuzzy C-means (FCM) [10] is a data clustering technique wherein each data point belongs to a cluster of some degree that is specified by a membership grade. This technique is an improvement on earlier clustering methods by providing a method to group data points that populate some multidimensional space into a specific number of separate clusters.

FCM starts with an initial guess for the cluster centers, which are intended to mark the mean location of each cluster. However, the initial guess for these cluster centers will most likely be incorrect. Additionally, FCM assigns every data point a membership grade for each cluster. By repeatedly re-calculating the cluster centers and the membership grades for each data point, FCM gradually moves the cluster centers to the appropriate location within a data set. This repetition is based on minimizing an objective function that represents the distance from any given data point to a cluster center weighted by that data point's membership grade.

CHAPTER 3 METHODS AND PROCEDURES

This study integrates the possibility of adopting Bayesian networks to analyze the relevance and uncertainty among TQIP indicators, and to devise a feasible mechanism to modify the structure and parameters of TQIP indicators. Accordingly, we have devised a nonlinear network of TQIP indicators to form a warning system which helps hospitals to control medical quality by determining if hidden relations exist among those indicators.

3.1 Problem Scope and Constraints

1. The variables in the problem field must be discrete data-types that satisfy the Bayesian network assumptions.
2. The data resource must be complete for Bayesian network implementation.
3. The data sets are independently and identically distributed within the Bayesian network.

3.2 Clustering + Bayesian Network Methodology

This study applies the clustering algorithm and Bayesian networking to the program of healthcare quality indicators. We then use kernel approximation [2] to verify similarities between the generated data behind the BN and the raw indicator data.

In order to reduce the network complexity and illustrate the whole indicator network more completely, this study proposes a “Clustering +Bayesian network” methodology to implement the program of healthcare quality indicators. The first part of this methodology uses the concepts and properties of the Fuzzy C-means (FCM) method to cluster indicators; in the second part, we add a mechanism for combining clustering with the Bayesian network. This mechanism essentially sets a “Radius”, which is a maximum distance, to determine the central point of each cluster to be the farthest point from this cluster. According to the “radius”, we re-calculate the new clusters again and look for the overlapping points between clusters after FCM implementation.

The third part uses “HUGIN Researcher”, an application package based on

the PC algorithm, to implement the structure learning process and to derive a structure of hidden relationships among the indicators. After that, we estimate the parameters by using the EM algorithm [30] in HUGIN Tool.

This research mechanism is shown in Figure 3.1.

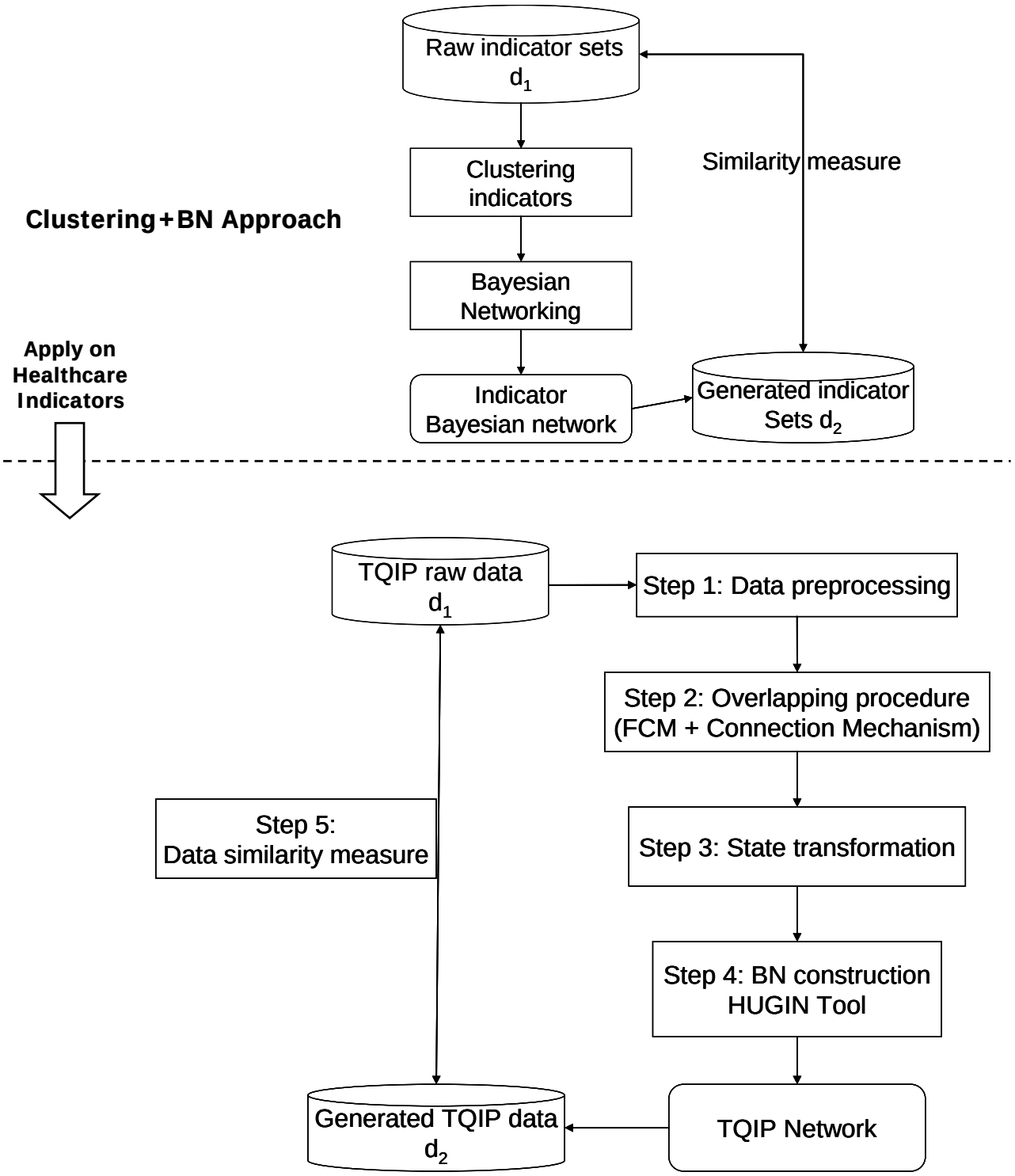

Figure 3.1 The research mechanism.

3.3 Fuzzy C-means Algorithm

Fuzzy C-means (FCM) is a clustering algorithm extended from the K-means algorithm. The difference in the FCM is that each data point belongs to a cluster that is specified by a membership grade denoted as [0, 1]. It provides a method for grouping data points that populate some multidimensional space into a specific number of different clusters.

Let $X_i=\{x_1,x_2,\cdots,x_N\}$ present a given set included of N feature data. $V=\{v_1,v_2,\cdots,v_C\}$ are the expected cluster centers. $U=(\mu_{ij})_{N\times C}$ is a fuzzy partition matrix, where each member μ_{ij} indicates the degree of membership between the data vector x_i and the cluster j. The values of matrix U should satisfy the following two conditions:

$$\mu_{ij}\in[0,1],\forall i=1,\cdots,N,\ \forall j=1,\cdots,C \tag{3.1}$$

And the other condition is that the sum of the membership grade for each cluster is 1:

$$\sum_{j=1}^{C}\mu_{ij}=1,\forall i=1,\cdots,N \tag{3.2}$$

The objective of FCM algorithm is to minimize the cost function formulated as follows.

$$J(U,V)=\sum_{j=1}^{C}\sum_{i=1}^{N}(\mu_{ij})^m\left(\sqrt{(x_i-v_j)^T(x_i-v_j)}\right)^2 \tag{3.3}$$

$\left((x_i-v_j)^T(x_i-v_j)\right)^2$ is the distance between a data point and cluster center. In this study, we adopt the *Euclidean distance*. The procedure of FCM is illustrated as follows.

Step 1: Initialize the membership matrix U with random values ranged [0, 1], where the conditions (3.1) and (3.2) are satisfied.

Step 2: Calculate the cluster centers v_j according to the equation:

$$v_j = \frac{\sum_{i=1}^{N} (\mu_{ij})^m x_i}{\sum_{i=1}^{N} (\mu_{ij})^m}, \forall j = 1, \cdots, C \tag{3.4}$$

Step 3: Calculate the new distance:

$$d_{ij} = \| x_i - v_j \|, \forall i = 1, \cdots, N \ \forall j = 1, \cdots, C \tag{3.5}$$

Step 4: Update the new matrix U :

If $d_{ij} > 0 \left(x_i \neq v_j \right)$, calculate the new membership grade μ_{ij} .

$$\mu_{ij} = \frac{1}{\sum_{k=1}^{C} \left(\frac{d_{ij}}{d_{ik}} \right)^{\frac{2}{m-1}}} \tag{3.6}$$

Else $\mu_{ij} = 1$.

Step 5: If the termination criterion has been met (e.g. maximum number of iterations), stop.

Otherwise, go to step 2.

3.4 The Connection Mechanism for Clustering + Bayesian Network

Take the Acute Care Indicators used at the domestic level of medical centers during 2002 for example. The scatter plot of the third and fourth features of the indicator data after FCM implementation is shown in Figure 3.2.

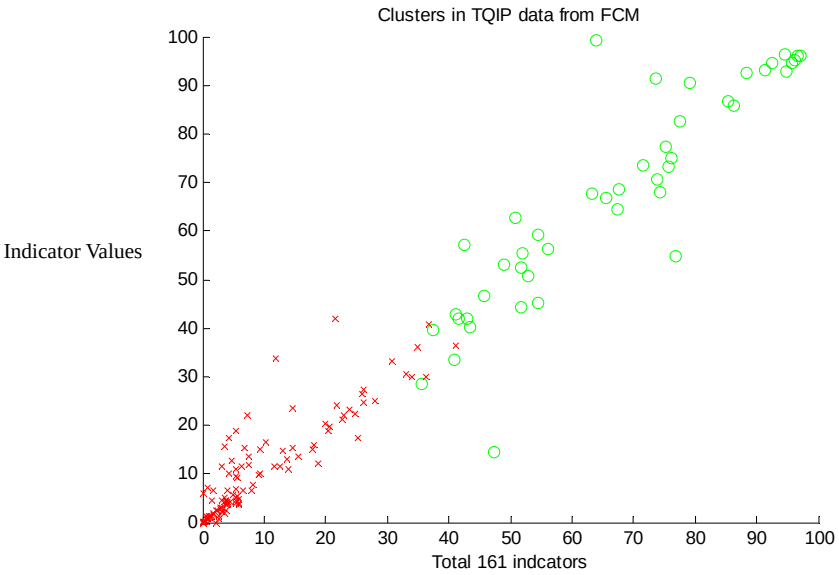

Figure 3.2 Two Clustered in TQIP by FCM.

