

Bayesian Network Based Netica for Respiratory Diseases

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Abstract. The disease of the influenza, whose early symptoms are similar to other diseases, it is very difficult to diagnose a patients. Such as viral colds, bacterial colds and early symptoms of pneumonia. Based on the structural characteristics of Bayesian network in statistical probability, we do a diagnostic analysis of human respiratory diseases, so that doctors can provide basis for diagnosis of patients' diseases. General principle is the use of Bayesian network based on probabilistic reasoning directed acyclic graph model, the complex relationship between variables in the specific problems are expressed in a network structure, and through the network model to reflect the dependencies between the variables in the field of applied research, expression and reasoning on uncertainty knowledge. This is an example of applying the Bias network to the diagnosis of disease.

1. Introduction

Bayesian theory originated in the paper published by Reverend Thomas Bayes “comments on the solution of probability problems”. In 1950s, the empirical Bayes method was combined with the classical method with Robbins as the representative. In 1980s, Pearl proposed the Bayesian network, and Bayesian network are applied to the field of artificial intelligence for probabilistic reasoning[1], based on this and Bayesian network successfully applied in the field of expert system, the Bayesian network has become one of the important methods of uncertainty reasoning and expert knowledge. With the continuous deepening of study theory and application level unceasing enhancement, a method of Bayesian network through the graphical representation and the use of probability knowledge, it has overcome the rule system based on many concepts and computational difficulties, it has been widely recognized in academic circles and attention. It mainly has the following characteristics: solid theoretical basis, flexible learning mechanism and strong knowledge expression, and the diversity of reasoning ability and application model [2,3].

First, several concepts and theorems are introduced.

- A priori probability: it refers to the probability obtained according to the previous experience and analysis.
- A posteriori probability: things have happened, and the reason for this thing to happen is the size of the possibility caused by a certain factor.
- Conditional probability: the occurrence probability of event A under the condition that another event B has already occurred, and the conditional probability is expressed as $P(A|B)$.

$$P(A|B) = \frac{P(A \cap B)}{P(B)} \quad (1)$$

- The whole probability formula: if the event is $B_1, B_2, \dots$ In the form of a complete set of events



and there is a positive probability, the following formula is established for any event A.

$$P(B) = \sum_{i=1}^n P(A_i)P(B|A_i) \quad (2)$$

- Bayes formula:

$$P(B_i|A) = \frac{P(AB_i)}{P(A)} = \frac{P(B_i)P(A|B_i)}{\sum_{i=1}^n P(B_i)P(A|B_i)} \quad (3)$$

● Bayesian networks: composed of a directed acyclic graph (DAG) and conditional probability table (CPT). The Bias network uses a directed acyclic graph to express the conditional dependence of a set of random variables with them. It is parameterized by conditional probability distribution. Each node is parameterized by $P(\text{node}|\text{Pa}(\text{node}))$, and $\text{Pa}(\text{node})$ represents the parent node in the network. For example, figure 1 is a simple Bayesian network, and its corresponding full probability formula is[3]:

$$P(A, B, C) = P(C|A, B)P(B|A)P(A) \quad (4)$$

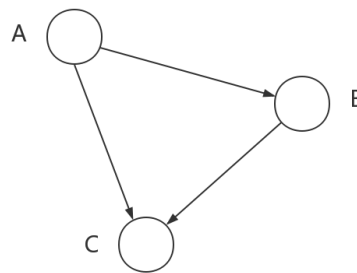


Figure 1. Bayesian network schematic diagram.

The structure of Bias network is divided into two steps: to determine the network topology and to determine the network parameters.

Determine the network topology:

- 1) Select a set of random variables $\{X_1, X_2, \dots, X_n\}$, which depict the problem.
- 2) Select a variable sequence $a = \{X_1, X_2, \dots, X_n\}$;
- 3) Starting from an empty graph, the variable is added to the network diagram in accordance with the order a.
- 4) When the variable X_i is added, the variables in the network diagram include $X_1, X_2, \dots, X_{(i-1)}$;
- 4.1) Using background knowledge, select a subset of the C as small as possible in these variables (X_i), makes the assumption that given the subset of C (X_i), X_i and other variables in the network diagram are independent and reasonable.
- 4.2 from a subset of C (X_i) in each node to add a pointer to a X_i directed edge.

Determining network parameters:

The Bias network parameter is the probability distribution of each variable, which is generally obtained by the training sample statistics.

