

# A Simple Node Ordering Method for the K2 Algorithm based on the Factor Analysis

Vahid Rezaei Tabar

*Department of Statistics, Faculty of mathematics and Computer Sciences, Allameh Tabataba'i University, Tehran, Iran  
vhrezaei@atu.ac.ir*

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**Abstract:** In this paper, we use the Factor Analysis (FA) to determine the node ordering as an input for K2 algorithm in the task of learning Bayesian network structure. For this purpose, we use the communality concept in factor analysis. Communality indicates the proportion of each variable's variance that can be explained by the retained factors. This method is much easier than ordering-based approaches which do explore the ordering space. Because it depends only on the correlation matrix. As well, experimental results over benchmark networks 'Alarm' and 'Hailfinder' show that our new method has higher accuracy and better degree of data matching.

## 1 INTRODUCTION

Bayesian networks (BNs) are directed acyclic graphs (DAGs), where the nodes are random variables, and the arcs specify the conditional independence structure between the random variables (Pearl, 1988; Geiger, 1990; Jensen, 1996; Friedman, 1997). The learning task in a BN can be separated into two subtasks, structure learning; that is to identify the topology of the network, and parameter learning; that is to estimate the parameters (conditional probabilities) for a given network topology (Heckerman, 1994; Ghahramani, 1998; Grossman, 2004). While there are large collections of variables in many applications, a fully BN approach for learning structure upon variables can be expensive and lead to high dimensional models (Friedman, 2000; Perrier, 2008). In other words, the number of BN structures is super-exponential in the number of random variables in the domain. To overcome such difficulties in terms of computational complexity, several approximations have been designed, such as imposing a previous ordering on the domain attributes or using other approaches trying to reduce the state space of this problem (Spirtes, 1993; Madigan, 1995). The K2 algorithm is one of the basic methods for effectively resolving the above problems (Cooper, 1992). This algorithm works with a node ordering as an input. It starts by assuming that a node lacks parents, after which in every step it

adds incrementally that parent whose addition most increases the probability of the resulting structure. K2 stops adding parents to the nodes when the addition of a single parent cannot increase the probability. As mentioned, the K2 algorithm receives as input a total ordering of the variables which can have a big influence on its result. Thus, finding a good ordering of the variables is also crucial for the algorithm success (Larranaga, 1996; Ruiz, 2005; Lamma, 2005; Chen, 2008).

The K2 algorithm reduces this computational complexity by requiring a prior ordering of nodes as an input, from which the network structure will be constructed.

Chow & Liu, (1968) proposed a method derived from the maximum weight spanning tree algorithm (MWST). This method associates a weight to each edge. This weight can be either the mutual information between the two variables or the score variation when one node becomes a parent of the other. When the weight matrix is created, a usual MWST algorithm gives an undirected tree that can be oriented given a chosen root. Based on the Heckerman et al. (1994) propose, one can use the oriented tree obtained with the maximum weight spanning tree algorithm (MWST) to generate the node ordering. The algorithm which uses the class node as a root called "K2+T" (Leray et al., 2004). Where the class node is the root node of the tree, the class node can be interpreted as a cause instead of a

consequence. That's why Leray et al. (2004) proposed the reverse order called "K2-T".

In general, node ordering algorithms are categorized into two groups; evolutionary algorithms and heuristic algorithms. Initial research on evolutionary algorithms has provided extensive experimental results through various crossover and mutation methods (Romero, 1994; Larranaga 1996; Hsu et al., 2007). In terms of heuristic methods, Hruschka et al. (2007) introduced the feature ranking-based node ordering algorithm, which is a type of feature selection method in the classification domain. It measures dependencies of variables over the class label using  $\chi^2$  statistical tests and information gain; it then sorts the variables by the dependence-based scores. The sorted variables are regarded as the node ordering. Chen et al. (2008) incorporated information theory and exhaustive search functions in their algorithm. The algorithm comprises three major phases. In the first two phases, it constructs an undirected structure through mutual information, independence tests, and d-separation. The last phase is related to determination of node ordering.

In this paper, we focus on the factor analysis for determining the node ordering as an input for K2 algorithm. The steps of our method are as follows:

- First right number of factors must be extracted.
- Once the extraction of factors has been completed, we use the "Communalities" which tells us how much of the variance in each of the original variables is explained by the extracted factors. In other words, communality is the proportion of each variable's variance that can be explained by the common factors.
- We consider the communality as a novel method for determining the node ordering as an input for K2 algorithm.

