Chapter One

Introduction

1.1General View

Lung cancer is the uncontrolled growth of abnormal cells in one or both of the lungs. While normal cells reproduce and develop into healthy lung tissue, these abnormal cells reproduce faster and never grow into normal lung tissue, lumps of cancer cells (tumors) then form and grow.Besides interfering with the way lung functions, cancer cells can spread from the tumor into the bloodstream or lymphatic system where they can spread to other organs.

Bayesian networks (or belief networks) are probabilistic graphical models representing a set of variables and their dependencies. The graphical nature of Bayesian networks and the ability of describing uncertainty of complex relationships in a compact manner provide a method for modeling almost any type of data.

Various cancer diagnosis algorithms have been proposed for the characterization of microcalcifications (MCs), an important indicator of malignancy. These algorithms are based on extracting image features from regions of interest (ROIs) and estimating the probability of malignancy for a given MC cluster. A variety of computer-extracted features and classification schemes have been used to automatically discriminate between benign and malignant MC clusters. The majority of these studies have followed two approaches. The first approach is based on computer extracted morphology/shape features of individual MCs or of MC clusters [1], since

morphology is one of the most important clinical factors in breast cancer diagnosis.CAD schemes that employ the radiologists' ratings of MCs morphology have also been proposed. The second approach employs texture features extracted from ROIs containing MC clusters [1].Lyra, M., et.al.,2008, investigated the use of mammograms texture features and classified an image based on the breast tissue index. The features used include the gray-level histogram, and texture features based upon the gray level co-occurrence matrix and moment based features obtained by Matlab program. The results indicate improvement that is related to breast density classification in mammograms. They noted that the proposed method can be applied to other imaging modalities like Ultrasound [2].

Artificial Neural Networks (ANN) is proved to be effective in medical diagnostic model. A number of researchers in Suez Canal University, 2006, suggested a model consists of artificial neural networks designed for classifying mammograms according to tumor type and risk level. A wavelets coefficients used as a network input pattern and a suit of Multi-Layer Perceptron (MLP) is used with the classic Back-Propagation learning algorithm. The proposed diagnosis system achieves good results in classifying the mammograms [3].

J.S.Leena Jasmine, et.al., 2010, presented a new approach for detecting microclassification and that by extracting the microclassification features from the contourlet coefficients of the image and these results are used as an input of neural network. The experiments demonstrated that approach provided better classification rate. The evaluation of the system is carried on Mammography Image Analysis society (MIAS) database [4].

1.2Statement of Problem:

Lungtumorsare among the most difficult medical investigation and used the X-Ray image to be read according to the overlap of lung tissues with thoracic cage bones, furthermore it is hard to detect the earlier lung cancer, because the tumor is too small to be picked up i.e. perceived by the eye. Thus the task of the radiologist is tedious and misdiagnosis of lung cancer most of the time occurs.

This research represents a simplified model to help diagnose the patients arriving at a respiratory clinic. A history of smoking has a direct influence on both, whether a patient has bronchitis or lung cancer.

1.3 Objectives:

The objectives of this research areto:

1. develop an algorithm that delineates the lung cancer on X-Ray images for the lung by Bayesian Neural Network.
2. choose the best subset of features that helps on visualization of lung tumors.
3. detectpresence or absence of lung cancer has direct influence on the results of a chest X-ray test.

1.4Methodology

In this research it isdoing probabilistic inference of lung cancer diagnosis involving features that are not directly related, and for which the conditional probability cannot be readily computed using:

1. Application of Bayesian Network example for exact probabilistic inference.
2. Pearl's message-passing algorithm to model the diagnostic of lung cancer.

1.5 Thesis Layout

In this research the implementation of one of the most advanced techniques to diagnose lung cancer is explained through the following:

The second chapter explains the Literature review.

The third chapter presents theoretical background about the Neural Network used in this model (Bayesian Neural Network) Bayesian Network basics, Structure & Probabilities. Also the Pearl's Belief Propagation Algorithm, Purpose of Algorithm with boundary conditions.In addition to general view for Lung;anatomically, physiologically and the main causes of Cancers with illustrations of cancer disease in different stages with different infusing factors.

In the fourth Chapter about the proposed system (Methodology) and result of using ofdemo that illustrates a simple Bayesian Network example for exact probabilistic inference using Pearl's message-passing algorithm to model the diagnostic of lung cancer with MatLab presence.

Results, conclusions and recommendations illustrated in chapter five.

Chapter Two

Literature Review

2.1 Literature review

1. Kornelpapik,Zalan,Dombovari,Zsolttulassay,Janos, feher and Belamolnar,1998, computer generated neural network and its applications have been described. A study of the applications of neural network in basic sciences, clinical medicine, signal processing and interpretation and medical image processing can be seen in Wan Hussain.
2. Wan Ishak (2002).Rusovick and Warner (1997) defined telemedicine as any instance of medical care occurring via the internet and using real-time video-teleconferencing equipment as well as more specialized technique.
3. Norsarini Salim (2004) discusses how Neural Network approach can diagnose disease using patient medical data such as breast cancer, heart failure, medical images, acidosis diseases, and lung cancer.
4. Peter M. Ravdin, et al(1992) and Wu, Y., et al developed a neural network model to diagnose breast cancer. Frenster, J.H. ,1990. described the Neural Network model for Pattern Recognition in Medical Diagnosis. A method of selecting training data for neural network is presentedEberhart, R.,Hernandez, C.A. et al. 1993.
5. Micheli-Tzanako ,1990. Dealt with various aspects and applications of neural networks in a wide spectrum of biomedical engineering problems. MengJooEr ,Shiqian Wu , Juwei Lu& Hock Lye Toh,1999. have developed

efficient neural network approach using a radial basis function (RBF) neural classifier to cope with small training sets of high dimension.

6. Jari J. Forsstrm , Kevin J. Dalton ,1995. developed connectionist models such as neural networks, which define relationships among input data that are not apparent when using other approaches. They also reviewed the use of neural networks in medical decision support.
7. Paulo J. Lisboa ,Azzam F. G. Taktak, 2006. Assessed the benefit of artificial neural networks (ANNs) as decision making tools in the field of cancer. In the work of G Wilym s. Lodwick,M.D.,RichardConners and Charles A. Harlow ,1979, an efficient neural network model has been developed to diagnose the carcinogenesis.
8. Neural network have been applied to breast cancer diagnosis. Kiyan and Yildirim, 2003.employed Radial Basis Function, General Regression Neural Network and Probabilistic Neural Network in order to get the suitable result.

Chapter Three

Theoretical Background

3.1 Bayesian Network

Bayesian networks (or belief networks) are probabilistic graphical models representing a set of variables and their dependencies. The graphical nature of Bayesian networks and the ability of describing uncertainty of complex relationships in a compact manner provide a method for modeling almost any type of data.

3.1.1 Bayesian network basics

A Bayesian network is a graphical structure that allows representing and reasoning about an uncertain domain. The nodes in a Bayesian network represent a set of random variables, X = X1,..Xi,...Xn, from the domain. A set of directed arcs (or links) connects pairs of nodes, Xi → Xj, representing the direct dependencies between variables. Assuming discrete variables, the strength of the relationship between variables is quantified by conditional probability distributions associated with each node. The only constraint on the arcs allowed in a BN is that there must not be any directed cycles, one cannot return to a node simply by following directed arcs. Such networks are called directed acyclic graphs, or simply dags. There are a number of steps that a knowledge engineer must undertake when building a Bayesian network. At this stage these steps are presented as a sequence; however it is important to note that in the real-world the process is not so simple [9].

3.1.2Bayesian Networks – Structure

Are simple, graphical notations for conditional independence assertions, hence for compact specifications of full joint distributions.

A BN is a directed graph with the following components:

1. **Nodes:** one node for each variable
2. **Edges:** a directed edge from node Ni to node Nj indicates that variable Xi has a direct influence upon variable Xj [10].

3.1.3Bayesian Networks – Probabilities

In addition to the structure, a conditional probability distribution is needed for the random variable of each node given the random variables of its parents (i.e. P(Xi | Parents(Xi))). Nodes/variables that are not connected are (conditionally) independent

3.1.4 Bayesian Networks Pearl's Belief Propagation Algorithm

3.1.4.1 Purpose of Algorithm

"... Deals with fusing and propagating the impact of new evidence and beliefs through Bayesian networks so that each proposition eventually will be assigned a certainty measure consistent with the axioms of probability theory."[Pearl, 1988] [13]

- Notations
- Algorithm

This propagation algorithm assumes that the Bayesian network is singly connected, ie. The graph is a directed acyclic graph (DAG)[10]. As shown in figure (3.1)that illustrate the section of a singly connected network around node X.