Considering the basic structure that two variables A and B are indirectly connected by third variables C, the Bayesian network can be divided into 3 substructure forms:

- Head-to-tail:

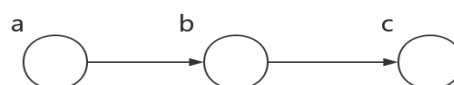


Figure 2. The structure of head-to-tail

$$P(a, b, c) = P(a)P(c|a)P(b|c) \quad (5)$$

As shown in Figure 2. In the case of known C, understanding of a will not affect the reliability of C, and it will not affect the reliability of B. The information channel between a and B is blocked, a and B are independent. But in the case of C, the understanding of a affects the reliability of the C and then affects the reliability of the B.

- Tail-to-tail:

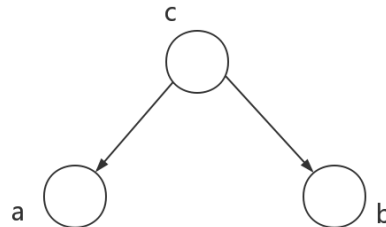


Figure 3.The structure of Tail-to-tail

$$P(a, b, c) = P(c) P(a|c) P(b|c) \quad (6)$$

As shown in Figure 3. In the case of unknown C, information can be passed between a and B. They are associated. When C is known, information can not be transferred between a and B. They are blocked and blocked. A and B are independent.

- Head-to-head:

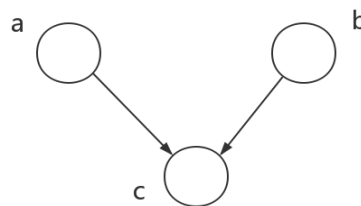


Figure 4.The structure of head-to-head

$$P(a, b, c) = P(a) P(b) P(c|a, b) \quad (7)$$

As shown in Figure 4. Completely opposite to the two previous cases. In the case of known C, a and B are interrelated. In the case of unknown C, a and B are blocked and are independent[4,5].

2. Preliminary

The clinical symptoms of bacterial and viral respiratory infections are similar. The following are some of the differences between bacterial and viral respiratory infections. 1, the viral respiratory infection has the characteristic of the obvious group disease, but the bacterial respiratory infection is mostly sporadic. 2, viral respiratory infection has no purulent secretion, and pyogenic sputum is an important evidence of bacterial infection. 3. The total number of leukocytes in the virus infected people is low or normal. In the case of bacterial infection, the total number of white blood cells is high. Therefore, it is difficult to determine whether it is a virus or a bacterium if the clinical blood is not tested. At the same time, there are some similarities between the symptoms of pneumonia at the early stage, so now we use Bayesian network to build a network topology based on Netica software to quickly identify the respiratory diseases of patients.

3. Model Architecture

According to the existing data, the incidence of some respiratory diseases and the typical clinical symptoms of these diseases are obtained, such as viral influenza, bacterial colds and pneumonia. Therefore, the Bayesian network is established according to the theoretical knowledge. As in Figure 5, a Bayesian network model like this does not use some of the patient's data and does not reflect the patient's actual situation. Even if there is not enough data, the Bayesian network can play a role, which is the power of it [6].