Our novel method is much easier than ordering-based approaches which do explore the ordering space. To the best of our knowledge, the most effective heuristic algorithm for determining the node ordering is the one proposed by Chen et al. (2008) whose time complexity is  $O(n^4)$ . However, our methodology has less complexity compared to other node ordering methods. Because our method depends only on the correlation matrix.

The paper is organized as follows. First an introduction to the Factor Analysis is presented. We then introduce our methodology for learning BN structure. We finally compare our results with the performance of other methods such as K2+T (K2

with MWST initialization), K2-T (K2 with MWST inverse initialization), Hruschka et al. method (2007), Chen et al. method (2008).

## 2 FACTOR ANALYSIS

Factor analysis is a method of data reduction (Kim, 1978; Johnson, 1992). It does this by seeking underlying unobserved variables (factors) that are reflected in the observed variables. Therefore it is needed to determine the number of factors to be extracted. The default in most statistical software packages is to retain all factors with eigenvalues greater than 1 (Kaiser, 1992). Alternate tests for factor retention include the scree test, Velicer's MAP criteria, and parallel analysis. It has been found that the parallel analysis commonly leads to accurate decision when applied to discreet data (Hayton, 2004).

Horn (1965) proposes parallel analysis, a method based on the generation of random variables, to determine the number of factors to retain. Parallel analysis, compares the observed eigenvalues extracted from the correlation matrix to be analysed with those obtained from uncorrelated normal variables.

An aim of factor analysis (FA) is to 'explain' correlations among observed variables in terms of a relatively small number of factors. Assume the  $p \times 1$  random vector  $\mathbf{X}$  has mean  $\boldsymbol{\mu}$  and covariance matrix  $\boldsymbol{\Sigma}$ . The factor model postulates that  $\mathbf{X}$  linearly depend on some unobservable random variables  $F_1, F_2, \dots, F_m$ , called common factors and  $p$  additional sources of variation  $\xi_1, \dots, \xi_p$  called errors or sometimes specific factors. The factor analysis model is:

$$\begin{aligned} X_1 - \mu_1 &= l_{11}F_1 + l_{12}F_2 + \dots + l_{1m}F_m + \xi_1 \\ X_2 - \mu_2 &= l_{21}F_1 + l_{22}F_2 + \dots + l_{2m}F_m + \xi_2 \\ &\vdots \\ X_p - \mu_p &= l_{p1}F_1 + l_{p2}F_2 + \dots + l_{pm}F_m + \xi_p \end{aligned} \quad (1)$$

As a matrix notation, we can write:

$$\mathbf{X} - \boldsymbol{\mu} = \mathbf{L}\mathbf{F} + \boldsymbol{\xi}$$

The coefficient  $l_{ij}$  is called loading of the  $i$ -th variable on the  $j$ -th factor, so  $\mathbf{L}$  is the matrix of factor loadings. Notice, that the  $p$  deviations  $X_i - \mu_i$  are expressed in terms of  $p + m$  random variables  $F_1, \dots, F_m$  and  $\xi_1, \dots, \xi_p$  which are all unobservable. There are too many unobservable quantities in the model. Hence we need further assumptions about  $\mathbf{F}$  and  $\boldsymbol{\xi}$ . We assume that:

$$E(\mathbf{F})=\mathbf{0}, \quad \text{Cov}(\mathbf{F})=E(\mathbf{F}\mathbf{F}^t)=\mathbf{I}, \quad E(\boldsymbol{\xi})=\mathbf{0}, \quad \text{Cov}(\mathbf{F}, \boldsymbol{\xi})=\mathbf{0}, \quad \text{cov}(\boldsymbol{\xi}\boldsymbol{\xi}^t)=\boldsymbol{\varphi} = \begin{pmatrix} \varphi_1 & 0 & \dots & 0 \\ 0 & \varphi_2 & \dots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \dots & \varphi_p \end{pmatrix}$$

Therefore, we have (Johnson , 2002):

$$\boldsymbol{\Sigma}=\text{Cov}(\mathbf{X}) =\mathbf{L}\mathbf{L}^t +\boldsymbol{\varphi}$$