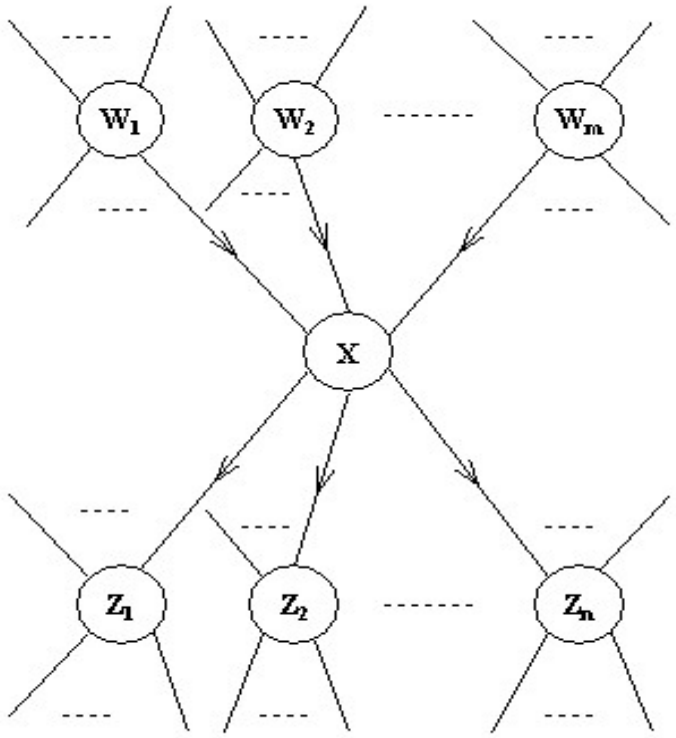


Fig.3.1 – Section of a singly connected network around node X.[9]

Propagation Rules

The likelihood vector is equal to the term-by-term product of the entire message passed from the node's children [9] as shown in formula 1 below.

$$\lambda(x) = \prod_{j=1}^{n} \lambda_{Z_j}(x) \quad \textbf{(1)}$$

The prior probabilities vector is equals to the dot product of the conditional probabilities matrix of X given all the possible combination values of its parents and the π message passed down from its parents; illustrated in formula 2 below.

$$\pi(x) = \sum_{\mathbf{W}} P(x \mid \mathbf{w}) \prod_{k=1}^{n} \pi_X(w_k) \quad \textbf{(2)}$$

It is believed that the values of X are equal to the normalized term-by-term product of the likelihood vector and the prior probabilities vector as shown in formula 3 below.

$$\begin{aligned} BEL(x) &\equiv \alpha\lambda(x)\pi(x) \\ &= \alpha \left[\prod_{j=1}^{n} \lambda_{Z_j}(x)\right] \left[\sum_{\mathbf{W}} P(x \mid \mathbf{w}) \prod_{k=1}^{n} \pi_X(w_k)\right] \end{aligned} \quad \textbf{(3)}$$

Updating λ

To explain the update, see examples. NB: If (x) is a unit vector (i.e. all 1's) then the output of the formula would also be a unit vector as illustrate in formula 4 below.

$$\lambda_X(w_i) = \beta \sum_x \lambda(x) \sum_{w_k : k \neq i} P(x \mid \mathbf{u}) \prod_{k \neq i} \pi_X(w_k) \quad \textbf{(4)}$$

Updating π

The message that X is going to pass onto a particular child is equals to the belief of X divided (term-by-term) by the message that child sent to X. Here, division by zero is only defined when the numerator is also equals to zero. Zero divided by zero is defined as zero in this case. See formula 5 below.

$$\begin{aligned} \pi_{Z_j}(x) &= \alpha \prod_{k \neq j} \lambda_{Y_k}(x) \pi(x) \\ &= \alpha \frac{BEL(x)}{\lambda_{Y_j}(x)} \\ &\quad \text{careful when } \lambda_{Y_j} \text{ contains zero values} \end{aligned} \quad \textbf{(5)}$$

3.1.4.2 Boundary Conditions

1. Root nodes: If X is a node with no parents, we set the π value equal to the prior probabilities of P(x).
2. Anticipatory nodes: If X is a childless node that has not been instantiated, we set the λ value as a vector of all 1's.
3. Evidence nodes: If evidence $X=x_i$ is obtained, we set the λ value to (0,...,0,1,0,...0) with 1 at the i_{th} position [9].

3.1.4.3Dealing with Cycles

Pearl's belief propagation assumes a single connected networkexists, so what happens when a multiple connected network like in Figure3.2 exists?

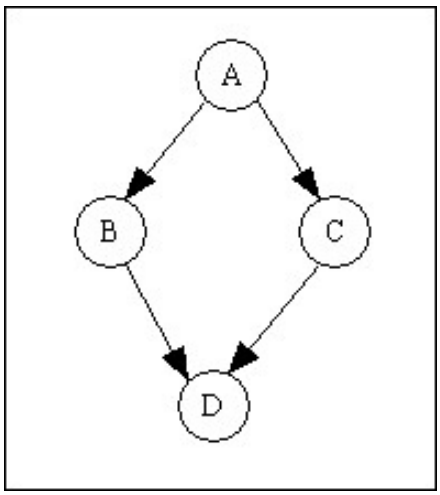


Fig. 3.2 - A multiple connected network. [9]

One method to deal with this situation is called clustering. It involves combining nodes together and treating them as a single node, albeit a more complex one. For example, in the above figure, we can combine the nodes B and C together as node Z, Figure 3.3

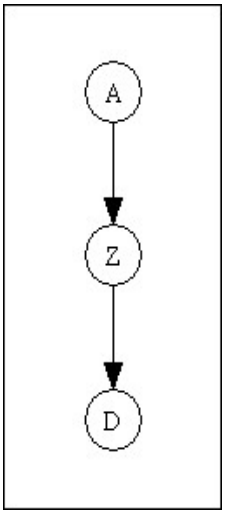


Fig3.3- Possible solution.[9]

This eliminates the cycle in the graph and Pearl's belief propagation can be used as normal with the exception the data for B and C has to be separated in Z if the need arises. A common way of selecting the clusters in a graph is called **junction trees**. Since it is not demonstrated in our applet or examples.

Another technique to deal with multiple connected network is called **stochastic simulation** which will be left here as a reference.

3.2Lung Cancer

3.2.1Introduction

Lung cancer is the number one cancer killer of men and women. Over 165,000 people die of lung cancer every year in the United States. Most cases of lung cancer are related to cigarette smoking. Therefore, it is best for smokers to stop smoking as soon as possible [11].

This reference summary will help better understanding of lung cancer and the treatment options that are available.

3.2.2 Anatomy

Lungs are a pair of large organs in the chest. They are part of the respiratory system. The right lung has three parts (lobes) and the left lung is smaller and has two lobes. A thin tissue (the pleura) covers the lungs and lines the inside of the chest. Between the two layers of the pleura is a very small amount of fluid (pleural fluid). Normally, this fluid does not build up.

Oxygen is vital for life, without it, death occurs very rapidly. The lungs allow oxygen to enter and supply the blood. During breathing- in, lungs expand with air and during breathing- out; air goes out of the lungs.

During breathing the air goes through the mouth and nose and comes in close contact with the blood in the lungs. The blood fills up with oxygen and releases wastes, like carbon dioxide back out into the air.

The air enters through the air pipe, known as the trachea and then it goes into smaller tubes, called bronchial tubes.Small balloon-like sacs called alveoli are at the end of the tubes. The walls of the alveoli are very thin. On the other side of the walls small blood vessels exist. The very thin wall of the alveoli allows the oxygen to go to the bloodstream and also allows Co2 to leave the blood to thelungs to be exhaled.

The inner lining of the bigger bronchial tubes secrete a special substance called mucus. The mucus helps trap dirt from the air. Mucus is continually expelled from the lungs. Just like with saliva, mucus is often swallowed, without thinking about it.

Very small brushes, known as cilia, continually push the mucus to the outside. The cilia are like the hairs, or bristles of a brush. If the mucus becomes sufficiently big, it is coughed out.

3.2.3 Cancer and Its Causes

The body is made up of billions of small cells. Together, many cells make up organs, like the lungs, the heart, or the bones. Usually, when the cells get old or damaged, they die and are replaced by new cells. Sometimes, cells continue to grow and divide when they aren't needed, causing an abnormal growth called a tumor.

There are two kinds of tumors. If the tumor does not invade nearby body parts, it is called a benign tumor or a non-cancerous growth. Benign tumors are rarely life threatening. Benign tumors usually do not need to be removed.