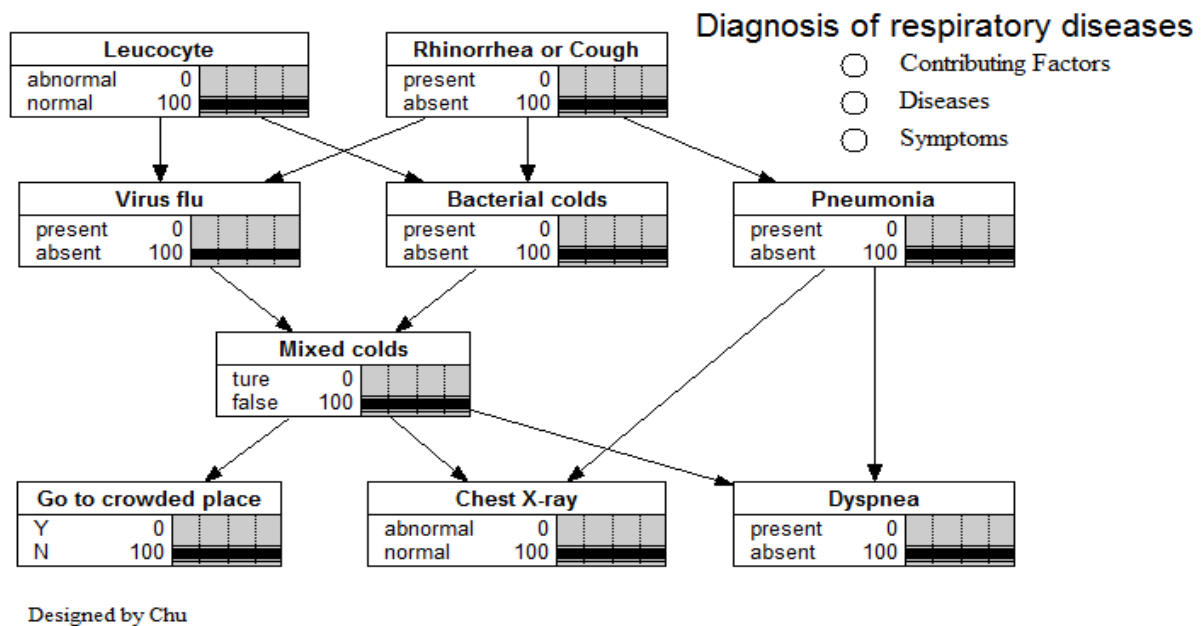
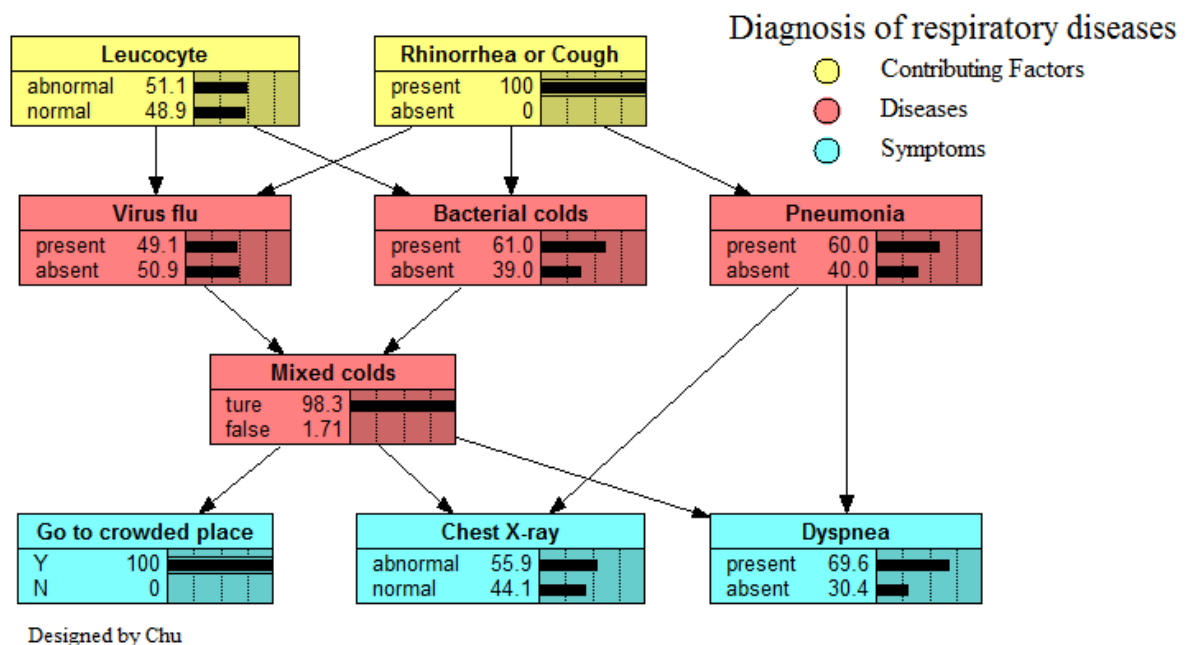
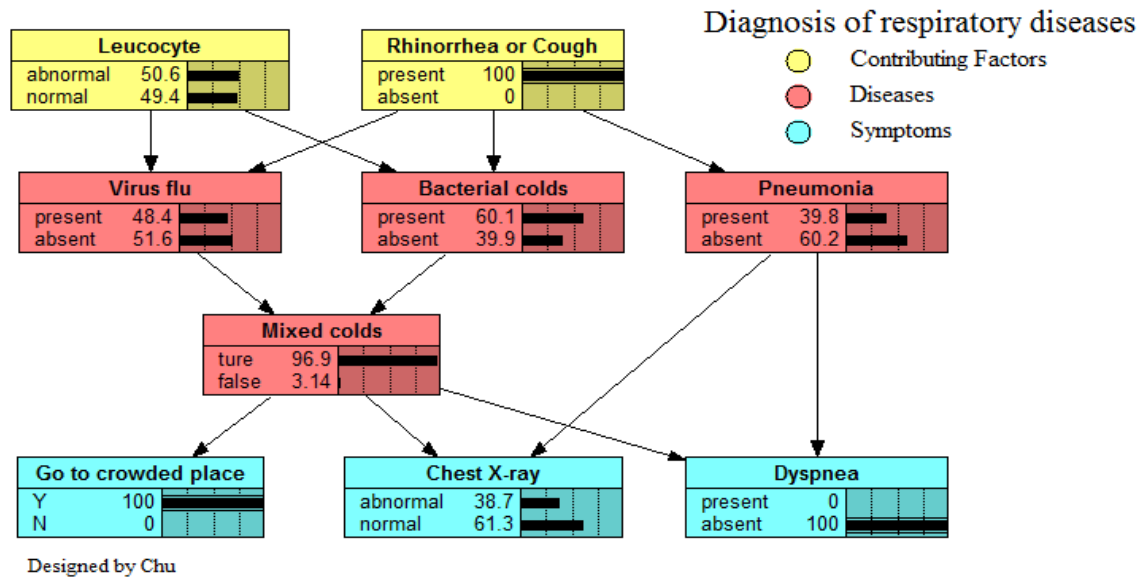
**Figure 5.** Initial state model