The decision about the number of common factors (m) to retain, must steer between the extremes of losing too much information about the original variables on one hand, and being left with too many factors on the other. For this purpose, we use the parallel analysis. Because we deal with the discrete datasets (Hayton, 2004). Once the extraction of factors has been completed, we use the ‘‘Communalities’’ as a method of determining the ordering among variables which tells us how much of the variance in each of the original variables is explained by the common factors. That proportion of  $\text{Var}(X_i) = \sigma_{ii}$  contributed by the m common factors is called the i-th communality  $h_i^2$  which can be defined as the sum of squared factor loadings for the variables. The proportion of  $\text{Var}(X_i)$  due to the specific factor is called the uniqueness, or specific variance. i.e.

$\text{Var}(X_i) = \text{communality} + \text{specific variance}$

$$\sigma_{ii} = l_{i1}^2 + l_{i2}^2 + \dots + l_{im}^2 + \varphi_i$$

Regarding

$$h_i^2 = l_{i1}^2 + l_{i2}^2 + \dots + l_{im}^2,$$

We get

$$\sigma_{ii} = h_i^2 + \varphi_i$$

If the data were standardized before analysis, the variances of the standardized variables are all equal to one. Then the specific variances can be computed by subtracting the communality from the variance as expressed below:

$$\varphi_i = 1 - h_i^2$$

Based on the fact that variables with high values of communalities are well represented in the common factor space, we can determine the variable ordering. It means that the variable with high communality extracts the largest amount of information from the data. Note that one can think of communalities as multiple  $R^2$  values for regression models predicting the variables of interest from the common factors.

### 3 STRUCTURE LEARNING FOR BAYESIAN NETWORK

The global joint probability distribution of the BN constructed by variables, given the representation of conditional independences by its structure and the set of local conditional distributions, can be written as:

$$P(X_1, \dots, X_n) = \prod_{i=1}^n P(X_i | \text{Parent}(X_i)) \quad (2)$$

where  $P(X_i | \text{Parent}(X_i))$  specified the parameter shown by  $\theta_{X_i | Pa(X_i)}$ . If we assume that  $X_i$  takes its  $k - th$  value and the variables in  $Pa(X_i)$  take their  $j$ -th configuration then  $\theta_{X_i | Pa(X_i)} = \theta_{ijk}$ . In theory, one could iterate over all possible BN structures and select the one that achieves the best likelihood/accuracy/whatever-score. In practices, this is of course not possible (Fridman, 2000).

The methods used for learning the structure of BNs can be divided into two main groups;

- Discovery of independence relationships using statistical test, e.g. PC and GS algorithm,
- Exploration and evaluation which use a score to evaluate the ability of the graph to recreate conditional independence within the model, e.g., K2

K2 algorithm is the basic method working with a node ordering as an input. It starts by assuming that a node lacks parents, after which in every step it adds incrementally that parent whose addition most increases the probability of the resulting structure (Cooper, 1992). K2 stops adding parents to the nodes when the addition of a single parent cannot increase the probability. The K2 algorithm receives as input a total node ordering which can have a big influence on its result. Thus, finding a good ordering of the variables is also crucial for the algorithm success. In other words, The K2 algorithm reduces this computational complexity by requiring a prior ordering of nodes as an input, from which the network structure will be constructed. The ordering is such that if node  $X_i$  comes prior to node  $X_j$  in the ordering, then node  $X_j$  cannot be a parent of node  $X_i$ . In other words, the potential parent set of node  $X_i$  can include only those nodes that precede it in the input ordering. The K2 algorithm is included below:

**Procedure K2**

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1. {Input: A set of n nodes, an ordering on the nodes,
an upper bound u on the number of parents a node may
have, and a database D containing m cases}
2. {Output: for each node, a printout of parents of the
node}
3. for i:=1 to n do
4.    $\pi_i := \emptyset$ ;
5.    $P_{old} = f(i, \pi_i)$ 
6.   OKToProceed:=true;
7.   While OKToProceed and  $|\pi_i| < u$  do
8.     Let z be the node in  $Pred(x_i) - \pi_i$  that maximize
 $f(i, \pi_i \cup \{z\})$ ;
9.      $P_{new} = f(i, \pi_i \cup \{z\})$ ;
10.    If  $P_{new} > P_{old}$  then
11.       $P_{old} = P_{new}$ ;
12.       $\pi_i = \pi_i \cup \{z\}$ 
13.    else OKToProceed:= false;
14.  end{while};
15. end{for}
16. end{K2}
    
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where

$$f(i, \pi_i) = \prod_{j=1}^{q_i} \frac{(r_i - 1)!}{(N_{ij} + r_i - 1)!} \prod_{k=1}^{r_i} N_{ijk}$$

$Pred(x_i)$ : is a set that is computed for every node during the algorithm and it includes the nodes that precede a node  $x_i$  in the ordering.