Here we add a mechanism for combining clustering with the Bayesian network in order to re-calculate the new clusters and look for the overlapping points between clusters after FCM implementation. The procedure for the connection mechanism is as follows.

Step 1: Find the centroids of each cluster by FCM.

Step 2: Calculate the *Euclidean distance* from each node to the centroid in each cluster in order to find out the maximum distance of the "Radius".

Step 3: Compute all the distances of each node to the cluster centroids.

Step 4: Compare the "radius" in each cluster to each node in the other cluster.

Step 5: If the radius is larger than the distance of the node in its cluster to the centroid in the other one, then reset the node to a new cluster.

Step 6: Repeat Step 4 to 5 until all nodes have been re-calculated.

The following is a sketch illustration of the mechanism.

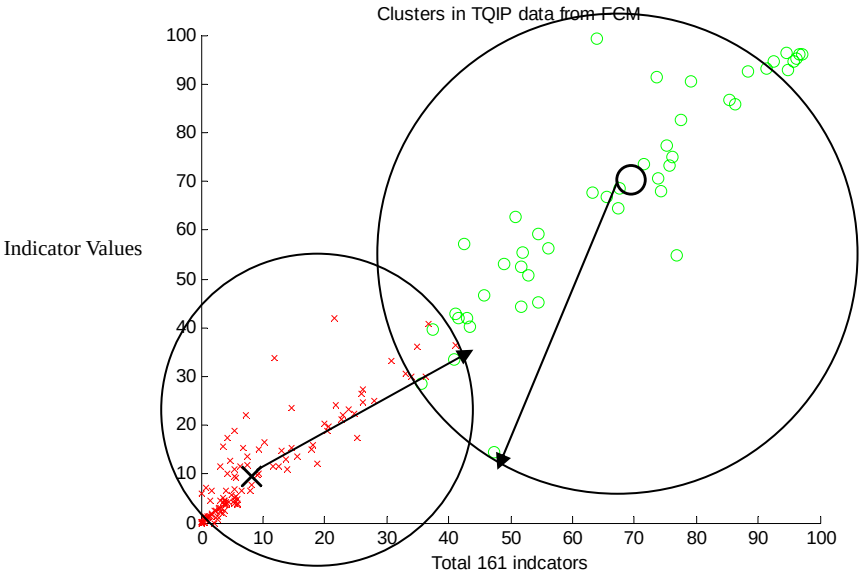

Figure 3.3 Overlapping by maximum distance from each cluster.

3.5 BN Construction by HUGIN Tool Based on PC Algorithm

The PC algorithm is the key for learning the structure of a Bayesian network of the HUGIN Tool [30] [33].

The PC algorithm assumes the *Causal Markov Condition* and the *Faithfulness Condition* as well as statistical decisions. As follows [34]:

Markov Assumption: Given a Bayesian network B, any variable is independent of all its descendants in B, given its parents.

Faithfulness Assumption: A graph G and a probability distribution P are faithful to one another if and only if each one and all independent relations in P are valid and entailed by the Markov assumption on G.

Let a database D serve as an input over a set of variables V, $I\left(X,Y\middle|S\right)$ serves as a test of conditional independence, and a significant level $0<\alpha<1$. The following is a sketch of the revised procedure [19].

Input: A database D over a set of variables V; $I\left(X,Y\middle|S\right)$: a test of conditional independence; $0<\alpha<1$: a significant level.

Output: An essential graph over V.

1) Construct the complete undirected graph over V.
2) For all ordered adjacent nodes X and Y, check a conditional independence relation $I(X,Y|S)$ if and only if all variables in S are adjacent to either X or Y. If X and Y are d-separated given S, delete edge X - Y; until all ordered pairs of adjacent variables have been tested for d-separation.
3) For each triple of nodes X, Y, Z such that X is adjacent to Y and Y is adjacent to Z but X is not adjacent to Z, orient X - Y - Z as $X \rightarrow Y \leftarrow Z$ if and only if Y is not in the set S that d-separates X and Y in 2).
4) Repeat, until no more edges can be directed:
   (a) Direct all arcs necessary to avoid new v-structures.
   (b) Direct all arcs necessary to avoid cycles.

Figure 3.4 The sketch of the revised procedure.

The procedure of the PC algorithm can be concluded with the following description [19]:

1) Test for conditional independence between each pair of variables ($X \perp Y \mid S$).
2) Identify the skeleton of the graph.
3) Identify collides ($X \rightarrow Y \leftarrow Z$).
4) Identify derived directions.

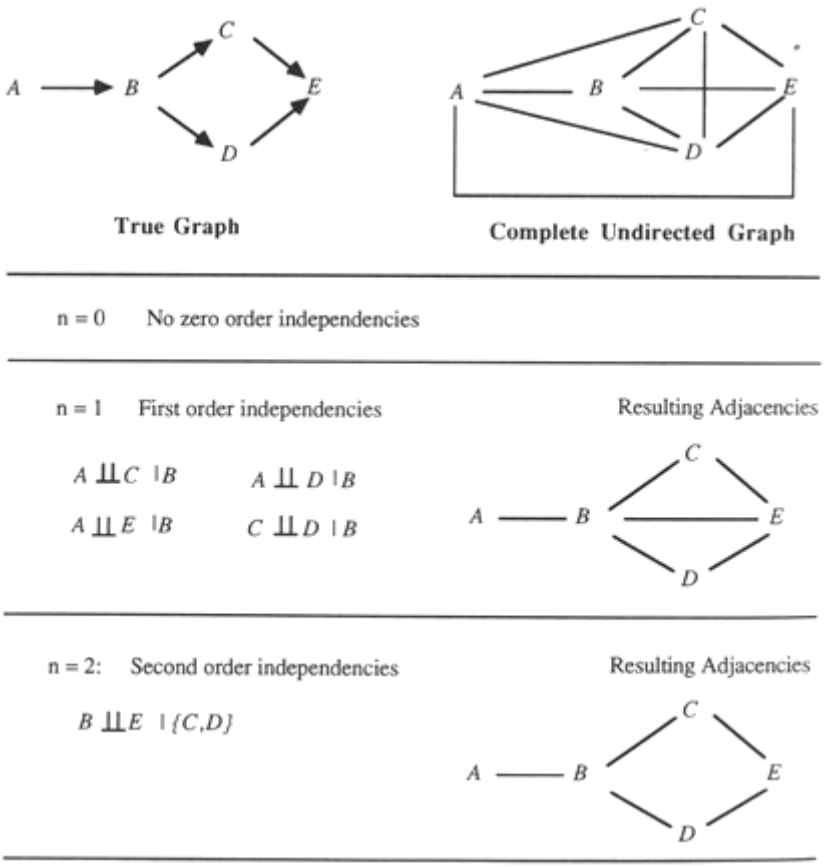

Figure 3.5 Traces the first two steps of the PC algorithm [43].

In step 1, a complete undirected graph is created. A hypothesis of any ordered adjacent nodes X and Y exists as conditionally independent by statistical tests given the set S within but not inclusive of X and Y. After the set of adjacencies has been identified and no conditional independent relation has been found in step 2, the triple set of variables with only two adjacencies and a skeleton of the second part in Figure 3.5 will be partially oriented in step 3, e.g.:

A-B-C; A-B-D;

C-B-D; B-C-E;

B-D-E; C-E-D

A collide E is found because E is not in set{C, D}. And we have none of the other triples from collides. In step 4, repeat the procedure and check to avoid new v-structures and cycles until no more edges can be oriented, e.g. If there is a directed path from A to B, and an edge between A and B, then orient A-B as A→B.

3.6 Parameter Estimation by HUGIN Tool Based on EM Algorithm

The EM algorithm [27] supports parameter estimation in the HUGIN Tool. Let a Bayesian network $B=(G,P)$, and the conditional probability distribution of the parameters of B such that $\theta_{ijk}=P(X_i=k|Pa(X_i)=j)$ for each i,j,k.

The log-likelihood function $l(\theta)$ given data D and DAG G is:

$$l(\theta)=\sum_{i=1}^{N}\log P(c_i|\theta) \tag{3.7}$$

The E-step computes expected counts for family $fa(X_i)$ and parent $Pa(X_i)$ configurations of each node X_i under θ:

$$\eta^*(Y)=E_\theta\{\eta(Y)|D\} \tag{3.8}$$

where Y is either $Pa(X_i)=j$ or $X_i=k,Pa(X_i)=j$. The M-step computes new estimates of θ^*_{ijk} from the expected counts under θ_{ijk}:

$$\theta^*_{ijk}=\frac{\eta^*(X_i=k,Pa(X_i)=j)}{\eta^*(Pa(X_i)=j)} \tag{3.9}$$

The E-M procedure is iterated until a convergence of $l(\theta)$. In the HUGIN Tool, when the difference between the log-likelihoods of two successive iterations is less than or equal to the numerical value of a threshold multiplied by the log-likelihood, the procedure stops. Alternatively, one can set the number of upper limit of iterations to ensure that the procedure terminates.

3.7 HUGIN Learning Wizard Tool

The BN learning of HUGIN Tool, which is supported through a “Learning Wizard” [33], is adopted in this study. A full learning cycle consists of three main steps: Data acquisition, structure learning, and parameter estimation.

Step 1: Data acquisition.

Read data from various sources and preprocess the data.

Step 2: Structure learning.

Check whether known dependencies or independencies have to be forced onto the algorithm, including constraints, node positions, and node labels, etc.

Step 3: Parameter estimation.

Specify parameters for the EM algorithm.