If the tumor does invade and destroy nearby cells, it is called a malignant tumor or cancer. Malignant lung tumors may grow back after being removed. Cancer can be lifethreatening. Cancerous cells spread by breaking from the original tumor. They enterblood vessels or lymph vessels, which branch into all the tissues of the body. The cancer cells attach to other organs and form new tumors that may damage those organs. The spread of cancer is called metastasis.

Cancer treatments aim to kill or control cancerous cells.

Cancers in the body are given names, depending on where they first began. Cancer that begins in the lungs will always be called lung cancer, even if it has spread to another place such as the liver, bones, or brain. Although doctors can locate where a cancer started, the cause of cancer in a patient cannot usually be identified.

Cells contain hereditary, or genetic, materials called chromosomes. This genetic material controls the growth of the cell. Cancer tends to run in families, so people with close relatives that have cancer should be examined regularly for any sign of it. Cancer always develops from changes that occur in the chromosomes. When the genetic material in a cell becomes abnormal, it can lose the ability to control its growth. Sudden changes in genetic material can occur for a variety of reasons. This tendency may be inherited.

Experts also agree that smoking tobacco, chewing tobacco and being exposed to tobacco smoke can all lead to lung cancer.Exposure to chemicals or other

factors in the environment, like pollution or asbestos (old wall insulation in homes), might increase cancer risk, too.

3.2.4Symptoms and Their Causes

There are two main types of lung cancer: non-small cell and small cell. Non-small cell lung cancer is more common, slow growing, and does not spread to other organs rapidly while small cell lung cancer is not as common as non-small cell, but it is fast growing and spreads very rapidly to other organs[5].

Cigarette smoking or exposure to second-hand smoke causes the majority of lungcancer cases.Cigarettes contain over 4000 chemicals; 40 of these chemicals can cause cancer.Smoking filtered or unfiltered cigarettes does not help prevent cancer. Chewingtobacco also causes cancer.Pipe and cigar smoking increases the risk of lung cancer, although not as severely as cigarette smoking.Exposure to pollution, radioactive materials, asbestos and other products also increases the chance of developing lung cancer.Stopping smoking and avoiding exposure to cancer-causing environments, like chemicals, lowers the risk of developing lung cancer, even after years of smoking.

Early stage lung cancer often does not cause symptoms. But as the cancer grows, common symptoms may include:

1. A cough that gets worse or does not go away.
2. Coughing up blood.
3. Hoarseness.
4. Shortness of breath, chest pain, or wheezing.

5. Weight loss with no known cause or loss of appetite.

Other symptoms of lung cancer include:

1. Swelling in the face or neck.
2. Repeated lung infections or bronchitis.
3. Fever.
4. General weakness - specifically in shoulder, arm, or hand.

3.2.5 Diagnosis

Chest X-rays are very useful in determining whether there are any abnormalities in the lungs.

A CAT scan of the lung, a more detailed X-ray of the lungs, helps determine the exact location of lesions found on a chest X-ray.

3.2.6Finding Lung Cancer Cells:

The only sure way to know if lung cancer is present is for a pathologist to check samples of cells or tissue. The pathologist studies the sample under a microscope and performs other tests like CT-Scan [11].

There are many ways to collect samples:

1. Sputum cytology: sputum is coughed up from the lungs
2. Thoracentesis: the doctor uses a long needle to remove pleural fluid from the chest.

3. Bronchoscopy: The doctor inserts a thin, lighted tube through the nose or mouth into the lung for examination and possible removal of cells.
4. Fine needle aspiration: the doctor uses a thin needle to remove tissue or fluid from the lung or lymph node.

After a biopsy of the lung lesion is done, the pathologist helps determine if the lesion is cancerous or not. If the lesion is found to be cancerous, the doctor will need more tests to see if the cancer has spread to other parts of the body, and to find out what stage the cancer is in. The further a cancer has spread, the higher is the stage. If it appears that the cancer has spread, further tests may be performed to determine the exact location of the cancer. A bone scan, a special radiological exam, may be done to check the bones.

A doctor may recommend a CAT scan to check for cancer that may have spread to the abdomen and pelvis areas. He may also recommend an MRI of the head to check for cancer that may have spread to the brain. Blood tests may be necessary to check for anemia, liver, or kidney problems.

However, lung lesions may not turn out to be cancerous. A lung lesion may indicate an old or new infection in the lungs. Lung lesions may also indicate benign tumors, as opposed to malignant tumors, which are cancerous. Benign tumors do not have cancer cells in them.

3.2.7Treatment

The treatment of lung cancer depends on the type of lung cancer and its stage. People with lung cancer may have surgery, chemotherapy, radiation therapy, targeted therapy, or a combination of treatments.

Cancer treatment is either local therapy or systemic therapy:

Local therapy: Surgery and radiation therapy are local therapy. They remove or destroy cancer in the chest.

Systemic therapy: Chemotherapy and targeted therapy are systemic therapies.

The drugs enter the bloodstream and destroy or control cancer throughout the body.

3.2.7.1 Surgery

Surgery for lung cancer removes the tissue that contains the tumor. The surgeon can remove part of the lung or the entire lung. Removal of a small part of the lung is a wedge resection; removal of a lobe of the lung is a lobectomy and a pneumonectomyis removal of the entire lung. The surgeon also removes nearby lymph nodes [11].

3.2.7.2Radiation Therapy

Radiation therapy uses high energy rays to kill cancer cells. It affects cells in the treated area. External radiation is the most common type of radiation therapy for lungcancer. Treatments are usually 5 days a week for several weeks. The side effectsdepend on the type of radiation therapy, the dose of radiation and the part of thebody that is treated.

3.2.7.3 Chemotherapy

Chemotherapy uses drugs to kill cancer cells. The drugs/medication enters the bloodstream and can affect cancer cells all over the body [7].

Chemotherapy is given in cycles. A patient has a rest period after each treatment period.

The side effects depend mainly on which drugs are given and the quantity of the dose. The drugs can harm normal cells that may divide rapidly [11].

3.2.7.4 Targeted Therapy

Targeted therapy uses drugs to block the growth and spread of cancer cells. These drugs target, or alter, a specific molecule or pathway needed for the cancer cells growth. Some patients with non-small cell lung cancer that has spread receive a targeted therapy [6].

If the lung cancer has not spread and is relatively small, surgery may be necessary to take the cancer out. Radiation therapy and chemotherapy may also be necessary to either try to cure the cancer or, at least, to slow its growth.

Summary

Lung cancer is not a rare disease. Prevention of lung cancer is the most effective way to fight it. Not smoking is the single most important thing anyone can do to avoid lung cancer.

Chapter Four

The proposed system (Methodology)

4.1 Introduction

Consider the following model, representing model to:

1. help diagnose the patients arriving at a respiratory clinic. A history of smoking has a direct influence on both whether or not a patient has bronchitis or lung cancer. In turn,
2. the presence or absence of lung cancer has direct influence on the results of a chest X-ray test.
3. A probabilistic inference involving features that are not directly related, and for which the conditional probability cannot be readily computed using an application of the Bayes' theorem is to be done.

4.2 Sample collection

Samples collected over 200 patients from four Medical Diagnostic Center in Khartoum state with full record of all demographic data including smoking history and all investigations records and follow up with their results to compared with results that issued by this diagnosis model .

Make the conditional probability percent to use as input data to the program as below:

4.1 Conditional Probability Table

Variables	CP True	CP False	Quantity in Sample
Smokers	0.20	0.8	40
Lung Cancer	0.30	0.005	60
X-Ray (LC)	0.60	0.02	36
Bronchitis	0.25	0.05	50

4.3Creating the Bayesian Network

A Bayesian network consists of a direct-acyclic graph (DAG) in which every node represents a variable and every edge represents a dependency between variables. We construct this graph by specifying an adjacency matrix where the element on row *i* and column *j* contains the number of edges directed from node *i* to node *j*. The variables of the models are specified by the graph's nodes: `S` (smoking history), `B` (bronchitis), `L` (lung cancer) and `X` (chest x-ray). The variables are discrete and can take only two values: true (t) or false (f) as described in appendix A.1.

In addition to the graph structure, the parameters of the model need to be specified, namely the conditional probability distribution. For discrete variables, this distribution can be represented as a table (Conditional Probability Table, `CPT`), which lists the probability that a node takes on each of its value, given the value combinations of its parents.

4.4Visualizing the Bayesian Network as a Graph

The network structure can be visualized using the `biograph` object. The properties of nodes and edges can be changed as described in appendix A.1 .