$\pi_i$ : set of parents of node  $x_i$

$q_i = |\varphi_i|$ ,  $\varphi_i$ : list of all possible instantiations of the parents of  $x_i$  in database **D**.

$r_i = |V_i|$ ,  $V_i$ : list of all possible values of the attribute  $x_i$

$N_{ijk}$ : Number of cases (i.e. instances) in **D** in which the attribute  $x_i$  is instantiated with its  $k$ -th value, and the parents of  $x_i$  in  $\pi_i$  are instantiated with the  $j$ -th instantiation in  $\varphi_i$ ;  $N_{ij} = \sum_{k=1}^{r_i} N_{ijk}$  That is, the number of instances in the database in which the parents of  $x_i$  in  $\pi_i$  are instantiated with the  $j$ -th instantiation in  $\varphi_i$ .

Our methodology for learning BN via communality concept is as follows:

- Because we conduct factor analysis on the correlation matrix (standardized variables), we need to use the proper correlation between variables, i.e., the correlation between ordinal variables referred as Spearman correlation
- Once the extraction of factors has been completed (here using parallel analysis), we use the communalities (the proportion of each variable's variance) and determine the node ordering.
- Finally K2 algorithm is used to construct a BN.

**4 EXPERIMENT**

In this section we present the empirical results. For this purpose, we use two well-known network structures; ALARM (Beinlich et al., 1998) and Hailfinder (Abramson, 1996). We sample four datasets from ALARM and Hailfinder BNs in order to perform multiple tests and estimate more precise metrics. Therefore we sample 1000, 5000, 10000 and 20000 cases for learning BN structures and repeat this procedure 10 times.

We consider the proportion of the variance of each variable which is accounted for by the common factors (communality) as the input for K2 algorithm. We also consider other node ordering methods such as K2+T, K2-T, Hruschka et al. method (2007) and Chen et al., method (2008) as input for K2 algorithm. We finally compare the results.

The existence of the known network structures allows us to define important terms, which indicate the performance of the method. For this purpose, the True Positive (TP), False Positive (FP), True Negative (TN) and False Negative (FN) values are computed. In addition, known measure such as, Positive Predictive Value (PPV), True Positive Rate (TPR) and F-score measure (F-measure) are considered (Powers, 2011). The F-measure score is defined as follows:

$$F - measure = 2 \frac{PPV \cdot TPR}{PPV + TPR}$$

F-measure is useful quantity used to compare learned and actual networks. Comparing this measure between different methods indicates which method is more efficient in the task of learning BNs. The algorithm with larger values for F-measure is more efficient in learning the skeleton of the network.

**4.1 ALARM Network**

The ALARM network has 37 variables; each one has two, three or four possible attributes. ALARM network shown in Figure 1.

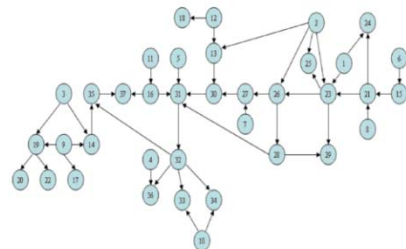


Figure 1: ALARM Network.



The 37 nodes in ALARM network can be viewed as ordinal variables; 27 variables have natural ordering and 10 variables are binary data which can be viewed as a special case of ordinal data with only two categories (for instance not having hypovolemia is better than having one). Therefore the Spearman correlation between variables for performing FA is considered.

The right number of factors is determined by parallel analysis. Figure 2 shows the number of eigenvalues of the data that are greater than simulated values. In other words, Parallel analysis suggests that the numbers of factors are 11, 12, 12 and 12 for sample sizes 1000, 5000, 10000 and 20000 respectively.