3.8 Performance Evaluation-Data Similarity

In the end, this study adopts kernel approximation [2] for the purpose of measuring the data similarity behind data structures. First, the kernel function is used to calculate the approximate structure behind the dataset. In kernel function, the "Smoothing Parameter as the Bandwidth" (3.10) is used to adjust the shape and control the smooth degree of kernel function. Furthermore, this study compares the values for the Gap (3.11) of bandwidth between two datasets in order to determine whether two datasets come from the same structure.

The bandwidth is formulated as follows:

$$h^{*}=\left(\frac{R(K)}{n\left(\int x^{2}K\right)^{2}R\left(f^{''}\right)}\right)^{\frac{1}{5}} \tag{3.10}$$

Where $R(K)$ is represented as the *Roughness of Gaussian* kernel function; $\left(\int x^{2}K\right)^{2}$ is represented as the *Square of the Second Moment of Gaussian* kernel function; $R\left(f^{''}\right)$ is used to approximate the estimated probability density function. In addition, the difference (interval) of bandwidth values is formulated as follows:

$$d_{h}=\left|h_{1}\text{-}h_{2}\right| \tag{3.11}$$

Here we set a threshold by our case to check the similarity between the raw indicator-data and the generated data behind the BN model.

CHAPTER 4 A BN-BASED HEALTHCARE QUALITY INDICATOR NETWORK

In this chapter, we apply the methods and procedures mentioned in chapter 3 to TQIP indicator sets. First, we determine the scope of selected indicators depending on the report key and eliminate the missing records. Second, we adopt a data-transformation mechanism, which is used for transforming the continuous data-type into a discrete type before using the BN learner.

4.1 Indicator Resource and Scope

1. Indicator data is provided by Taiwan Joint Commission on Hospital Accreditation.
2. Acute Care Indicators adopted in domestic medical centers are the objective of this study.
3. Report key showed in "-7[*]" and "-99[†]" is not within the scope of selected indicators.
4. Indicators range is from January 1 2000 to December 31 2004 and a total of 60 cases (records) of each indicator item.
5. Time is not a function of this study.

The following is the indicator list of the medical centers.

Table 4.1 Indicator lists of the medical centers.

Year	I.D.	Indicator Set	Total # Measurements Not Recorded	Total # of Indicator Measurements
2000	Group 1[‡]	AC	39	162
2001	Group 1	AC	86	184
2002	Group 1	AC	86	192
2003	Group 1	AC	86	200
2004	Group 1	AC	90	228

[*] -7 (NR): No Records in the database at the facility level, or No valid Records at the aggressive level (no hospital rates≧0).
[†] -99 (NA): Not Able to calculate or display value due to low facility count.
[‡] Group 1: the level of Medical Centers.

4.2 Research Tools

The experiments in this study were conducted on a Pentium 4 2.80 GHz PC with 512 MB of RAM running under Windows XP Professional SP2. The data sets were stored in MS-Excel formats, which were used for the data preprocessing as well. In addition, MATLAB, an application-software, was used for numerical computation, data visualization and simulation. In this study, the clustering algorithm and connection mechanism were programmed using MATLAB. In addition, the BN learning of HUGIN Tool, which is supported through a “Learning Wizard”, was adopted in this experiment.

4.3 Data Preprocessing and State Discretization

The data-type of TQIP indicators is presented as continuous data-type (shown in Table 4.2 & 4.3); though the data-type of problem domains dealt with in Bayesian networks is presented as discrete values. In addition, different indicator items have different numerical values. Therefore, we utilize a state-transformation for value discretization of TQIP indicators.

Table 4.2 Partial indicator data sets of A1.1 (Resource: TJCHA).

I.D.	Indicator Set	Indicator	Measure	Year	Month	Weighted Mean
Group 1	AC	A1	A1.1	2000	1	0.8546
Group 1	AC	A1	A1.1	2000	2	1.305
Group 1	AC	A1	A1.1	2000	3	1.1855
Group 1	AC	A1	A1.1	2000	1Q	1.0965
Group 1	AC	A1	A1.1	2000	4	0.9918
Group 1	AC	A1	A1.1	2000	5	1.0129
Group 1	AC	A1	A1.1	2000	6	1.1675
Group 1	AC	A1	A1.1	2000	2Q	1.0558
Group 1	AC	A1	A1.1	2000	7	1.1887
Group 1	AC	A1	A1.1	2000	8	1.1252
Group 1	AC	A1	A1.1	2000	9	1.2437
Group 1	AC	A1	A1.1	2000	3Q	1.1862
Group 1	AC	A1	A1.1	2000	10	1.1327
Group 1	AC	A1	A1.1	2000	11	1.0771

I.D.	Indicator Set	Indicator	Measure	Year	Month	Weighted Mean
Group 1	AC	A1	A1.1	2000	12	1.0243
Group 1	AC	A1	A1.1	2000	4Q	1.0777

Table 4.3 Partial indicator data sets of A1.1a.

I.D.	Indicator Set	Indicator	Measure	Year	Month	Weighted Mean
Group 1	AC	A1	A1.1a	2000	1	20.1389
Group 1	AC	A1	A1.1a	2000	2	19.3878
Group 1	AC	A1	A1.1a	2000	3	21.3389
Group 1	AC	A1	A1.1a	2000	1Q	20.2192
Group 1	AC	A1	A1.1a	2000	4	24.7899
Group 1	AC	A1	A1.1a	2000	5	28.0899
Group 1	AC	A1	A1.1a	2000	6	25.3472
Group 1	AC	A1	A1.1a	2000	2Q	26.1034
Group 1	AC	A1	A1.1a	2000	7	27.5934
Group 1	AC	A1	A1.1a	2000	8	25.8915
Group 1	AC	A1	A1.1a	2000	9	23.0878
Group 1	AC	A1	A1.1a	2000	3Q	25.2591
Group 1	AC	A1	A1.1a	2000	10	25.5814
Group 1	AC	A1	A1.1a	2000	11	31.1864
Group 1	AC	A1	A1.1a	2000	12	25.5521
Group 1	AC	A1	A1.1a	2000	4Q	27.3013

In Table 4.1, each item of indicators has its range of weighted means. In order to satisfy the discrete data-type conditions of Bayesian networks, a transformation procedure will be used in this study.

From the outset, we adopt equally weighted discretization depending on *Frequency distribution*. The following describes the procedure.

Step 1: Sort the data points and compute the Range.

$$\text{Range}=\text{Max}-\text{Min} \tag{4.1}$$

Step 2: Divide up the numbers of discrete state k.

$$k=\log_2 n+1 \tag{4.2}$$

where n is denoted as the total sample size.

Step 3: Compute the divided range of each state.

$$\text{State Width}=\frac{\text{Range}}{k} \tag{4.3}$$

Step 4: Transform each indicator into the corresponding state.

Take A1.1 for example. A total number of records $n=60$; Max=1.9463, Min=0.8546, then Range=Max－Min=1.0917. The numbers of discrete state $k=\log_2 n+1\fallingdotseq 7$; each state width=$1.0917/7=0.156$. Thus the corresponding state-transformation is shown in Table 4.4

Table 4.4 The corresponding state transformation of A1.1.

Indicator/ Records	A1.1	Corresponding state	Indicator/ Records	A1.1	Corresponding state
1	0.8546	0	31	1.5821	4
2	1.305	2	32	1.5256	4
3	1.1855	2	33	1.5536	4
4	0.9918	0	34	1.476	3
5	1.0129	1	35	1.3836	3
6	1.1675	2	36	1.3205	2
7	1.1887	2	37	1.3862	3
8	1.1252	1	38	1.4679	3
9	1.2437	2	39	1.4314	3
10	1.1327	1	40	1.6648	5
11	1.0771	1	41	1.549	4
12	1.0243	1	42	1.4533	3
13	1.2891	2	43	1.5039	4
14	1.1529	1	44	1.561	4
15	1.1932	2	45	1.5588	4
16	1.2068	2	46	1.4777	3
17	1.2977	2	47	1.3506	3
18	1.5062	4	48	1.3571	3
19	1.4631	3	49	1.7943	6
20	1.2775	2	50	1.772	5
21	1.2815	2	51	1.7498	5
22	1.2518	2	52	1.743	5
23	1.1768	2	53	1.8342	6
24	1.18	2	54	1.8176	6
25	1.3974	3	55	1.9463	6
26	1.3934	3	56	1.9397	6

Indicator/ Records	A1.1	Corresponding state	Indicator/ Records	A1.1	Corresponding state
27	1.3506	3	57	1.8183	6
28	1.3412	3	58	1.7167	5
29	1.4613	3	59	1.8061	6
30	1.5015	4	60	1.7196	5

Here is another example A1.1a. The total numbers of records $n = 60$; Max=32.173, Min=18.6901, then Range=Max－Min=13.4829. The numbers of discrete state $k=\log_2 n + 1 \fallingdotseq 7$; each state width=$13.4829/7 = 1.926$. As a result, the corresponding state is shown in Table 4.5.

Table 4.5 The corresponding state transformation of A1.1a.

Indicator/ Records	A1.1a	Corresponding state	Indicator/ Records	A1.1a	Corresponding state
1	20.1389	0	31	21.1838	1
2	19.3878	0	32	25.0177	3
3	21.3389	1	33	24.9304	3
4	24.7899	3	34	24.4364	2
5	28.0899	4	35	28.1528	4
6	25.3472	3	36	25.1472	3
7	27.5934	4	37	23.5374	2
8	25.8915	3	38	19.0939	0
9	23.0878	2	39	24.5627	3
10	25.5814	3	40	22.8457	2
11	31.1864	6	41	26.1484	3
12	25.5521	3	42	24.9201	3
13	18.6901	0	43	23.8647	2
14	19.9297	0	44	23.4934	2
15	22.8238	2	45	20.9691	1
16	21.2481	1	46	24.6847	3
17	21.7503	1	47	23.6422	2
18	22.5873	2	48	24.6804	3
19	24.8019	3	49	27.014	4
20	25.7874	3	50	28.7339	5
21	27.5154	4	51	31.6253	6
22	21.8563	1	52	32.173	7

Indicator/ Records	A1.1a	Corresponding state	Indicator/ Records	A1.1a	Corresponding state
23	23.0769	2	53	29.2774	5
24	22.3958	1	54	28.71	5
25	20.1674	0	55	30.6839	6
26	19.6151	0	56	27.6484	4
27	23.7679	2	57	27.4445	4
28	22.4745	1	58	28.2417	4
29	21.346	1	59	29.9551	5
30	19.6881	0	60	27.6431	4

4.4 Prior Information Involved

Within indicator sets, parts of indicators are related to their detailed measurements depending on certain formula-relations. For example, A1.1 is formulated as follows:

A1.1=

$$\frac{\text{Person - time of Unscheduled Returns to the Emergency Department}}{\text{Total Person - time of Emergency Department}} \times 100\% \tag{4.4}$$

And its detailed measure “A1.1a” is formulated as follows:

A1.1a=

$$\frac{\text{Person - time of unscheduled returns resulting in an inpatient admission}}{\text{Person - time of Unscheduled Returns to the Emergency Department}} \times 100\% \tag{4.5}$$

Hence, while learning the structure within the BN, we designate a “Design Relation” to serve as the prior information, which is a formula-relation between AC indicators and their detailed measurements.

