An Improved K2 Algorithm for Symptom-Disease Bayesian Network

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Abstract. This paper establishes a Bayesian network for pre-diagnosis based on symptom-disease knowledge from clinical data. In order to solve the local optimal problem, the idea of simulated annealing algorithm is introduced into an improved K2 algorithm, and the BDE scoring function is used to determine the optimal network structure of the Bayesian network. Performance evaluation indexes are used to evaluate the performance of the network. The experimental results show that the improved K2 algorithm outperformed the K2 algorithm.

1. Introduction
The clinical data contains a lot of useful knowledge, so relative clinical knowledge extraction has become a hot topic in academics in recent years. This paper builds a Bayesian network based on acquired symptom-disease knowledge from clinical text data.

K2 algorithm was firstly proposed by Herskovits and Cooper in 1992[1]. Liu et al. proposed an improved K2 algorithm combining mutual information and ant colony algorithm[2], so that the problem that K2 algorithm relies on prior knowledge could be solved, and the search space of ant colony algorithm is reduced. Wei et al. proposed an improved K2 algorithm based on conditional mutual information and probability jump mechanism[3]. Li proposed an improved K2 algorithm based on particle swarm optimization algorithm[4].

Inspired by the idea of simulated annealing algorithm, we proposed a simulated annealing alike K2 algorithm to construct Bayesian network, and the network is evaluated by a BDE scoring function.

2. A Simulated Annealing Alike K2 Algorithm to Construct Bayesian Network

2.1. BDE Scoring Function
Scoring function is used to evaluate the fitting degree between network structure and data set, which is an important index to judge the structure of Bayesian network [5]. At present, the commonly used scoring functions are Bayesian Dirichlet-Likelihood Equivalence (BDE)[6], Minimum Description Length (MDL)[7], Akaike Information Criterion (AIC)[8] and Bayesian Information Criterion (BIC)[9]. BDE scoring function is one of the earliest scoring functions for judging the Bayesian network data fit [10].

The formula of the BDE score is shown in (1):

\[
p_{\text{BDE}}(D, B_{\hat{B}}) = p(b_{\hat{B}}^{\hat{B}}) \prod_{i=1}^{n} \prod_{j=1}^{q} \frac{\Gamma(a_{ij})}{\Gamma(a_{ij} + N_{ij})} \prod_{k=1}^{a} \frac{\Gamma(a_{ijk} + N_{ijk})}{\Gamma(a_{ijk})}
\]

(1)
Where, \( n \) is the number of variables, \( q \) is the number of configurations of the \( i \)-th variable \( X_i \) and the set of parent nodes \( P_i(X_i) \). \( N_{ijk} \) is the sample number of variable \( X_i \) in sample data \( D \) when its parent node set \( P_i(X_i) \) takes the \( j \)-th configuration and the variable state is \( k \). \( N_j \) is the sum of all state values of \( N_{ijk} \), that is \( N_j = \sum_{k=1}^{r} N_{ijk} \). \( \alpha_{ij} \) is a hyper-parameter of Dirichlet distribution in Bayesian network parameters. \( \alpha_{ij} = \frac{\alpha_i}{\sum_{k=1}^{r} \alpha_{ijk}} \), \( \Gamma(n) \) is gamma function, for any \( n(n \in \mathbb{N}) \), \( \Gamma(n) = (n-1)! \).

2.2. The Simulated Annealing Alike K2 Algorithm

K2 algorithm needs to know the node order in advance, otherwise it is easy to fall into local optimization during network construction[11]. In order to solve this problem, this paper proposes an improved K2 algorithm by introducing the idea of simulated annealing into the process of network construction.

By integrating the idea of simulated annealing algorithm with some changes, this paper proposes an improved K2 algorithm. The specific changes are as follows:

(1) Stack for reserving Solutions

Simulated annealing algorithm retains only one feasible solution in one iteration, but the improved K2 algorithm builds a stack for reserving multiple candidate optimal solutions. The stack not only holds the optimal solution, but also some suboptimal solution with a certain probability. It is possible to reserve some temporal suboptimal solution which may convert into an optimal solution in the following iterations.