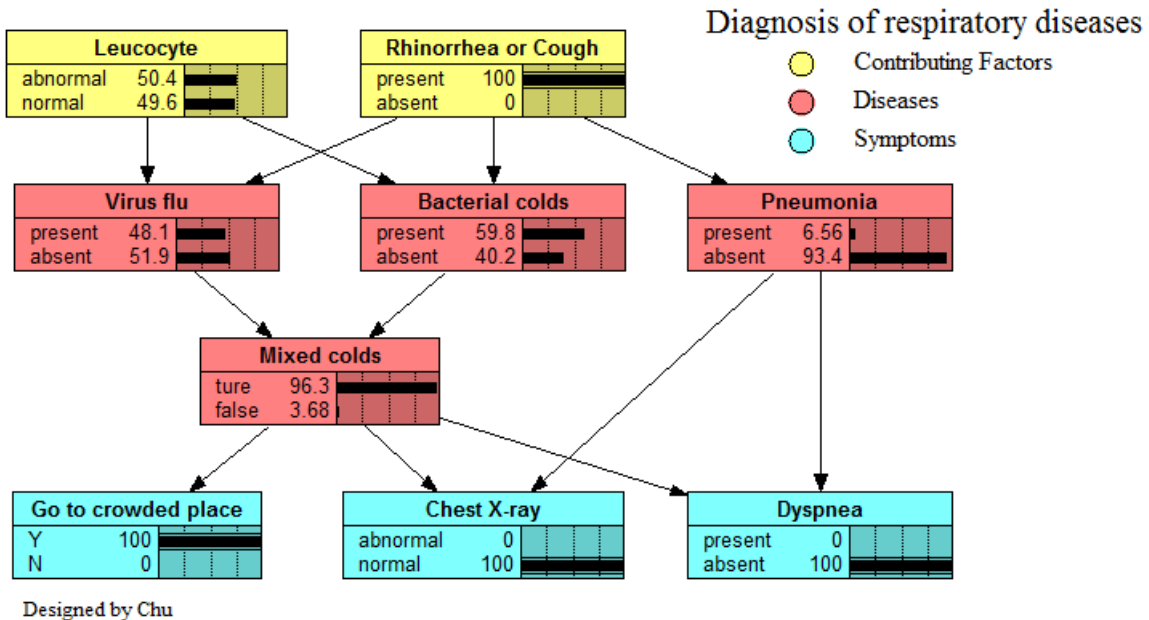
Figure 6 reflects a new patient to seek medical advice from a clinic. We inquired about the patient's condition. We learned that we had been to the crowds recently, and there were some runny nose or cough. Inputting information into the network, the probability of the three diseases increased because of the risk of infection.