4.5 Indicators Clustering

After the data preprocessing and state-discretization, a total of 121 indicators are selected in this study. In order to reduce the complexity of the final network, the expected cluster is set as $2(V=2)$. The scatter plot of the first and second columns by FCM clustering is shown in Figure 4.1.

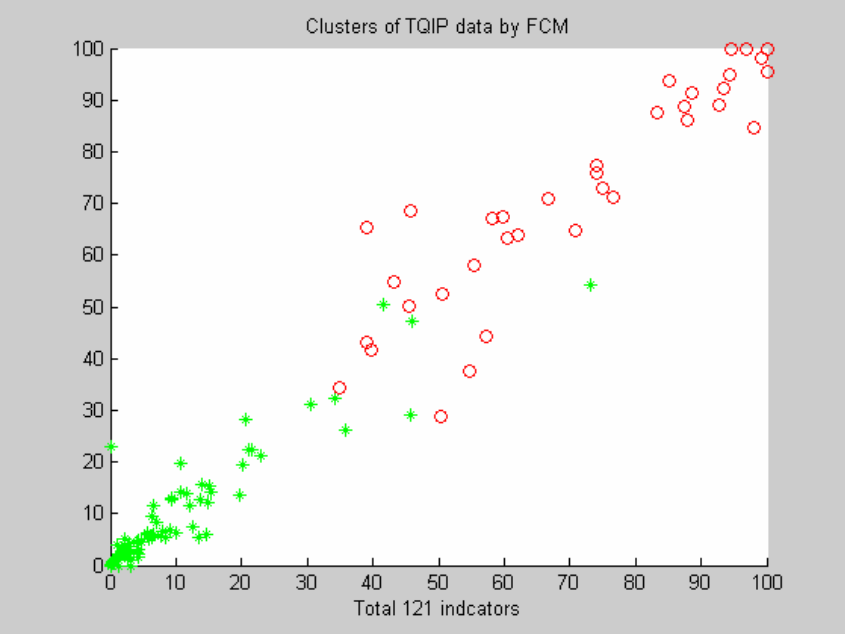

Figure 4.1 Clusters of TQIP data by FCM.

And below is the result of objective function by FCM.

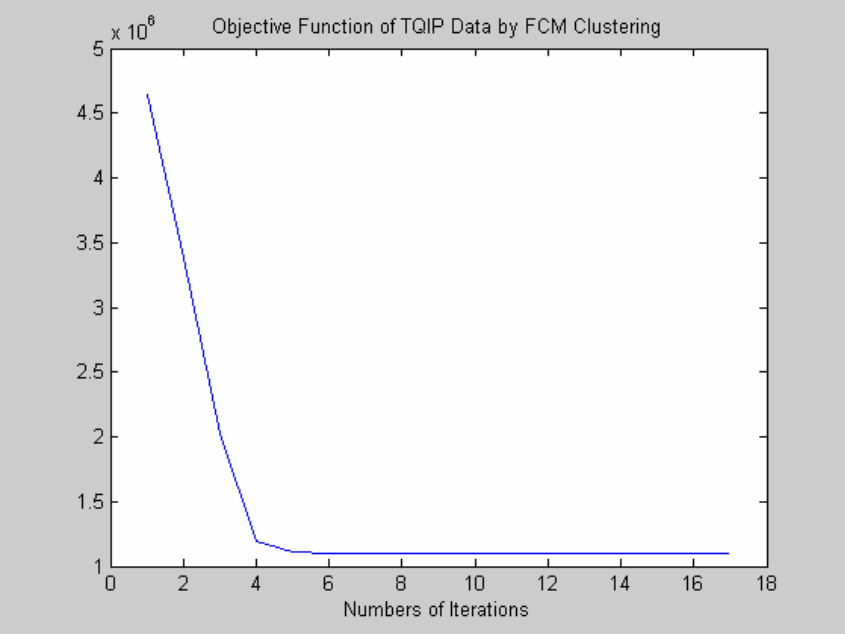

Figure 4.2 The objective function of TQIP data by FCM clustering.

After FCM implementation, the connection mechanism of clustering + BN, which is mentioned in Sec. 3.4, is used for the next procedure. We re-calculate the maximum distance from each point to the centroid in each cluster and look

for the overlapping points between two clusters after FCM implementation. The following is the result of the connection mechanism.

Table 4.6 The first new cluster by the connection mechanism.

New Cluster One			
Count	Indicator Measure	Count	Indicator Measure
1	1b.3	20	2b.4d
2	1b.5	21	2b.5
3	1b.6	22	2b.5c
4	1b.7	23	2b.6
5	1b.8	24	2b.6c
6	1b.10	25	6.2
7	1b.11	26	6.5
8	1b.12	27	12.1f
9	1b.13	28	12.1j
10	1b.15	29	12.1m
11	2b.1	30	13.1a
12	2b.1c	31	13.2
13	2b.1d	32	13.2a
14	2b.2	33	A2.1
15	2b.2c	34	A2.1a
16	2b.3	35	A2.2a
17	2b.3c	36	A2.3a
18	2b.4	37	A2.4a
19	2b.4c		
Total count of indicators=37.			

Table 4.7 The second new cluster by the connection mechanism.

New Cluster Two							
Count	Indicator	Count	Indicator	Count	Indicator	Count	Indicator
1	1a.1	23	3.7	45	12.1	67	A1.2a
2	1a.2	24	3.8	46	12.1a	68	A1.3
3	1a.3	25	3.9	47	12.1b	69	A1.3a
4	1a.5	26	3.12	48	12.1c	70	A2.1b
5	1a.6	27	4.3	49	12.1d	71	A2.1d
6	1a.7	28	4.4	50	12.1e	72	A2.1e
7	1a.8	29	4.8	51	12.1k	73	A2.2

Count	Indicator	Count	Indicator	Count	Indicator	Count	Indicator
8	1a.10	30	5.1	52	12.1l	74	A2.2b
9	1a.11	31	5.2	53	12.1m	75	A2.2d
10	1a.12	32	5.3	54	12.1n	76	A2.2e
11	1a.13	33	5.4	55	12.2	77	A2.3
12	1a.15	34	5.5	56	12.3	78	A2.3b
13	1b.2	35	5.6	57	13.1	79	A2.3d
14	1b.7	36	6.1	58	13.1b	80	A2.3e
15	2a.7	37	6.3	59	13.1c	81	A2.4
16	2b.1d	38	6.4	60	13.1d	82	A2.4b
17	2b.6d	39	7.1	61	13.2b	83	A2.4d
18	3.1	40	9.1	62	13.2c	84	A2.4e
19	3.2	41	10.1	63	13.3	85	A4.1
20	3.3	42	11.3	64	A1.1		
21	3.4	43	11.4	65	A1.1a		
22	3.6	44	11.6	66	A1.2		
Total count of indicators=85.							

After implementing the connection mechanism, we obtain two overlapping points: “1b.7” and “12.1m”.

4.6 BN Learner based on HUGIN Tool

4.6.1 BN Learner with Prior Information Involved

Before performing the BN learner, we adopt the state-transformation procedure, which is mentioned in Sec. 4.3, to implement the data discretization. The discretization procedure performs the state-transformations on a total of 121 indicators.

After the state-transformations, we import the “prior information” and the clustered data into the HUGIN Tool’s learning wizard to perform the structure learning for the BN learner (shown in Figure 4.3).

In this study, because the indicator data sets in TQIP are subject to time periods it is difficult to acquire sufficient indicator records. We have therefore lessened the significant level $\alpha = 0.2$.

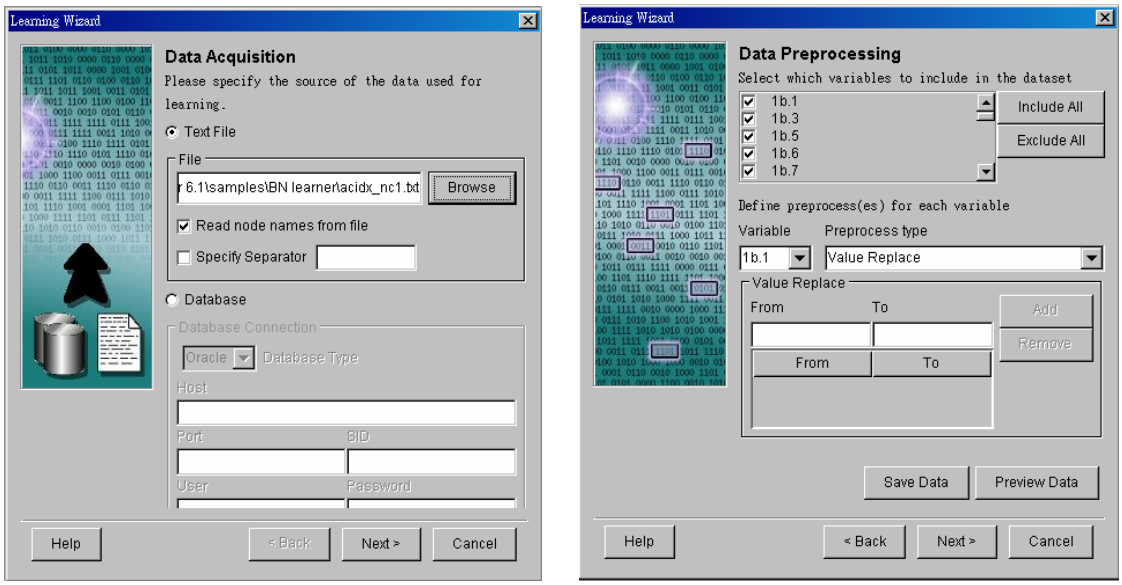

Figure 4.3 Data Acquisition and Data Preprocessing.