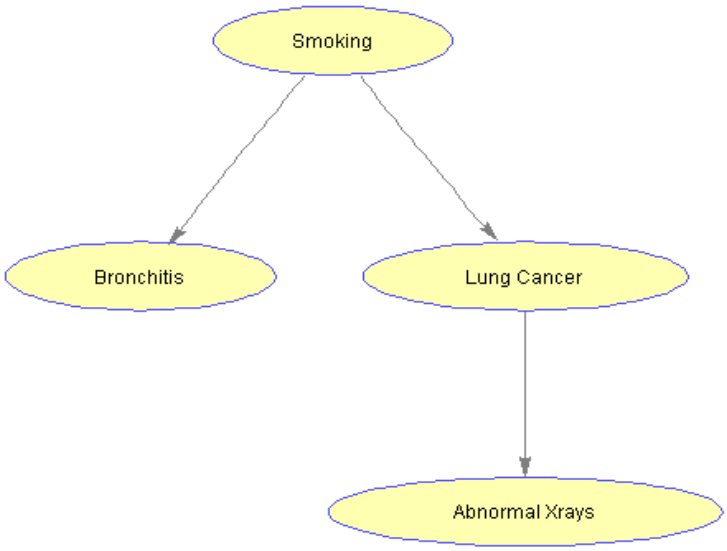


Fig 4.1 Bayesian Network – Graph structure

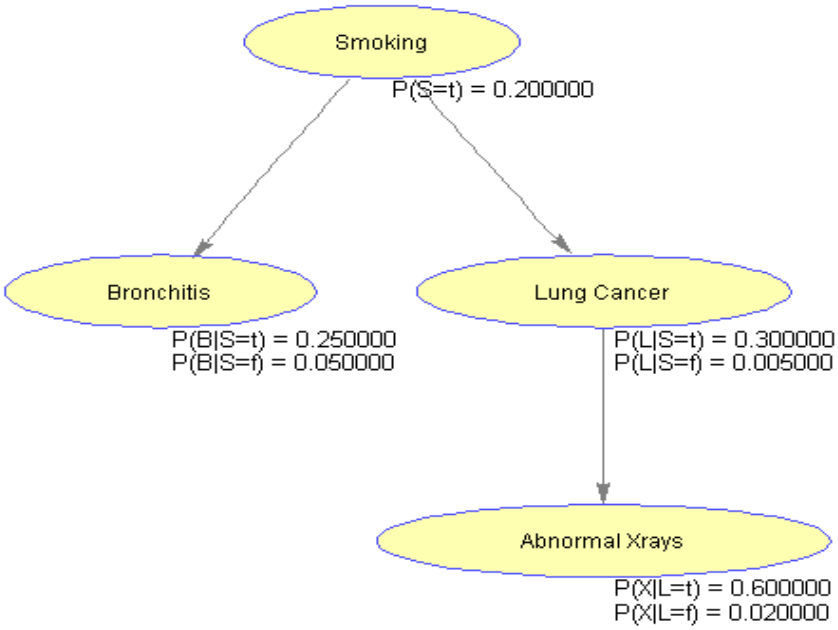


Fig 4.2 Bayesian Network Graph structure – CPT

4.5Initializing the Bayesian Network

The process of computing the probability distribution of variables given specific evidence is called probabilistic inference. By exploiting local independencies among nodes, Pearls [13] developed a message-passing algorithm for exact inference in singly-connected networks. The algorithm can compute the conditional probability of any variable given any set of evidence by propagation of beliefs between neighboring nodes. For more information about the message-passing algorithm see [12]. A Bayesian network for the example under consideration can be create and initiate as follows:

The algorithm parameters, including the conditional probability of each node given the evidence, are stored in the fields of the MATLAB structures

`nodes`and `edges`. Using the function `customnodedraw`, the distribution of the conditional probability can be visualized given an empty set of evidence in a series of pie charts, as shown below.

Results:

```
P(S|[]) = 0.2
P(B|[]) = 0.09
P(L|[]) = 0.064
P(X|[]) = 0.05712
```

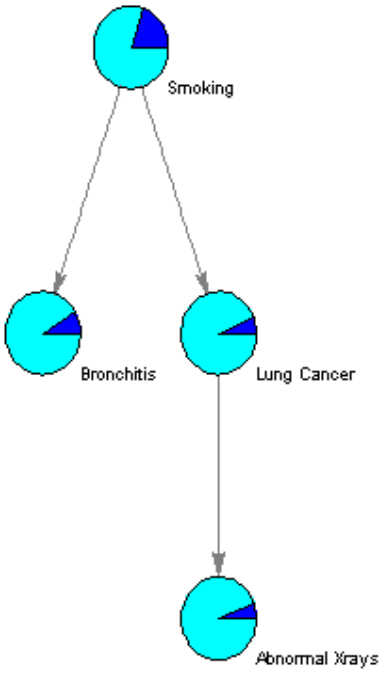


Fig 4.3 Distribution of conditional probability

To evaluate the likelihood that a patient with bronchitis has lung cancer, instantiate B=t (true) and update the network as follows in appendix A1 and get the result:

Result

```
P(S|B=t) = 0.55556
P(B|B=t) = 1
P(L|B=t) = 0.16889
P(X|B=t) = 0.11796
```

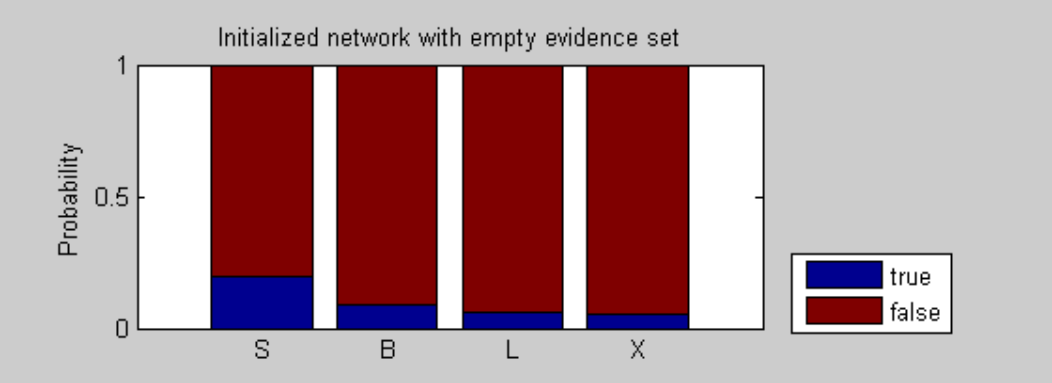


Fig 4.4 Initialized network with empty evidence set

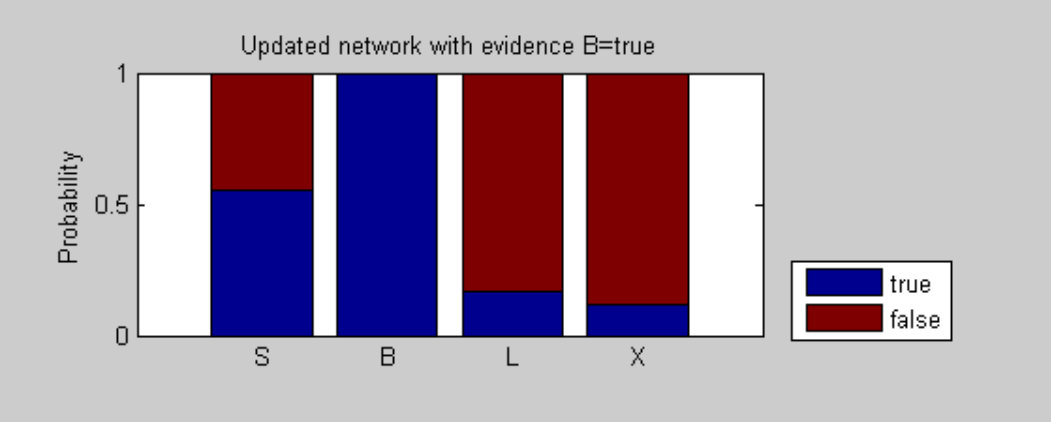


Fig. 4.5 Initialized network with evidence B=true

With the observation that the patient has bronchitis (`B = t`), the probability of a true condition for all other nodes has increased. In particular, the probability of smoking history increases because smoking is one leading cause of chronic bronchitis. In turn, because smoking is also associated with lung cancer, the probability of lung cancer increases and so does the probability of an abnormal chest X-ray test.