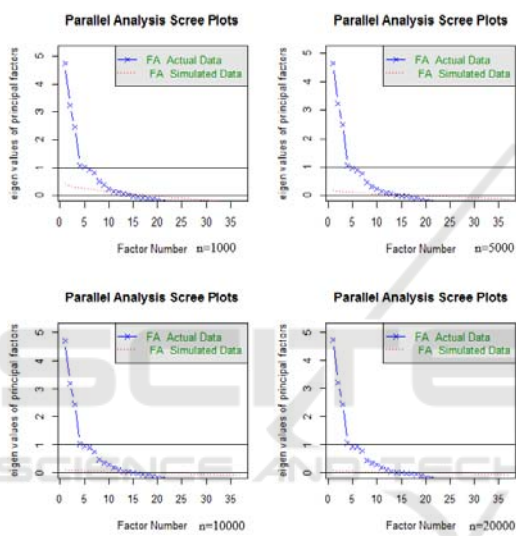


Figure 2: Factor Numbers Using parallel analysis; Alarm network.

As mentioned before, we sample 1000, 5000, 10000 and 20000 cases and repeat this procedure 10 times and report the mean of TPs, FPs, F-measures and the standard deviation (std) of F-measures. According to the Tables 1- 4, our proposed method for determination of node ordering as input for K2 algorithm receives higher value of F-measure.

Table 1: Comparing different methods (Sample size: 1000, network=Alarm).

Method	TP	FP	F	std
PROPOSED	22.12	44.37	<b>0.39</b>	0.011
K2 + MWST	16.25	44.38	0.3	0.031
K2-MWST	22.75	58.87	0.35	0.012
Chen et al.	20.62	58.62	0.32	0.023
Hruschka et al	20.87	61.50	0.32	0.019

Table 2: Comparing different methods (Sample size: 5000, network =Alarm).

Method	TP	FP	F	std
PROPOSED	22.25	44.5	<b>0.39</b>	0.010
K2 + MWST	15.62	45.62	0.29	0.011
K2-MWST	22.25	57.12	0.35	0.022
Chen et al.	20.75	51.75	0.35	0.013
Hruschka et al	21.12	56.87	0.34	0.012

Table 3: Comparing different methods (Sample size: 10000, network =Alarm).

Method	TP	FP	F	std
PROPOSED	21.37	42.75	<b>0.40</b>	0.023
K2 + MWST	18.87	37.25	0.36	0.013
K2-MWST	18.25	46.50	0.33	0.012
Chen et al.	22.50	53.62	0.36	0.018
Hruschka et al	22.37	53.12	0.36	0.016

Table 4: Comparing different methods (Sample size: 20000, network =Alarm).

Method	TP	FP	F	std
PROPOSED	22.37	36.12	<b>0.41</b>	0.020
K2 + MWST	16.50	45.50	0.30	0.021
K2-MWST	23.12	57.25	0.36	0.016
Chen et al.	23.12	52.37	0.38	0.014
Hruschka et al	22.87	49.50	0.38	0.014

## 4.2 Hailfinder Network

Hailfinder is a BN designed to forecast severe summer hail in northeastern Colorado. The number of nodes and arcs are 56 and 66 respectively (Figure 3). The 56 nodes in Hailfinder network can be viewed as ordinal variables; therefore the Spearman correlation between variables can be considered for performing FA.

Figure 4 shows the number of eigenvalues of the data that are greater than simulated values. Parallel analysis suggests that the numbers of factors are 13, 18, 19 and 21 for sample sizes 1000, 5000, 10000 and 20000 respectively.

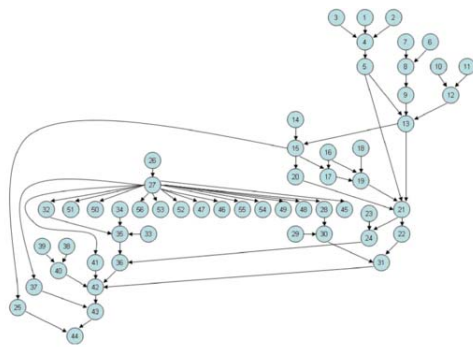


Figure 3: Hailfinder Network.