Then, we take the design relations as the “prior information”, which is mentioned in Sec. 4.4, before performing the structure learning (shown in Figure 4.4).

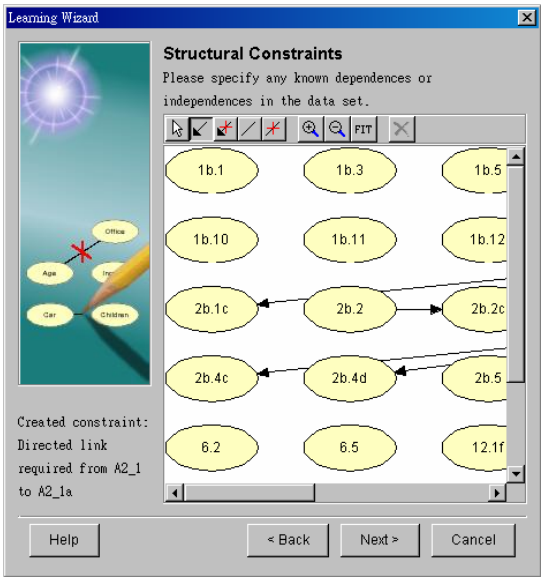

Figure 4.4 Prior Information Involved.

Next, with the significant level $\alpha = 0.2$, learning the BN structure using the PC algorithm is continued. Furthermore, the parameters among these indicators are estimated using EM-learning (shown in Figure 4.5).

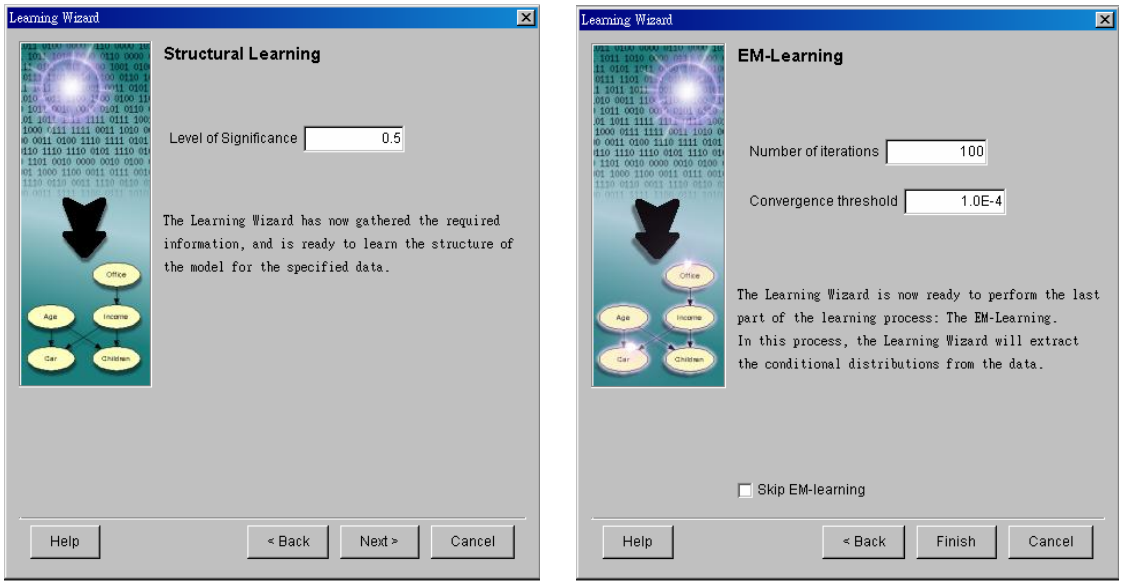

Figure 4.5 Structure Learning and Parameter Estimation.

As such we construct two Bayesian networks by using indicator sets (shown in Figure 4.6 and 4.7).

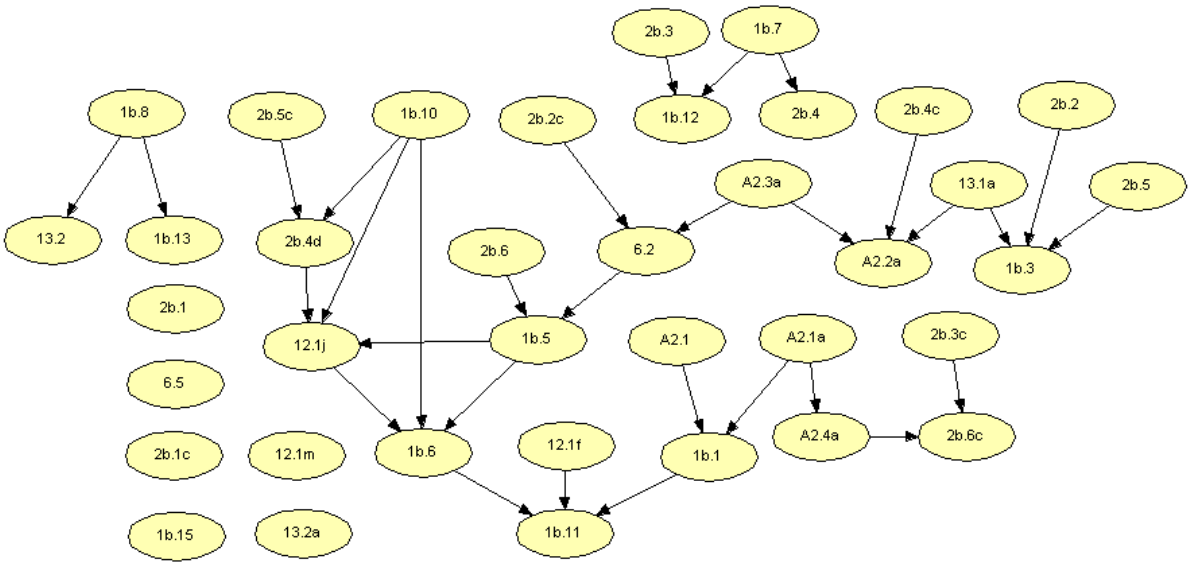

Figure 4.6 The first BN of TQIP indicators with design relations involved.

Below is the second BN of TQIP indicator set.

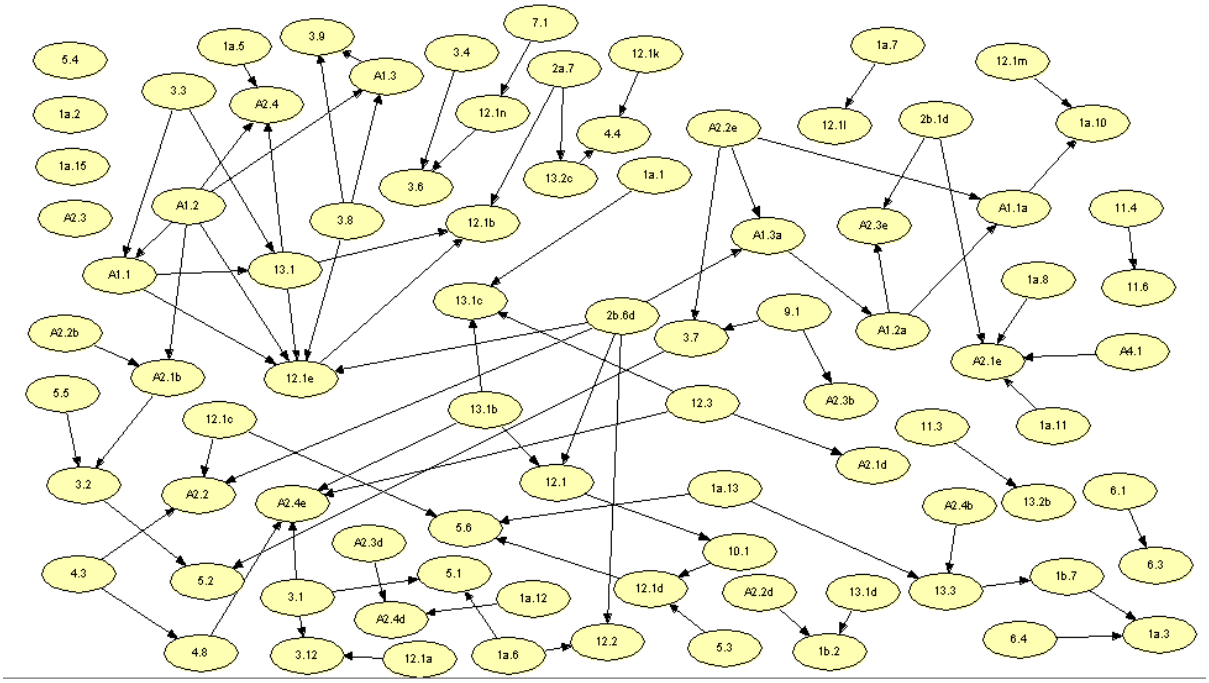

Figure 4.7 The second BN of TQIP indicators with design relations involved.

4.6.2 BN Learner without constraints

It should be mentioned that the design relations among indicators are not concerned with the BN learner. Learning the structure and estimating the parameters to obtain Bayesian networks uses the indicator sets directly. The BNs simply illustrate the hidden relations among TQIP indicators.

The following is the Bayesian networks without constraints.