In case the patient has not been evaluated for bronchitis but the chest X-ray shows some abnormalities, the network instantiated `X = t` and initialized again with the new evidence. `evNode = X;`

Result:

```
P(S|X=t) = 0.67927
P(B|X=t) = 0.18585
P(L|X=t) = 0.67227
P(X|X=t) = 1
```

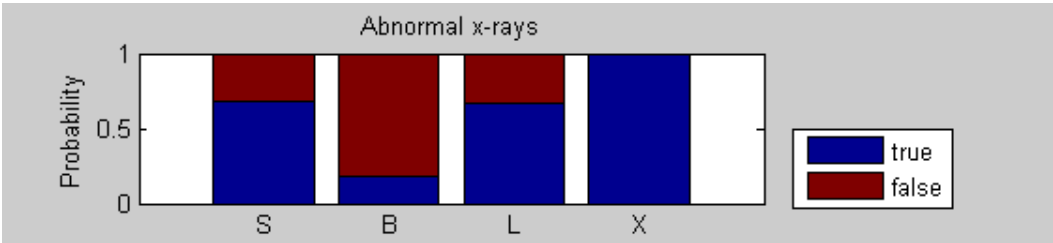


Fig 4.6 Abnormal X-rays

Given the observed abnormal X-ray results, the probability of lung cancer has increased significantly because of the direct dependency of node `X` (X-rays) on node `L` (lung cancer).

Finally, suppose the patient has both been diagnosed with bronchitis and received positive results for his/her chest X-ray, the previous state of the network (`X = t`) is updated with the new evidence (`B = t`),:

Result:

```
P(S|B=t,X=t) = 0.91372
P(B|B=t,X=t) = 1
P(L|B=t,X=t) = 0.85908
P(X|B=t,X=t) = 1
```

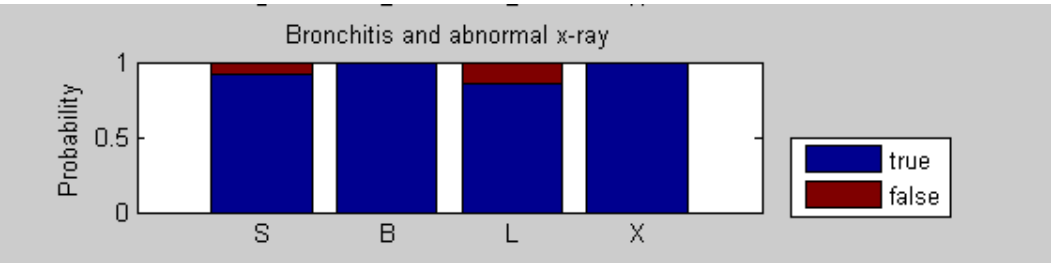
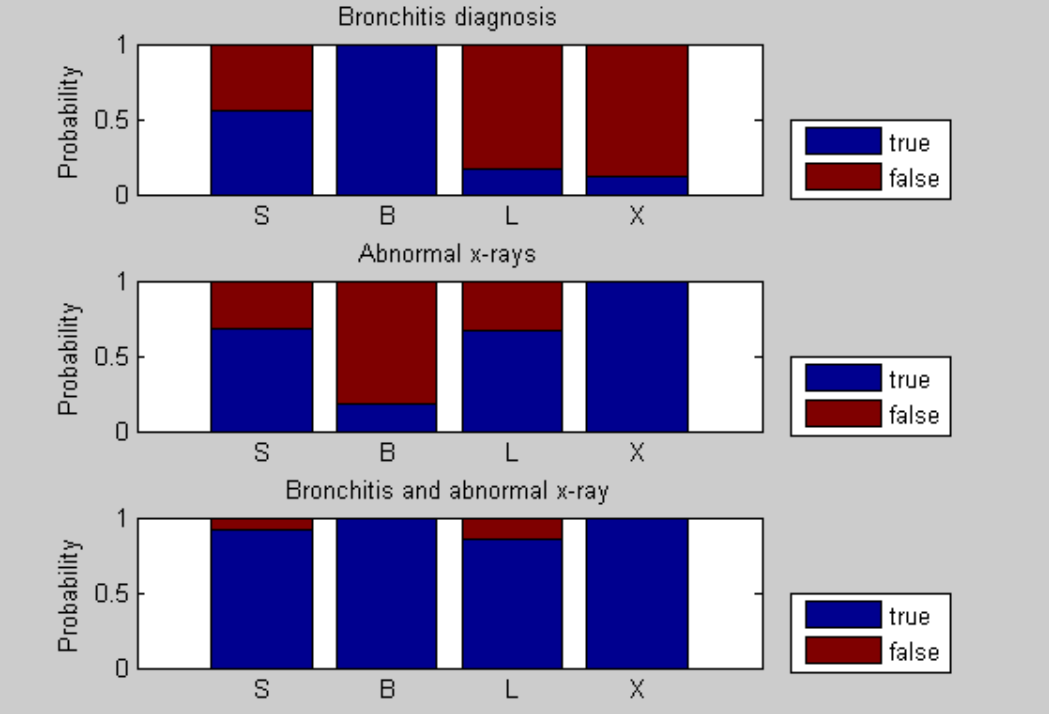


Fig 4.7 Bronchitis and abnormal X-rays

The three situations can be compared by plotting the probabilities as bar charts as shown in figures below. Evidence of bronchitis and evidence of abnormal X-rays increase the probability of lung cancer with smoking history, one directly and the other indirectly.

Results:

When compare the three situations by plotting the probabilities, it is observe that the evidence of bronchitis and evidence of abnormal X-rays increase the probability of lung cancer with smoking history, one directly and the other indirectly as illustrated in Figure 4.8 below:



4.8 The comparing of three situations by plotting probabilities

The effect of a positive versus negative bronchitis diagnosis in presence of abnormal X-ray results can now be compared. Instantiate`B = f` (false) and compare with previous estimates `B = t` (true).

Result

```
P(S|B=f,X=t) = 0.62575
P(B|B=f,X=t) = 0
P(L|B=f,X=t) = 0.62962
P(X|B=f,X=t) = 1
```

When bronchitis is ruled out (`B = f`), the probability of smoking history decreases with respect to the case in which the bronchitis is confirmed (`B = t`). The effect is propagated across the network and affects the probability of lung cancer in a similar manner as shown in figure 4.9 below

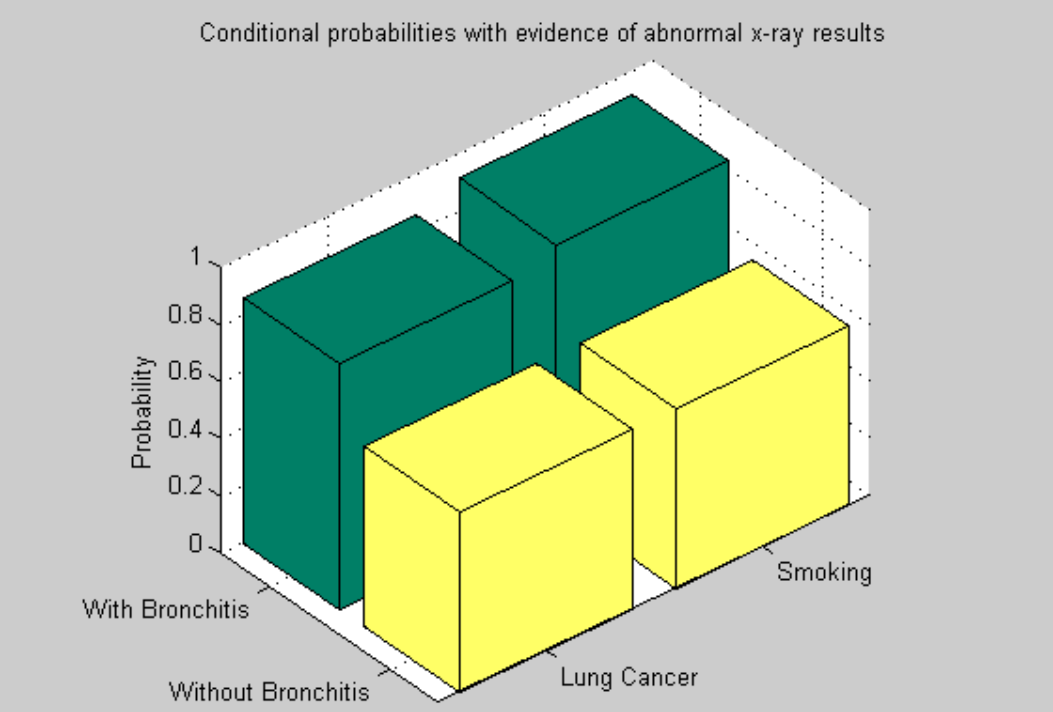


Fig. 4.9Conditional probability with evidence of abnormal x-ray Result

4.6Expanding the Network

Among various symptoms related to lung cancer and bronchitis is shortness of breath (dyspnea).modeling therelationships of this condition within the considered Bayesian Network is done by introducing a node D and modify the adjacency matrix accordingly.