**Figure 6.** Primary diagnostic model

Look at the detailed inference process: the probability of bacterial colds increased to 61%, and the probability of abnormal breathing and X rays increased correspondingly. At present, the information is too small, and we can not conclude the patient's disease. Continue to ask whether the patient has symptoms of dyspnea. The patient answered "no". The information obtained now affects the Bayesian model, such as Figure 7.

**Figure 7.** Second diagnosis model

At this time the probability of the three diseases is reduced, especially the pneumonia to 20.2%, which is because the cause of dyspnea is more prone to pneumonia. In order to exclude the possibility of pneumonia, we asked the patient to do a chest X-ray. The results showed normal. The network changed to figure 8. From the chart, we could see that the influence factor of pneumonia dropped to 6.56%. If the patient did not have obvious symptoms, he could basically exclude pneumonia.

**Figure 8.** Third diagnosis model

Now we can roughly determine that the patient has a cold, but it is not sure whether it is viral or bacterial. For further confirmation, we asked the patient to test the blood. The results of the blood test showed an increase in the leukocytes of the patient, as shown in Figure 9.

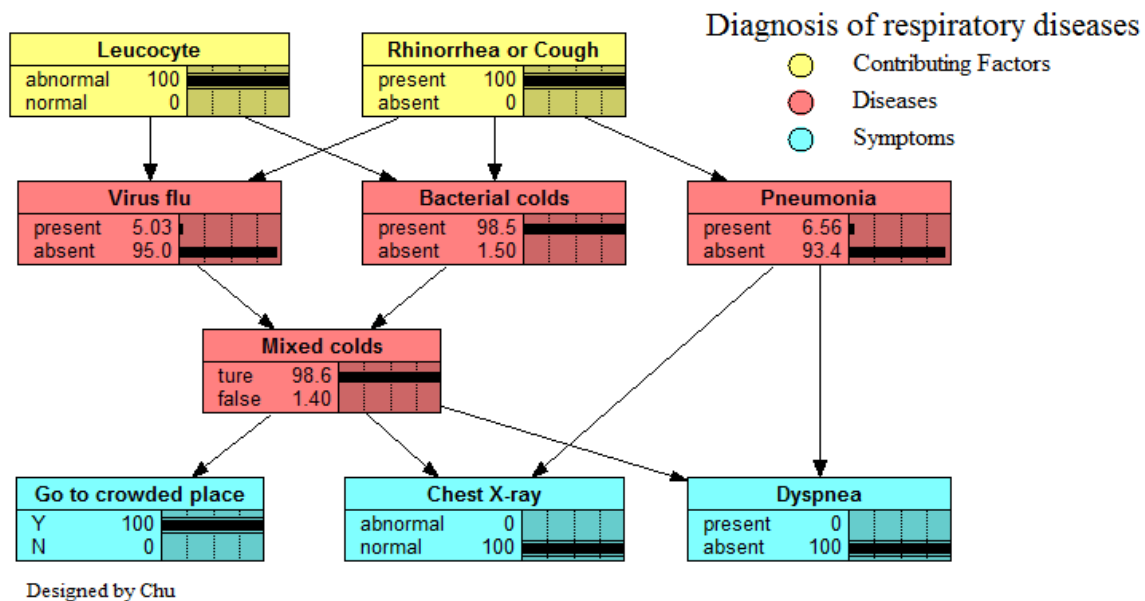


Figure 9. Final diagnosis model

This can basically determine the patient is suffering from bacterial cold, can be the right medicine. If white blood cells are shown to be normal, the probability of a cold is the highest.

4. Conclusions

When we consult the patient information, the probability of the Bayesian network will be automatically adjusted, which is the most perfect and powerful of the Bayesian inference. The most powerful feature of Bayesian network is that the probability obtained from each stage is reflected by mathematics and science. In other words, if we know enough information of patients, we can get statistical knowledge based on these information, and Bayesian network can draw reasonable inference[7]. When the current Bayesian network is unable to give clear results, we can add other inspection items to further test. Even though the current Bayesian network does not include these tests, it is easy to expand, just add extra nodes as the diagnostic program from the new statistical data. We don't have to throw away any part of the past. This is another powerful function of the Bayesian network. They are easy to expand to adapt to changing needs and changes in knowledge.

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