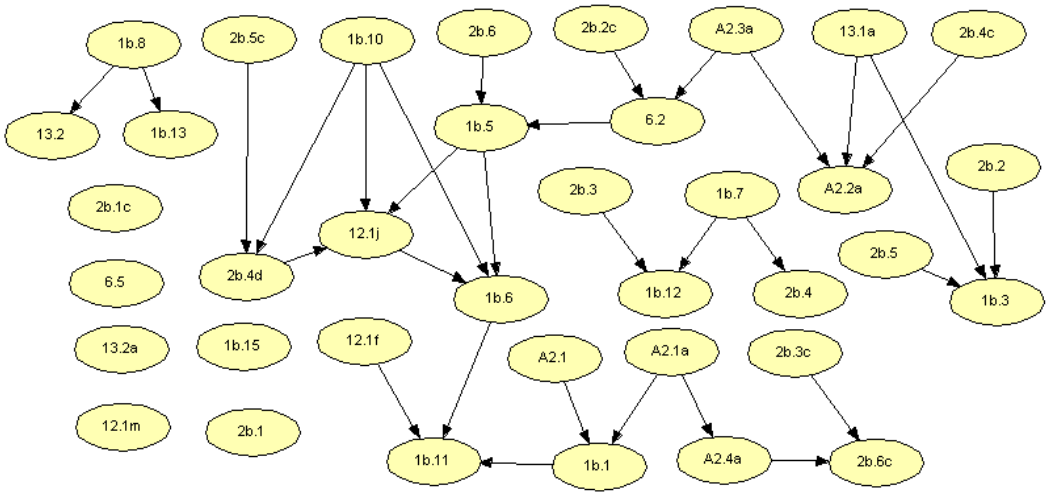

Figure 4.8 The first BN of TQIP indicators without constraints.

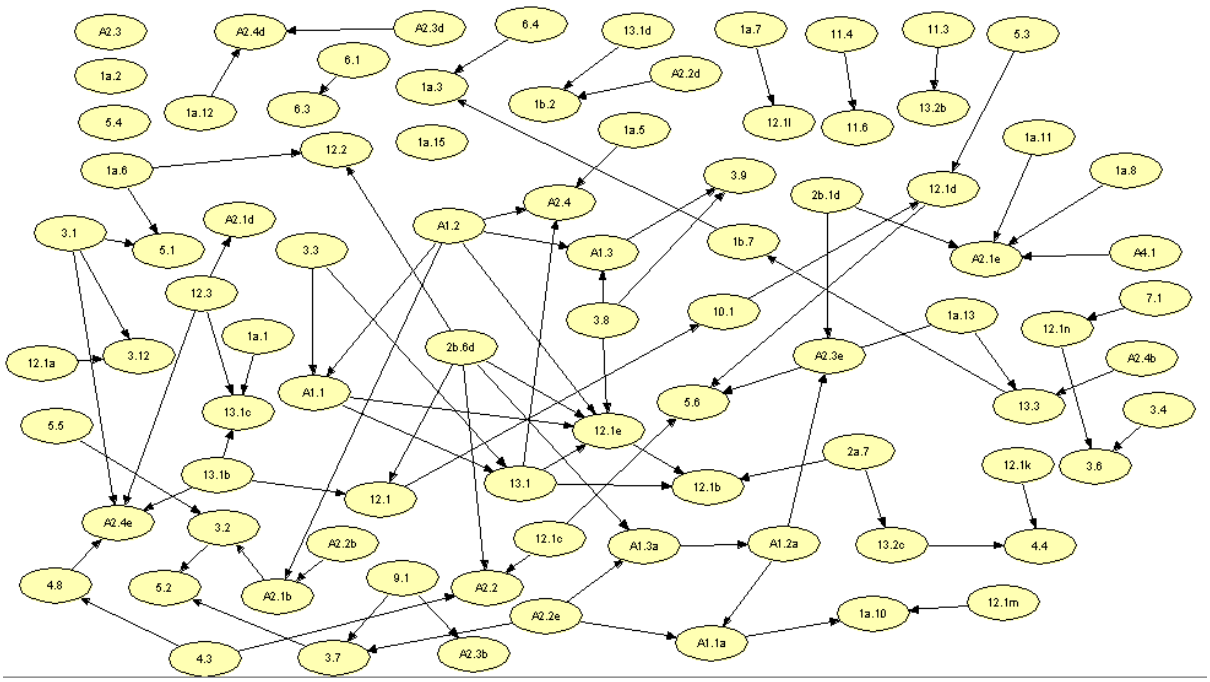

Figure 4.9 The second BN of TQIP indicators without constraints.

4.7 Performance Evaluation－Data Similarity

The diagrams in Sec. 4.6 may help to illustrate the overlapping of multiple, simultaneous Bayesian networks when used with the TQIP indicator sets. In Part One, we realized that the overlapping indicators of 1b.7 and 12.1m connect the two separate Bayesian networks.

In Figure 4.6, indicator 12.1m is isolated without any direct dependency on other indicators. However, indicator 1b.7 has two direct links to the indicators 1b.12 and 2b.4. The causal relationship among the three indicators is shown as 1b.12←1b.7→2b.4. That is, the causal relationship of 1b.12←1b.7→2b.4 is a diverging relationship, i.e., when 1b.7 is known, it blocks the evidence of indicator 1b.12 and 2b.4. On the other hand, when indicator 1b.7 is instantiated, 1b.12 and 2b.4 are d-separated.

Next, in Figure 4.7, indicator 1b.7 has a direct dependency on indicator 1a.3, and the causal relationship is shown as 13.3→1b.7→1a.3, which is the causal relationship of a serial relation. When 1b.7 is known, it blocks the evidence of indicator 13.3 and 1a.3. In addition, when indicator 1b.7 is instantiated, indicator 13.3 and 1a.3 become d-separated. In addition, indicator 12.1m has a causal relationship with indicator 1a.10, e.g., 12.1m→1a.10. The following is the dependency-relation sketch of two sub-BNs.

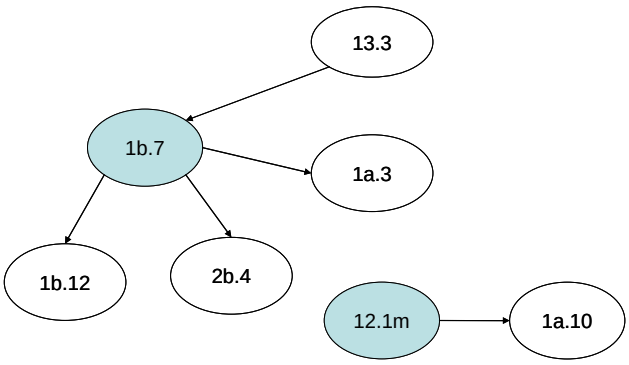

Figure 4.10 The connection sketch of two sub-BNs.

In this way, we measure the similarity between the original indicator data and the indicator data generated from Bayesian networks based on the two formulas of bandwidth h^* (3.10) and the gap of bandwidth d_h (3.11).

First, we compute the bandwidth values of the complete five-year original TQIP records and generate five-year indicator records with the Bayesian network. The following is the result of measuring the overlapping indicators when the "prior information", i.e. the design relations (see in Sec.4.4), is involved.

Table 4.8 The bandwidth value of the original and generated indicators (I).

Indicators	Original h_1	Generated h_2	d_h	Remark (BN I)
1b.1	0.5976	0.6463	0.0487	
1b.3	0.6159	0.7333	0.1174	
1b.5	0.103	0.107	0.004	
1b.6	0.5855	0.5282	0.0573	
1b.7	0.5936	0.1032	0.4904	Overlapping
1b.8	0.138	0.1418	0.0038	
1b.10	0.6451	0.132	0.5131	
1b.11	0.1073	0.5288	0.4215	
1b.12	0.4697	0.11	0.3597	Child indicator
1b.13	0.7444	0.1362	0.6082	
1b.15	0.6735	0.518	0.1555	
2b.1	0.1067	0.1304	0.0237	
2b.1c	0.5184	0.552	0.0336	
2b.2	0.6553	0.5344	0.1209	
2b.2c	0.61	0.7444	0.1344	

Indicators	Original h_1	Generated h_2	d_h	Remark (BN I)
2b.3	0.121	0.1034	0.0176	
2b.3c	0.1023	0.5264	0.4241	
2b.4	0.7963	0.7178	0.0785	Child indicator
2b.4c	0.7379	0.62	0.1179	
2b.4d	0.88	0.9011	0.0211	
2b.5	0.089	0.0702	0.0188	
2b.5c	0.1186	0.1345	0.0159	
2b.6	0.7063	0.7864	0.0801	
2b.6c	0.132	0.3813	0.2493	
6.2	0.1392	0.1304	0.0088	
6.5	0.8095	0.6236	0.1859	
12.1f	0.4796	0.1337	0.3459	
12.1j	0.1263	0.1383	0.012	
12.1m	0.7075	0.1387	0.5688	Overlapping
13.1a	0.1082	0.1124	0.0042	
13.2	0.7025	0.4997	0.2028	
13.2a	0.1152	0.1094	0.0058	
A2.1	0.0898	0.071	0.0188	
A2.1a	0.0995	0.0925	0.007	
A2.2a	0.5715	0.7733	0.2018	
A2.3a	0.107	0.5646	0.4576	
A2.4a	0.4876	0.6169	0.1293	

Table 4.9 The bandwidth value of the original and generated indicators (II).

Indicators	Original h_1	Generated h_2	d_h	Remark (BN II)
1a.1	0.4874	0.4765	0.0109	
1a.2	0.6135	0.1228	0.4907	
1a.3	0.6555	0.5485	0.107	Child indicator
1a.5	0.5266	0.4628	0.0638	
1a.6	0.1285	0.5895	0.461	
1a.7	0.4563	0.1276	0.3287	
1a.8	0.1095	0.0666	0.0429	
1a.10	0.6209	0.1546	0.4663	Child indicator
1a.11	0.7105	0.7473	0.0368	

Indicators	Original h_1	Generated h_2	d_h	Remark (BN II)
1a.12	0.8558	0.5824	0.2734	
1a.13	0.6521	0.6358	0.0163	
1a.15	0.1225	0.1150	0.0075	
1b.2	0.0882	0.6109	0.5227	
1b.7	0.5936	0.6414	0.0478	Overlapping
2a.7	0.4887	0.6483	0.1596	
2b.1d	0.7767	0.6537	0.123	
2b.6d	0.737	0.1724	0.5646	
3.1	0.0904	0.0933	0.0029	
3.2	0.6326	0.1508	0.4818	
3.3	0.1672	0.6898	0.5226	
3.4	0.5513	0.0806	0.4707	
3.6	0.6892	0.1413	0.5479	
3.7	0.1054	0.0809	0.0245	
3.8	0.1086	0.0995	0.0091	
3.9	0.0992	0.0776	0.0216	
3.12	0.0702	0.0810	0.0108	
4.3	0.1215	0.1231	0.0016	
4.4	0.5904	0.5338	0.0566	
4.8	0.5651	0.5595	0.0056	
5.1	0.637	0.6563	0.0193	
5.2	0.0669	0.0724	0.0055	
5.3	0.4981	0.1494	0.3487	
5.4	0.1072	0.1205	0.0133	
5.5	0.5302	0.1204	0.4098	
5.6	0.1004	0.5082	0.4078	
6.1	0.6335	0.0760	0.5575	
6.3	0.6648	0.1360	0.5288	
6.4	0.605	0.1235	0.4815	
7.1	0.5583	0.5850	0.0267	
9.1	0.159	0.6816	0.5226	
10.1	0.1102	0.1040	0.0062	
11.3	0.0706	0.0498	0.0208	
11.4	0.0782	0.0759	0.0023	
11.6	0.466	0.1052	0.3608	
12.1	0.5667	0.1122	0.4545	