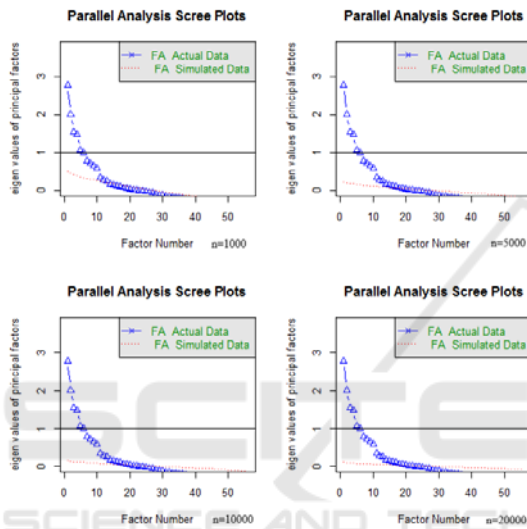


Figure 4: Factor Numbers Using parallel analysis; Hailfinder.

We also sample 1000, 5000, 10000 and 20000 cases from Hailfinder and repeat this procedure 10 times and report the mean of TPs, FPs, F-measures and the standard deviation of F-measures.

As shown in Tables 5-8, if we deal with a large data set, our proposed method for determining the node ordering among variables has higher accuracy as input for K2 algorithm.

Table 5: Comparing different methods (Sample size: 1000, network =Hailfinder).

Method	TP	FP	F	std
PROPOSED	29.37	72	<b>0.35</b>	0.013
K2 + MWST	20.5	64.5	0.27	0.012
K2-MWST	19.12	67.5	0.25	0.009
Chen et al.	20.87	60.62	0.28	0.011
Hruschka et al	26.37	81.12	0.3	0.010

Table 6: Comparing different methods Sample size: 5000, network =Hailfinder).

Method	TP	FP	F	std
PROPOSED	28.12	63.25	<b>0.35</b>	0.015
K2 + MWST	21.87	61.62	0.29	0.012
K2-MWST	20.75	63.25	0.27	0.009
Chen et al.	22.87	61.62	0.30	0.012
Hruschka et al	25.12	73.25	0.30	0.014

Table 7: Comparing different methods (Sample size: 10000, network =Hailfinder).

Method	TP	FP	F	std
PROPOSED	31.12	62.12	<b>0.39</b>	0.013
K2 + MWST	22.00	61.87	0.29	0.015
K2-MWST	21.87	61.87	0.29	0.011
Chen et al.	26.25	58.75	0.34	0.011
Hruschka et al	25.75	62.37	0.33	0.017

Table 8: Comparing different methods (Sample size: 20000, network =Hailfinder).

Method	TP	FP	F	std
PROPOSED	33.12	58.5	<b>0.42</b>	0.017
K2 + MWST	27.75	61.75	0.35	0.019
K2-MWST	22.62	61.75	0.3	0.016
Chen et al.	22.75	61.87	0.3	0.010
Hruschka et al	31.00	65.87	0.38	0.013

## 5 COMPARISON OF CONSUMED TIME AND COMPLEXITY

Yielding more effective node ordering is an important issue for the K2 algorithm. However, the most effective heuristic algorithm is the one proposed by Chen et al. (2008) whose time is  $O(n^4)$ . We introduce a very simple node ordering method as input of K2 algorithm that the time complexity was thereby reduced to  $O(n^2)$ . We also compare the time consumption by the node ordering methods. In this comparison, less time reflects better performance. The results are presented in Table 9. It shows that our method has the better performance. So we can conclude that the proposed ordering method is much accurate and simple compared with other ordering space exploring approaches.

Table 9: Time consumed (s) during node ordering (including the K2 algorithm).

Method	Alarm	Hailfinder
PROPOSED	8.98 s	31.35 s
K2 + MWST	11.28 s	33.62 s
K2-MWST	12.36 s	34.70 s
Chen et al.	75.19 s	300.94 s
Hrushka et al.	236.22	984.95 s

## 6 CONCLUSIONS

The BN-learning problem is NP-hard, so many approaches have been proposed for this task is quite complex and hard to implement. In this paper, we propose a very simple and easy-to-implement method for addressing this task. Our method is based on the single order yielded by factor analysis. It does not explore the space of the orderings. So, it is much easier than ordering-based approaches which do explore the ordering space. Because factor analysis is based on the correlation matrix of the variables involved.

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