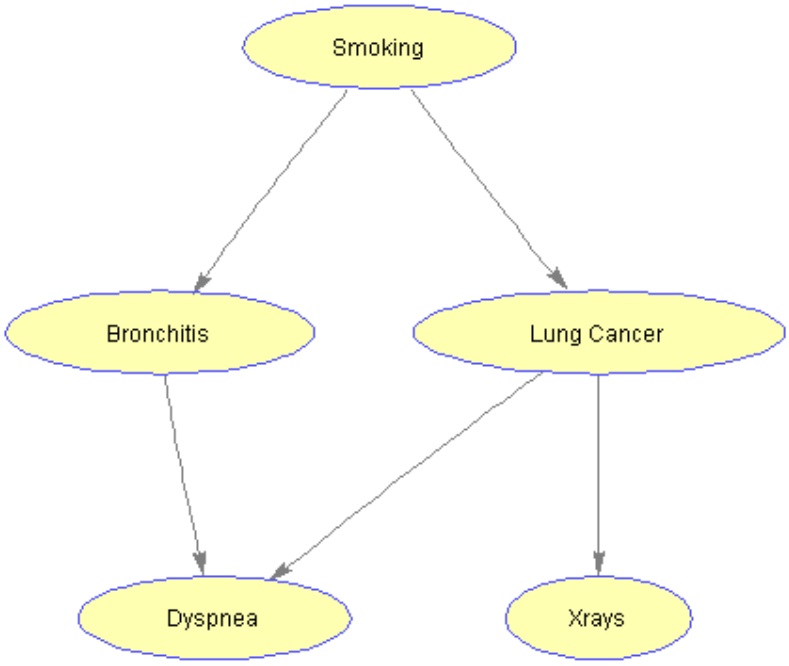


Fig 4.10 Bayesian Network – Graph structure - Expanded

With the introduction of node `D`, the network is not singly-connected anymore. In fact, there is more than one chain between any two nodes (i.e., `S` and `D`). This property can be checked by considering the undirected graph associated with the network and verifying that it is not acyclic.

```
isAcyclic = graphisdag(sparse(adj | adj'))
isAcyclic =
     0
```

In order to use the algorithm for exact inference described above, the new, multiply-connected network must be transferred into a singly-connected network. Several approaches can be used, including clustering of parent nodes (in this case `B` and `L`) into a single node as follows.

First, the adjacency matrix entries corresponding to the nodes `B` and `L`are combinedinto one entry associated to node `BL`. The node `BL` can take up to four values, corresponding to all possible combinations of values of the original nodes `B` and `L`. Then, update the conditional probability distribution considering that `B` and `L` are conditionally independent given the node `S`, that is P(BL|S) = P(B,L|S) = P(B|S) * P(L|S).

Result

```
P(S|[]) = 0.2
P(BL|[]) = 0.0152
P(X|[]) = 0.4128
P(D|[]) = 0.08634
```

4.7Drawing the Expanded Network

```
Biograph object with 4 nodes and 3 edges.
```

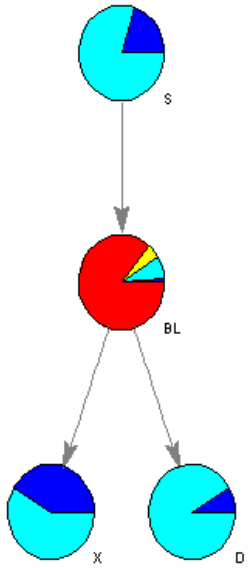


Fig 4.11Biograph object with 4 nodes and 3 edges.

4.8Performing Exact Inference on Clustered Trees

Suppose a patient complains of dyspnea (`D=t`). His likelihood that this symptom is related to either lung cancer or bronchitis can be evaluated.

```
[n5, e5, A5, a5] = bnMsgPassUpdate(cNodes, cEdges, [], [], D, t);
```

Because node `B` and node `L` are clustered into the node `BL`, their individual conditional probabilities must be calculated by considering the appropriate value combinations. The conditional probabilities in `BL` correspond to the following `B` and `L` value combinations: `BL = tt` if `B = t` and `L = t`; `BL = tf` if `B = t` and `L = f`; `BL = ft` if `B = f` and `L = t`; `BL = ff` if `B = f` and `L = f`. Therefore P(B|evidence) is equal to the sum of the first two elements of P(BL|evidence), and similarly, P(L|evidence) is equal to the sum of the first and third elements in P(BL|evidence). `p(1,:) = n5(S).P;`

Result

```
P(S|D=t) = 0.49224
P(B|D=t) = 0.21867
P(L|D=t) = 0.41464
P(X|D=t) = 0.48293
P(D|D=t) = 1
```

When dyspnea is present, both the likelihood of bronchitis and lung cancer increases. This makes sense, since both illnesses have dyspnea as symptom and the patient is indeed exhibiting this symptom.

4.9Explaining Away the Lung Cancer

As it can be seen in the graph, the dyspnea symptom has dependency both on bronchitis and lung cancer. Consider the effect of a bronchitis diagnosis on the likelihood of lung cancer.

Result

```
P(S|B=t,D=t) = 0.41667
P(B|B=t,D=t) = 1
P(L|B=t,D=t) = 0.33898
P(X|B=t,D=t) = 0.4678
P(D|B=t,D=t) = 1
```

When a patient complains of dyspnea and is diagnosed with bronchitis, the conditional probability of lung cancer is lower.

Consider now the effect of a lung cancer diagnosis on the likelihood of bronchitis.

Result

```
P(S|L=t,D=t) = 0.21531
P(B|L=t,D=t) = 0.12919
P(L|L=t,D=t) = 1
P(X|L=t,D=t) = 0.6
P(D|L=t,D=t) = 1
```

If a patient is diagnosed with lung cancer in presence of dyspnea, the likelihood of bronchitis decreases significantly. This phenomenon is called "explaining away" and refers to the situations in which the chances of one cause decrease significantly when the chances of the competing cause increase.

The "explaining away" phenomenon can be observed in the two situations described above by comparing the conditional probabilities of node `L` and `B` in the two cases. When the evidence for `B` is high, the likelihood of `L` is relatively low, and vice versa, when the evidence for `L` is high, the likelihood of `B` is low.

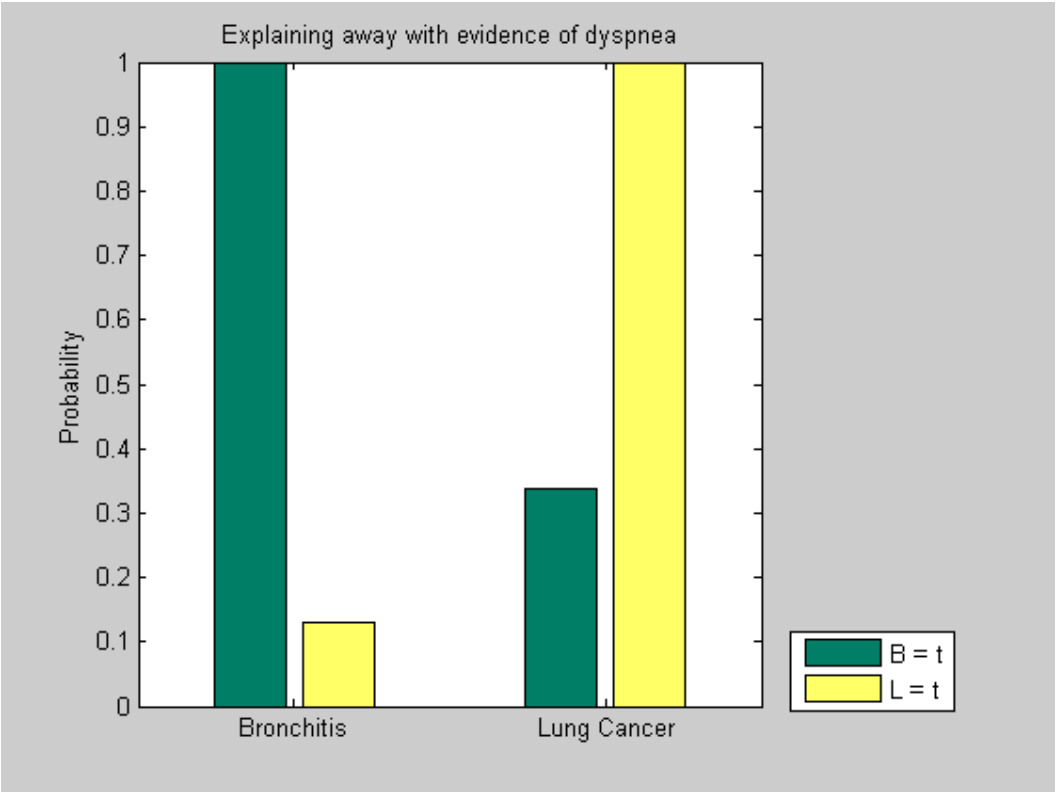


Fig 4.12 Explaining away with evidence of dyspnea

The "explaining away" phenomenon can be observed in the two situations described above by comparing the conditional probabilities of node `L` and `B` in the two cases. When the evidence for `B` is high, the likelihood of `L` is relatively low, and vice versa, when the evidence for `L` is high, the likelihood of `B` is low.