Indicators	Original h_1	Generated h_2	d_h	Remark (BN II)
12.1a	0.7324	0.6069	0.1255	
12.1b	0.1514	0.6474	0.496	
12.1c	0.9008	0.4052	0.4956	
12.1d	0.6374	0.1752	0.4622	
12.1e	0.1191	0.7269	0.6078	
12.1k	0.4223	0.1731	0.2492	
12.1l	0.098	0.0826	0.0154	
12.1m	0.7075	0.6825	0.025	Overlapping
12.1n	0.5514	0.1135	0.4379	
12.2	0.1422	0.1697	0.0275	
12.3	0.1039	0.0748	0.0291	
13.1	0.5946	0.5150	0.0796	
13.1b	0.6203	0.5641	0.0562	
13.1c	0.1177	0.7601	0.6424	
13.1d	0.7216	0.1331	0.5885	
13.2b	0.0883	0.0671	0.0212	
13.2c	0.111	0.1151	0.0041	
13.3	0.7528	0.7980	0.0452	
A1.1	0.7004	0.1320	0.5684	
A1.1a	0.8266	0.5537	0.2729	
A1.2	0.866	0.7868	0.0792	
A1.2a	0.6515	0.7721	0.1206	
A1.3	0.8852	0.7443	0.1409	
A1.3a	0.7758	0.9210	0.1452	
A2.1b	0.6226	0.6535	0.0309	
A2.1d	0.1157	0.0939	0.0218	
A2.1e	0.0994	0.6798	0.5804	
A2.2	0.0869	0.5021	0.4152	
A2.2b	0.698	0.7165	0.0185	
A2.2d	0.5575	0.5135	0.044	
A2.2e	0.6942	0.1268	0.5674	
A2.3	0.1399	0.1363	0.0036	
A2.3b	0.612	0.1256	0.4864	
A2.3d	0.0901	0.1087	0.0186	
A2.3e	0.7781	0.7218	0.0563	
A2.4	0.6438	0.6441	0.0003	

Indicators	Original h_1	Generated h_2	d_h	Remark (BN II)
A2.4b	0.8128	0.7152	0.0976	
A2.4d	0.8528	0.6275	0.2253	
A2.4e	0.6491	0.4945	0.1546	
A4.1	0.8148	0.6928	0.122	

Then, when no constraints (See in Sec. 4.6.2) are applied, we achieve the same results as when applying design relations (See in Sec. 4.6.1). In Figure 4.8, indicator 12.1m is isolated without any connections. Indicator 1b.7 has a causal relationship among other two indicators of 1b.12 and 2b.4, which is shown as 1b.12←1a.7→2b.4. It is a diverging relationship, so that when 1b.7 is known, it blocks the evidence of indicator 1b.12 and 2b.4. In addition, in Figure 4.9, indicator 1b.7 has a serial relation shown as 13.3→1b.7→1a.3, which is to say that when 1b.7 is known, it blocks the evidence of indicator 13.3 and 1a.3 (shown in Figure 4.11).

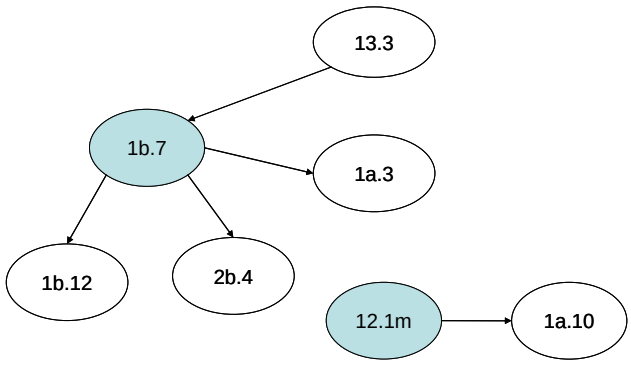

Figure 4.11 The connection sketch of two sub-BNs under no constraints.

Again, we measure the similarity between the original indicator data and the indicator data generated from Bayesian networks based on the two formulas of bandwidth h^* (3.10) and the gap of bandwidth d_h (3.11).

In the same way, we re-compute the bandwidth values of the complete five-year original TQIP records, and once again generate five-year indicator records from the Bayesian network. The following is the result of measuring the overlapping indicators when no constraints are involved.

Table 4.10 The bandwidth value of the original and generated indicators (I)

Indicators	Original h_1	Generated h_2	d_h	Remark (BN I)
1b.1	0.5976	0.1291	0.4685	
1b.3	0.6159	0.4950	0.1209	
1b.5	0.103	0.0886	0.0144	
1b.6	0.5855	0.5712	0.0143	
1b.7	0.5936	0.4592	0.1344	Overlapping
1b.8	0.138	0.1005	0.0375	
1b.10	0.6451	0.0896	0.5555	
1b.11	0.1073	0.4872	0.3799	
1b.12	0.4697	0.4830	0.0133	Child indicator
1b.13	0.7444	0.1496	0.5948	
1b.15	0.6735	0.5870	0.0865	
2b.1	0.1067	0.0993	0.0074	
2b.1c	0.5184	0.0768	0.4416	
2b.2	0.6553	0.6600	0.0047	
2b.2c	0.61	0.5810	0.029	
2b.3	0.121	0.1206	0.0004	
2b.3c	0.1023	0.1115	0.0092	
2b.4	0.7963	0.1338	0.6625	Child indicator
2b.4c	0.7379	0.7116	0.0263	
2b.4d	0.88	0.6455	0.2345	
2b.5	0.089	0.0926	0.0036	
2b.5c	0.1186	0.1245	0.0059	
2b.6	0.7063	0.1398	0.5665	
2b.6c	0.132	0.1291	0.0029	
6.2	0.1392	0.6480	0.5088	
6.5	0.8095	0.1575	0.652	
12.1f	0.4796	0.4423	0.0373	
12.1j	0.1263	0.6313	0.505	
12.1m	0.7075	0.1099	0.5976	Overlapping
13.1a	0.1082	0.1134	0.0052	
13.2	0.7025	0.6106	0.0919	
13.2a	0.1152	0.1084	0.0068	
A2.1	0.0898	0.0585	0.0313	
A2.1a	0.0995	0.1197	0.0202	
A2.2a	0.5715	0.6630	0.0915	

Indicators	Original h_1	Generated h_2	d_h	Remark (BN I)
A2.3a	0.107	0.1102	0.0032	
A2.4a	0.4876	0.7594	0.2718	

Table 4.11 The bandwidth value of the original and generated indicators (II).

Indicators	Original h_1	Generated h_2	d_h	Remark (BN II)
1a.1	0.4874	0.6663	0.1789	
1a.2	0.6135	0.1213	0.4922	
1a.3	0.6555	0.4985	0.157	Child indicator
1a.5	0.5266	0.0993	0.4273	
1a.6	0.1285	0.1322	0.0037	
1a.7	0.4563	0.1309	0.3254	
1a.8	0.1095	0.0989	0.0106	
1a.10	0.6209	0.5641	0.0568	Child indicator
1a.11	0.7105	0.8660	0.1555	
1a.12	0.8558	0.5447	0.3111	
1a.13	0.6521	0.5869	0.0652	
1a.15	0.1225	0.1411	0.0186	
1b.2	0.0882	0.5737	0.4855	
1b.7	0.5936	0.5737	0.0199	Overlapping
2a.7	0.4887	0.0728	0.4159	
2b.1d	0.7767	0.7019	0.0748	
2b.6d	0.737	0.3917	0.3453	
3.1	0.0904	0.0814	0.009	
3.2	0.6326	0.6356	0.003	
3.3	0.1672	0.1071	0.0601	
3.4	0.5513	0.5024	0.0489	
3.6	0.6892	0.6270	0.0622	
3.7	0.1054	0.1236	0.0182	
3.8	0.1086	0.0899	0.0187	
3.9	0.0992	0.1286	0.0294	
3.12	0.0702	0.0814	0.0112	
4.3	0.1215	0.1086	0.0129	
4.4	0.5904	0.4154	0.175	
4.8	0.5651	0.4959	0.0692	

Indicators	Original h_1	Generated h_2	d_h	Remark (BN II)
5.1	0.637	0.1259	0.5111	
5.2	0.0669	0.0714	0.0045	
5.3	0.4981	0.1440	0.3541	
5.4	0.1072	0.0756	0.0316	
5.5	0.5302	0.1190	0.4112	
5.6	0.1004	0.4951	0.3947	
6.1	0.6335	0.1196	0.5139	
6.3	0.6648	0.6835	0.0187	
6.4	0.605	0.1035	0.5015	
7.1	0.5583	0.7848	0.2265	
9.1	0.159	0.6503	0.4913	
10.1	0.1102	0.1065	0.0037	
11.3	0.0706	0.0966	0.026	
11.4	0.0782	0.0871	0.0089	
11.6	0.466	0.5177	0.0517	
12.1	0.5667	0.6057	0.039	
12.1a	0.7324	0.5299	0.2025	
12.1b	0.1514	1.0048	0.8534	
12.1c	0.9008	0.5570	0.3438	
12.1d	0.6374	0.1787	0.4587	
12.1e	0.1191	0.6126	0.4935	
12.1k	0.4223	0.1606	0.2617	
12.1l	0.098	0.0930	0.005	
12.1m	0.7075	0.1243	0.5832	Overlapping
12.1n	0.5514	0.0858	0.4656	
12.2	0.1422	0.1482	0.006	
12.3	0.1039	0.1085	0.0046	
13.1	0.5946	0.1167	0.4779	
13.1b	0.6203	0.5431	0.0772	
13.1c	0.1177	0.8209	0.7032	
13.1d	0.7216	0.6607	0.0609	
13.2b	0.0883	0.0979	0.0096	
13.2c	0.111	0.1027	0.0083	
13.3	0.7528	0.5156	0.2372	
A1.1	0.7004	0.5200	0.1804	
A1.1a	0.8266	0.6613	0.1653	