(2) Weak-to-strong mode

In the new iterative process, with the addition of a new node, if the score of some solution in stack is better than the current optimal score, the weak-to-strong mode would start: the candidate solution would be popped from the stack and replace the original optimal solution, and the original optimal one would be pushed into the stack.

The process of the improved K2 algorithm is as follows:

Input:
\( \lambda \) : a set of feature words \( \{\tau_0, \tau_1, \cdots, \tau_n\} \)
\( \mu \) : maximum number of parent nodes

Output: Bayesian Network \( B_i \) with the largest score \( V \)

1. \( B_i \) is a borderless graph consisting of symptom word node \( \tau_0, \tau_1, \cdots, \tau_n \) and target disease \( Y \).
2. \( \pi_i \leftarrow \emptyset \)
3. \( \tau_{opt} \leftarrow \tau_0, V_{opt} \leftarrow score(Y, \pi_j \cup \{\tau_0\}) \) ( \( score(Y, \pi_j \cup \{\tau_0\}) \) represents a network score consisting of the target disease \( Y \) and a set of feature words \( \pi_j \) containing \( \tau_j \).
4. for \( i = 1 \) to \( \mu \)
5. flag \leftarrow false
6. for \( j = 0 \) to \( n \)
7. \( V_j \leftarrow score(Y, \pi_j \cup \{\tau_j\}) \)
8. if \( (p(Y | \tau_j) > \theta_1) \) and \( (p(\tau_j | \bar{Y}) < \theta_2) \) (\( \theta_1, \theta_2 \) are threshold)
9. if ($V_j < V_{opt}$)
10. if ($|V_{opt} - V_j| < \text{threshold}$) (threshold is the given threshold)
11. if ($\text{random}(0,1) < \exp\left(\frac{V_j - V_{opt}}{K}\right)$) ( $K$ represents a given coefficient, $K > 0$, increase as the difference between $V_{opt}$ and $V_j$ increases)
12. stack$_i$.push($\pi_i \cup \{\tau_j\}$) (stack$_i$ is a stack that stores the temporary solution of the layer $i$)
13. end if
14. end if
15. else
16. $V_{opt} \leftarrow V_j, \pi_{opt} \leftarrow \pi_i \cup \{\tau_j\}$
17. flag $\leftarrow$ true
18. while (stack$_{i-1} \neq \phi$)
19. $\pi_{imp} \leftarrow \text{stack}_{i-1}.\text{pop}()$
20. $V_{imp} \leftarrow \text{score}(Y, \pi_{imp} \cup \{\tau_j\})$
21. if ($V_j < V_{imp}$)
22. if ($|V_{imp} - V_j| < \text{threshold}$) and ($\text{random}(0,1) < \exp\left(\frac{V_j - V_{imp}}{K}\right)$)
23. stack$_i$.push($\pi_i \cup \{\tau_j\}$)
24. $V_{opt} \leftarrow V_{imp}, \pi_{opt} \leftarrow \pi_{imp} \cup \{\tau_j\}$
25. end if
26. else
27. if ($|V_{imp} - V_j| < \text{threshold}$) and ($\text{random}(0,1) < \exp\left(\frac{V_{imp} - V_j}{K}\right)$)
28. stack$_i$.push($\pi_{imp} \cup \{\tau_j\}$)
29. end if
30. end if
31. end while
32. end if
33. end if
34. end for
35. if (flag=false) and ($\pi_j \neq \phi$)
36. break
37. else
38. Add an edge $\tau_{opt} \rightarrow Y$ to $B_s$
39. end if
40. end for
41. output $B_s$
3. Numerical Example

About 4,000 records of gastrointestinal diseases were extracted, where 2,000 records are training data and 2,000 records are test data. Take the disease "gastritis" as an example to construct its network. The specific process is as follows:

(1) Symptom words

About 12 symptoms words are to be chosen as symptoms of "gastritis", with the notations shown in Table 1:

| Feature words                                      | Symbol |
|----------------------------------------------------|--------|
| stomach ache/stomachache/pain                      | $C_1$  |
| gastric acid/acid reflux                           | $C_2$  |
| stomach distension/stomach swelling                | $C_3$  |
| stomach fever/stomach heat/heartburn               | $C_4$  |
| vomiting/retching                                   | $C_5$  |
| loss of appetite/unwillingness/inability to eat    | $C_6$  |
| diarrhea/ loose stool                               | $C_7$  |
| belly pain/stomachache/abdominal pain/abdominal pain| $C_8$  |
| stool does not form/loose stool                     | $C_9$  |
| left lower abdomen/left abdomen                     | $C_{10}$ |
| hematochezia/purulent blood/hemorrhage after defecation/bloody stool | $C_{11}$ |
| fever/high fever                                    | $C_{12}$ |

(2) Bayesian Network Construction with the Improved K2 Algorithm

The optimal network BDE score obtained by the K2 algorithm and the improved K2 algorithm for "gastritis" disease are shown in Figure 1:

![Figure 1. BDE scores of K2 and improved K2 algorithm for "gastritis" disease](image)

It can be seen from Fig.1, with the increase of sample size, BDE score function shows an upward trend, and the improved K2 algorithm can obtain a network structure with better BDE scores in most cases.

The parent nodes and specific scores of the network structure under different sample sizes are shown in Table 2:
Table 2. Optimal Networks for "Gastritis" with K2 and improved K2 Algorithm

| Sample size | K2 algorithm | Improved K2 algorithm |
|-------------|--------------|-----------------------|
|             | BDE sore     | Parent node           | BDE sore     | Parent node           |
| 500         | -323.6960    | $C_i$ & sour & hiccup | -323.6960    | $C_i$ & hiccup & sour |
| 1000        | -323.6338    | $C_i$ & sour & hiccup | -322.7797    | $C_i$ & $C_2$ & $C_4$ |
| 1500        | -321.4953    | $C_i$ & sour & $C_4$  | -320.0310    | $C_i$ & $C_2$ & $C_4$ |
| 2000        | -320.8789    | $C_i$ & sour & $C_4$  | -319.6585    | $C_i$ & $C_2$ & $C_4$ |

As shown in Fig.1 and Table 2, the improved K2 algorithm outperforms the K2 algorithm. The performances of K2 algorithm and improve K2 algorithm for "acute enteritis" is shown in Fig. 2:

Figure 2. BDE scores of K2 and improved K2 algorithm for "acute enteritis" disease

From Fig. 1 and Fig. 2, it can be seen that the optimal BDE scores of the improved K2 algorithm are better than the optimal BDE scores of the original K2 algorithm.

(3) Comparison with evaluation indexes

Applying the constructed Bayesian network for diagnosis on test sample, and the comparative results are shown in Table 3.

Table 3. Results for two diseases

| Disease       | Gastritis | Acute enteritis |
|---------------|-----------|----------------|
| Algorithm     | K2        | Improved K2    |
| Parent node   | $C_i$ & acid | $C_i$ & $C_2$ & $C_4$ | $C_i$ & $C_7$ & $C_8$ |
|               | Improved K2 | K2             |
|               | $C_i$ & $C_2$ & $C_4$ | $C_i$ & $C_7$ & $C_8$ |
|               | Improved K2 | $C_i$ & $C_2$ & $C_4$ | $C_i$ & $C_7$ & $C_8$ |
|      | TP  | 245 | 241 | 117 | 117 |
|------|-----|-----|-----|-----|-----|
| FN   | 189 | 193 | 291 | 291 |     |
| FP   | 210 | 197 | 108 | 108 |     |
| TN   | 1356| 1369| 1419| 1419|     |
| Precision | 80.05% | 80.5%  | 79.38% | 79.38% |     |
| Accuracy   | 53.85%  | 55.02%  | 52%  | 52%  |     |
| Recall     | 56.45%  | 55.53%  | 28.68% | 28.68% |     |

In summary, among the two diseases, the performance index of using the improved K2 algorithm to construct the optimal network is better than or equal to the optimal network constructed by the traditional K2 algorithm, so the effectiveness of the improved algorithm is confirmed.

4. Conclusion
This paper proposes an improved K2 algorithm by incorporating the idea of simulated annealing algorithm. The experimental results show that the simulated annealing alike K2 algorithm can build a more robust Bayesian network. By extracting knowledge from clinical text data, the constructed Bayesian model can be used to assist pre-diagnosis in clinic and has practical significance.

5. References
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