4.10 Results of using model:

All the results illustrated through this chapter with all graphs will appear with model.The main results when using this model are:

1. The distribution of the conditional probability can be visualized given an empty set of evidence in a series of pie charts.
2. To evaluate the likelihood that a patient with bronchitis has lung cancer, instantiate evidence of bronchitis is true and updates the network.
3. The observation of patient has bronchitis is true, the probability of a true condition has increased. In particular, the probability of smoking history increases because smoking is one leading cause of chronic bronchitis. In turn, because smoking is also associated with lung cancer, the probability of lung cancer increases and so does the probability of an abnormal chest X-ray test.
4. The evidence of bronchitis and evidence of abnormal X-rays increase the probability of lung cancer with smoking history, one directly and the other indirectly.
5. When bronchitis is ruled out (bronchitis is false)the probability of smoking history decreases with respect to the case in which the bronchitis is confirmed bronchitis is true.The effect is propagated across the network and affects the probability of lung cancer in a similar manner.
6. If a patient is diagnosed with lung cancer in presence of dyspnea, the likelihood of bronchitis decreases significantly. This phenomenon is called "explaining away" and refers to the situations in which the chances of one cause decrease significantly when the chances of the competing cause increase.
7. The "explaining away" phenomenon can be observed in the two situations by comparing the conditional probabilities of node lung cancer and bronchitis in the two cases. When the evidence for bronchitis is high, the likelihood of

lung cancer is relatively low, and vice versa, when the evidence for lung cancer is high, the likelihood of bronchitis is low.

Chapter five

Conclusion and Recommendations

5.1 Conclusion

1. The application of the Bayes' theorem that illustrates a Bayesian Network that is effectivefor exact probabilistic inference using Pearl's message-passing algorithm to model the diagnostic of lung cancer.
2. Bayesian Network very useful in applications with probabilistic inference of lung cancer diagnosis involving features that are not directly related, and for which the conditional probability cannot be readily computed using other network approach, develop an algorithm that delineates the lung cancer on X-Ray images for the lung by Bayesian Neural Network andchoose the best subset of features that helps on visualization of lung tumors.

5.2 Recommendations

For future work that aim todevelop this research, The recommendations are to:

1. using other features directly or not directly to lung cancer to contribute in diagnosis development by new approach.
2. implement the wide range of Bayesian network for different diagnostics category with different features & conditional probability.