Indicators	Original h_1	Generated h_2	d_h	Remark (BN II)
A1.2	0.866	0.7184	0.1476	
A1.2a	0.6515	0.6909	0.0394	
A1.3	0.8852	0.6930	0.1922	
A1.3a	0.7758	0.8565	0.0807	
A2.1b	0.6226	0.6377	0.0151	
A2.1d	0.1157	0.1107	0.005	
A2.1e	0.0994	0.6415	0.5421	
A2.2	0.0869	0.4966	0.4097	
A2.2b	0.698	0.1306	0.5674	
A2.2d	0.5575	0.5273	0.0302	
A2.2e	0.6942	0.7555	0.0613	
A2.3	0.1399	0.1293	0.0106	
A2.3b	0.612	0.6224	0.0104	
A2.3d	0.0901	0.1026	0.0125	
A2.3e	0.7781	0.7613	0.0168	
A2.4	0.6438	0.4718	0.172	
A2.4b	0.8128	0.7275	0.0853	
A2.4d	0.8528	0.7392	0.1136	
A2.4e	0.6491	0.4920	0.1571	
A4.1	0.8148	0.7450	0.0698	

In our study, we set two thresholds of 0.01 and 0.05 used as significant levels depending on our two cases. In the above two cases, we can see that regardless of design relations or non-constraints, the similarity between data gathered from the original indicators and the indicators generated from the Bayesian network partially falls within the settled interval (0.01 and 0.05) of this study (shown in Table 4.12, 4.13, and 4.14). In concern with the quantity of the compared data sets, this is because the original indicators are identically recorded and independent of each other, and because the Bayesian network molds the generated indicators to possess causal relationships among themselves. Furthermore, the state-transformation might affect the similarity between the two compared data sets.

Table 4.12 The interval of bandwidth of indicators within BN (I).

Indicators	d_h	Remark
1b.5	0.004	BN I
1b.8	0.0038	
6.2	0.0088	
13.1a	0.0042	
13.2a	0.0058	
A2.1a	0.007	
1a.15	0.0075	
3.1	0.0029	
3.8	0.0091	
4.3	0.0016	
5.2	0.0055	
10.1	0.0062	
11.4	0.0023	
13.2c	0.0041	
A2.4	0.0003	
Indicators	d_h	Remark
2b.1	0.0074	BN II
2b.2	0.0047	
2b.3	0.0004	
2b.3c	0.0092	
2b.5	0.0036	
2b.5c	0.0059	
2b.6c	0.0029	
13.1a	0.0052	
13.2a	0.0068	
A2.3a	0.0032	
1a.6	0.0037	
3.1	0.009	
3.2	0.003	
5.2	0.0045	
10.1	0.0037	
11.4	0.0089	
12.1l	0.005	
12.2	0.006	
12.3	0.0046	
13.2b	0.0096	
13.2c	0.0083	
A2.1d	0.005	

Table 4.13 The interval of bandwidth of indicators within BN (II).

Indicators	d_h	Remark
1b.1	0.0487	BN I
1b.5	0.004	
1b.8	0.0038	
2b.1	0.0237	
2b.1c	0.0336	
2b.3	0.0176	
2b.4d	0.0211	
2b.5	0.0188	
2b.5c	0.0159	
6.2	0.0088	
12.1j	0.012	
13.1a	0.0042	
13.2a	0.0058	
A2.1	0.0188	
A2.1a	0.007	
1a.1	0.0109	
1a.8	0.0429	
1a.11	0.0368	
1a.13	0.0163	
1a.15	0.0075	
1b.7	0.0478	
3.7	0.0245	
3.8	0.0091	
3.9	0.0216	
3.12	0.0108	
4.3	0.0016	
4.8	0.0056	
5.1	0.0193	
5.2	0.0055	
5.4	0.0133	
7.1	0.0267	
10.1	0.0062	
11.3	0.0208	
11.4	0.0023	
12.1m	0.025	
12.2	0.0275	
12.3	0.0291	

13.2b	0.0212	
13.2c	0.0041	
13.3	0.0452	
A2.1b	0.0309	
A2.1d	0.0218	
A2.2b	0.0185	
A2.2d	0.044	
A2.3	0.0036	
A2.3d	0.0186	
A2.4	0.0003	

Table 4.14 The interval of bandwidth of indicators within BN (II).

Indicators	d_h	Remark
1b.5	0.0144	BN II
1b.6	0.0143	
1b.8	0.0375	
1b.12	0.0133	
2b.1	0.0074	
2b.2	0.0047	
2b.2c	0.029	
2b.3	0.0004	
2b.3c	0.0092	
2b.4c	0.0263	
2b.5	0.0036	
2b.6c	0.0029	
12.1f	0.0373	
13.1a	0.0052	
13.2a	0.0068	
A2.1	0.0313	
A2.1a	0.0202	
A2.3	0.0032	
1a.6	0.0037	
1a.8	0.0106	
1a.15	0.0186	
1b.7	0.0199	
3.1	0.009	
3.2	0.003	
3.4	0.0489	
3.7	0.0182	

3.8	0.0187	
3.9	0.0294	
3.12	0.0112	
4.3	0.0129	
5.2	0.0045	
5.4	0.0316	
6.3	0.0187	
10.1	0.0037	
11.3	0.026	
11.4	0.0089	
11.6	0.0517	
12.1	0.039	
12.1l	0.005	
12.2	0.006	
12.3	0.0046	
13.2b	0.0096	
13.2c	0.0083	
A1.2a	0.0394	
A2.1b	0.0151	
A2.1d	0.005	
A2.2d	0.0302	
A2.3	0.0106	
A2.3b	0.0104	
A2.3d	0.0125	
A2.3e	0.0168	

However, by utilizing BN Learner, we construct a Bayesian network based on TQIP Acute Care indicators. Within the Bayesian network, in terms of raw data, the overlapping-indicators 1b.7 and 12.1m could be the key to surveying the quality of medical care in hospitals.

In addition, in terms of data, indicator 1b.7 “Ventilator use in the CCU” affects three indicators of 1b.12 “Indwelling urinary catheter use in the CCU”, 2b.4 “Antibiotic prophylaxis for appendectomy” and 1a.3 “Central line-associated bloodstream infections in the MICU”. In addition, indicator 13.3 “Repeat Falls” affects indicator 1b.7, and indicator 12.1m “Physical restraint events initiated between 3:00 p.m. and 10:59 p.m.” affects indicator 1a.10 “Ventilator-associated pneumonia in the SICU”. Hence, we can realize the two signal-indicators of 1b.7 and 12.1m within the Bayesian network and give

hospitals an auxiliary-assessment objectively utilizing the Acute Care TQIP indicators.

Furthermore, in this study, we still can get a portion of indicators falls within the settled thresholds (shown in Table 4.15). Although the bandwidth selection is a further point that needs to be considered, we still consider that the thresholds are fit to TQIP indicator-data sets. Thus, a similar data structure between the two indicator sets could be satisfied.

Table 4.15 The portion (%) of bandwidth-value within thresholds.

Type/thresholds	d_h<0.01	d_h<0.05
Design relations involved	12.4	40.5
Without constraints	18.2	42.1

As result, it seems reasonable to suggest that, in the final analysis, this study primarily to provide an explanation or understanding of how data are generated. Accordingly, we may view our quest for understanding how indicator-data is generated or how indicators work as a quest for acquiring the ability to make prediction under wider range of circumstances, including things are taken apart or reconfigured among TQIP indicators.

CHAPTER 5 CONCLUSIONS AND FUTURE RESEARCH

In this study, the *Equally-weighted discretization technique* is used to divide the individual TQIP indicators into standardized intervals. In addition, the *FCM clustering algorithm*, which is used to cluster TQIP indicators, reduces the complexity of the network structure while utilizing the Bayesian network construction.

Bayesian networks are built by using the HUGIN Tool, which is based on the PC algorithm. We construct two separate Bayesian networks for TQIP indicators depending either on the use of design relations or without the use of design relations. In summary, in terms of raw data, this study provides a method for hospitals to survey the provision of quality medical services. In addition, an integrated representation of Bayesian networks is provided to determine probability relationships among these TQIP indicators of healthcare quality settings, and also to identify any deficiency among indicators while surveying the performance of medical quality in hospitals.

In addition, we may view our quest for understanding how indicator-data is generated or how indicators work as a quest for acquiring the ability to make prediction under wider range of circumstances, including things are taken apart or reconfigured among TQIP indicators.

This study proposes a method to analyze the relevance and uncertainty among TQIP indicators. In addition, we devise a feasible mechanism to deal with the structure and parameters of TQIP indicators, and to form a nonlinear Bayesian network. However, in order to improve the TQIP network more completely, there are several further directions that need to be explored in future research.

1. This study is not concerned with the function of time. As collecting long-term data for TQIP indicators would better illustrate the healthcare system’s quality performance, a solution for integrating dynamic time-series data into the Bayesian networks should be explored.
2. In this study, the TQIP indicators are continuous variables. However, discrete or categorical data can be used efficiently in Bayesian networks. Here, we

adopt the equally weighted state-transformation depending on the ranges of indicators. Nevertheless, univariate discretization of indicators may destroy hidden patterns in data. Hence, a feasible merging-method might be considered that could divide continuous variables based on similar multivariate distributions across all variables and combinations of variables.

3. As a large quantity of TQIP indicators must be analyzed, an efficient method of combining clustering and the Bayesian network is a further point that needs to be considered. It is hoped that the problem complexity can be reduced and the explanative power of the Bayesian model can be increased.
4. If the large quantity of data is a constraint, using more sparse data with greater dimensionality is an issue to be considered. These issues of data capacity, complexity, and generalization must be settled if the BN is to interpret data appropriately.
5. In this study, in terms of data, two thresholds of 0.01 and 0.05 are set to fit our data sets. Deciding the appropriate bandwidth-selection by cases will be a further point that needs to be considered.

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