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Appendix A1

MATLAB program used as tool in this modeling

```
%% Creating the Bayesian Network

%=== setup
adj = [0 1 1 0; 0 0 0 0; 0 0 0 1; 0 0 0 0]; %
adjacency matrix
nodeNames = {'S', 'B', 'L', 'X'};           % nodes
S = 1; B = 2; L = 3; X = 4;                 % node
identifiers
n = numel(nodeNames);                       % number
of nodes
t = 1; f  = 2;                              % true
and false
values = cell(1,n);                         % values
assumed by variables
for i = 1:numel(nodeNames)
values{i} = [t f];
end


%=== Conditional Probability Table
CPT{S} = [.2 .8];
```

```
CPT{B}(:,t) = [.25 .05] ; CPT{B}(:,f) = 1 -
CPT{B}(:,t);
% CPT{L}(:,t) = [.03 .0005]; CPT{L}(:,f) = 1 -
CPT{L}(:,t);
CPT{L}(:,t) = [.3 .005]; CPT{L}(:,f) = 1 -
CPT{L}(:,t);
CPT{X}(:,t) = [.6 .02]; CPT{X}(:,f) = 1 -
CPT{X}(:,t);

%=== draw the network
nodeLabels = {'Smoking', 'Bronchitis', 'Lung Cancer',
'Abnormal Xrays'};
bg = biograph(adj, nodeLabels, 'arrowsize', 3);
set(bg.Nodes, 'shape', 'ellipse');
bgInViewer = view(bg);

%=== save as figure
bgFig = figure;
copyobj(bgInViewer.hgAxes,bgFig)

%=== annotate using the CPT
[xp, xn] = find(adj);     % xp = parent id, xn = node
id
pa(xn) = xp;              % parents
pa(1) = 1;                % root is parent of itself
```

```
s1 = cell(1,n); s2 = cell(1,n); pos = zeros(n,2);
for i = 2:n
pos(i,:) = bgInViewer.Nodes(i).Position;
s1{i} = sprintf('P(%s|%s=t) = %f', nodeNames{i},
nodeNames{pa(i)}, CPT{i}(1,t));
s2{i} = sprintf('P(%s|%s=f) = %f', nodeNames{i},
nodeNames{pa(i)}, CPT{i}(2,t));
end

pos(1,:) = bgInViewer.Nodes(1).Position; % root
s1{1} = sprintf('P(%s=t) = %f', nodeNames{1},
CPT{1}(1));
s2{1} = ' ';

text(pos(:,1)+2, pos(:,2)-10, s1)
text(pos(:,1)+2, pos(:,2)-15, s2)


%% Initializing the Bayesian Network


root = find(sum(adj,1)==0); % root is any node with
no parent
[nodes, edges] = bnMsgPassCreate(adj, values, CPT);
[nodes, edges] = bnMsgPassInitiate(nodes, edges,
root)
```

```
%=== conditional probability given the empty set []
for i = 1:n
disp(['P(' nodeNames{i}, '|[]) = '
num2str(nodes(i).P(1))]);
end

%=== assign relevant info to each node handle
nodeHandles = bgInViewer.Nodes;
for i = 1:n
nodeHandles(i).UserData.Distribution = [nodes(i).P];
end

%=== draw customized nodes
bgInViewer.ShowTextInNodes = 'none';

set(nodeHandles, 'shape','circle')
bgInViewer.CustomNodeDrawFcn = @(node)
customnodedraw(node);
%bgInViewer.Scale = .7
bgInViewer.dolayout



%=== inference with B = t
evNode = B;
```

```
evValue = t;
[n1, e1, A1, a1] = bnMsgPassUpdate(nodes, edges, [],
[], evNode, evValue);

for i = 1:n
disp(['P(' nodeNames{i}, '|B=t) = '
num2str(n1(i).P(1))]);
end

%== plot and compare
figure(); subplot(2,1,1);
x = cat(1,nodes.P);
bar(x, 'stacked'); set(gca, 'xticklabel', nodeNames);
ylabel('Probability');
title('Initialized network with empty evidence set')
legend({'true', 'false'}, 'location',
'SouthEastOutside')
hold on; subplot(2,1,2);
x1 = cat(1,n1.P);
bar(x1, 'stacked'); set(gca, 'xticklabel',
nodeNames);
ylabel('Probability');
title('Updated network with evidence B=true')
legend({'true', 'false'}, 'location',
'SouthEastOutside')
```

```
evNode = X;
evValue = t;
[n2, e2, A2, a2] = bnMsgPassUpdate(nodes, edges, [],
[], evNode, evValue);

for i = 1:n
disp(['P(' nodeNames{i}, '|X=t) = '
num2str(n2(i).P(1))]);
end



evNode = B;
evValue = t;
[n3, e3, A3, a3] = bnMsgPassUpdate(n2, e2, A2, a2,
evNode, evValue);

for i = 1:n
disp(['P(' nodeNames{i}, '|B=t,X=t) = '
num2str(n3(i).P(1))]);
end



figure(); subplot(3,1,1);
```

```
bar(x1,  'stacked'); set(gca, 'xticklabel',
nodeNames);
ylabel('Probability'); title('Bronchitis diagnosis');
legend({'true', 'false'}, 'location',
'SouthEastOutside')
hold on; subplot(3,1,2);
x2 = cat(1,n2.P);
bar(x2,'stacked'); set(gca, 'xticklabel', nodeNames);
ylabel('Probability'); title('Abnormal x-rays');
legend({'true', 'false'}, 'location',
'SouthEastOutside')
hold on; subplot(3,1,3);
x3 = cat(1,n3.P);
bar(x3, 'stacked'); set(gca, 'xticklabel',
nodeNames);
ylabel('Probability'); title('Bronchitis and abnormal
x-ray');
legend({'true', 'false'}, 'location',
'SouthEastOutside')

evNode = B;
evValue = f;
[n4, e4, A4, a4] = bnMsgPassUpdate(n2, e2, [], [],
evNode, evValue);

for i = 1:n
```

```
disp(['P(' nodeNames{i}, '|B=f,X=t) = '
num2str(n4(i).P(1))]);
end

figure();
bar3([n3(S).P(:,t) n4(S).P(:,t); n3(L).P(:,t)
n4(L).P(:,t)]);
colormap(summer); zlabel('Probability');
set(gca,'xticklabel',{'Smoking','Lung
Cancer'},'yticklabel', {'With Bronchitis', 'Without
Bronchitis'});
set(gca,'xticklabel',{'With Bronchitis','Without
Bronchitis'},'yticklabel', {'Smoking','Lung
Cancer'});
title('Conditional probabilities with evidence of
abnormal x-ray results')
view(50,35);

%=== add node D to the network
D = 5;
CPT{D}(:,:,t) = [.75 .1; .5 .05];
CPT{D}(:,:,f) = 1 - CPT{D}(:,:,t);
values{D} =  [1 2];
adj(end+1,:) = [0 0 0 0];
adj(:,end+1) = [0 1 1 0 0];
```

```
%=== draw the updated network
nodeLabels = {'Smoking', 'Bronchitis', 'Lung Cancer',
'Xrays', 'Dyspnea'};
nodeSymbols = {'S', 'B', 'L', 'X', 'D'};
bg = biograph(adj, nodeLabels, 'arrowsize', 4);
nodeHandles= bg.Nodes;
set(nodeHandles, 'shape', 'ellipse');
view(bg)



isAcyclic = graphisdag(sparse(adj | adj'))



%=== combine B and L
adj(B,:) = adj(B,:) | adj(L,:);
adj(:,B) = adj(:,B) | adj(:,L);
adj(L,:) = []; adj(:,L) = [];

%=== update the probability distribution accordingly
b1 = kron(CPT{B}(1,:), CPT{L}(1,:));
b2 = kron(CPT{B}(2,:), CPT{L}(2,:));
x = [CPT{X}(1,:) CPT{X}(1,:)];
d =  reshape((CPT{D}(:,:,1))', 1, 4);

%=== update the node values
```

```
S = 1; BL = 2; X = 3; D = 4;
nodeNames = {'S', 'BL', 'X', 'D'};
tt = 1; tf = 2; ft = 3; ff = 4;
values{BL} = 1:4;
values(L) = [];

%=== create a clustered Conditional Probability Table
cCPT{S} = CPT{S};
cCPT{BL}(t,:) = b1; cCPT{BL}(f,:) = b2;
cCPT{D}(:,t) = d; cCPT{D}(:,f) = 1 - d;
cCPT{X}(:,t) = x; cCPT{X}(:,f) = 1 - x;

%=== create and intiate the net
root = find(sum(adj,1)==0); % root (node with no
parent)
[cNodes, cEdges] = bnMsgPassCreate(adj, values,
cCPT);
[cNodes, cEdges] = bnMsgPassInitiate(cNodes, cEdges,
root);

for i = 1:n
disp(['P(' nodeNames{i}, '|[]) = '
num2str(cNodes(i).P(1))]);
end

%% Drawing the Expanded Network
```

```
%=== draw the network
nodeLabels = {'Smoking', 'Bronchitis or Lung Cancer',
'Abnormal X-rays', 'Dyspnea'};
cbg = biograph(adj, nodeNames, 'arrowsize', 4);
set(cbg.Nodes, 'shape', 'ellipse');
cbgInViewer = view(cbg);

%=== assign relevant info to each node handle
cnodeHandles = cbgInViewer.Nodes;
for i = 1:n
cnodeHandles(i).UserData.Distribution =
[cNodes(i).P];
end

%=== draw customized nodes
set(cnodeHandles, 'shape','circle')
colormap(summer)
cbgInViewer.ShowTextInNodes = 'none';
cbgInViewer.CustomNodeDrawFcn = @(node)
customnodedraw(node);
cbgInViewer.Scale = .7
cbgInViewer.dolayout

[n5, e5, A5, a5] = bnMsgPassUpdate(cNodes, cEdges,
[], [], D, t);
```

```
p(1,:) = n5(S).P;
p(2,:) = [sum(n5(BL).P([tt,tf])), 1-
sum(n5(BL).P([tt,tf]))];     % P(B|evidence)
p(3,:) = [sum(n5(BL).P([tt,ft])), 1-
sum(n5(BL).P([tt,ft]))]; % P(L|evidence)
p(4,:) = n5(X).P;
p(5,:) = n5(D).P;

for i = 1:5
disp(['P(' nodeSymbols{i}, '|D=t) = '
num2str(p(i,1))]);
end

%=== adjust the CPT to reflect B = 1 before
clustering into BL node
B = 2; L = 3;
CPT{B}(:,1) = [1 1] ; CPT{B}(:,2) = 1 - CPT{B}(:,1);
b1 = kron(CPT{B}(1,:), CPT{L}(1,:));
b2 = kron(CPT{B}(2,:), CPT{L}(2,:));

%=== create a clustered Conditional Probability Table
BL = 2;
cCPT{BL}(1,:) = b1; cCPT{BL}(2,:) = b2;

%=== create and intiate the net
```

```
root = find(sum(adj,1)==0); % root (node with no
parent)
[cNodes, cEdges] = bnMsgPassCreate(adj, values,
cCPT);
[cNodes, cEdges] = bnMsgPassInitiate(cNodes, cEdges,
root);

%=== instantiate for F = 1
[n7, e7, A7, a7] = bnMsgPassUpdate(cNodes, cEdges,
[], [], D, t);
w(1,:) = n7(S).P;
w(2,:) = [sum(n7(BL).P([tt,tf])), 1-
sum(n7(BL).P([tt,tf]))];     % P(B|evidence)
w(3,:) = [sum(n7(BL).P([tt,ft])), 1-
sum(n7(BL).P([tt,ft]))]; % P(L|evidence)
w(4,:) = n7(X).P;
w(5,:) = n7(D).P;

for i = 1:5
disp(['P(' nodeSymbols{i}, '|B=t,D=t) = '
num2str(w(i,1))]);
end

%=== adjust the CPT to reflect L = 1 before
clustering into BL node
B = 2; L = 3;
```

```
CPT{B}(:,t) = [.25 .05] ; CPT{B}(:,f) = 1 -
CPT{B}(:,t);
CPT{L}(:,t) = [1 1]; CPT{L}(:,f) = 1 - CPT{L}(:,t);

b1 = kron(CPT{B}(t,:), CPT{L}(t,:));
b2 = kron(CPT{B}(f,:), CPT{L}(f,:));

BL = 2;
cCPT{BL}(t,:) = b1; cCPT{BL}(f,:) = b2;

%=== create and intiate the net
root = find(sum(adj,1)==0); % root (node with no
parent)
[cNodes, cEdges] = bnMsgPassCreate(adj, values,
cCPT);
[cNodes, cEdges] = bnMsgPassInitiate(cNodes, cEdges,
root);

%=== instantiate for D = 1
[n8, e8, A8, a8] = bnMsgPassUpdate(cNodes, cEdges,
[], [], D, t);
v(1,:) = n8(S).P;
v(2,:) = [sum(n8(BL).P([tt,tf])), 1-
sum(n8(BL).P([tt,tf]))];     % P(B|evidence)
v(3,:) = [sum(n8(BL).P([tt,ft])), 1-
sum(n8(BL).P([tt,ft]))]; % P(L|evidence)
```

```
v(4,:) = n8(X).P;
v(5,:) = n8(D).P;

for i = 1:5
disp(['P(' nodeSymbols{i}, '|L=t,D=t) = '
num2str(v(i,1))]);
end

y = [w(2:3,1)  v(2:3,1)];
figure();
bar(y);
set(gca, 'xticklabel', {'Bronchitis', 'Lung
Cancer'});
ylabel('Probability'); title('Explaining away with
evidence of dyspnea')
legend('B = t', 'L = t', 'location',
'SouthEastOutside');
colormap(summer)
```