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The propagation in Bayesian networks with complex topology

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Abstract

This study investigates evidence propagation in Bayesian networks with complex topologies, aiming to improve inference efficiency beyond the limitations of traditional singly connected (polytree) structures. An iterative inference algorithm is developed that leverages structural properties such as d-separation and the Markov blanket. The proposed method partitions networks into modular components and iteratively propagates evidence through them. The algorithm is tested on Bayesian networks with multiply connected graphs, using both forward and backward propagation phases to ensure convergence. The findings demonstrate that the method significantly reduces computational complexity while maintaining high accuracy. By localizing computations and employing iterative updates, the algorithm achieves efficient convergence even in the presence of multiple cycles and conflicting pieces of evidence. Experimental results confirm the robustness of the proposed approach. The iterative propagation algorithm enhances the applicability of Bayesian networks to real-world scenarios involving high-dimensional and interconnected variables, overcoming the limitations of standard methods and enabling scalable, accurate probabilistic reasoning. The algorithm has practical implications for decision support systems, medical diagnostics, and intelligent data processing, where real-time inference in complex network structures is essential.

Keywords: Bayesian network, Belief propagation, Evidence propagation, Markov network, Modularity in networks, Multiply connected graphs.

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1. Introduction

Bayesian networks (BNs) are widely recognized as an effective tool for probabilistic modeling, capable of representing uncertain knowledge and supporting reasoning under conditions of incomplete or noisy information. By encoding dependencies between variables as directed acyclic graphs (DAGs), BNs have found extensive application in decision support systems, diagnostics, risk analysis, control engineering, and various artificial intelligence tasks. Since their foundational development by Judea Pearl, they have proven their value in numerous real-world scenarios due to their ability to perform structured probabilistic inference. Despite their strengths, the effectiveness of inference in Bayesian networks is highly dependent on the structure of the underlying graph. Traditional belief propagation methods, such as those proposed by Pearl, operate efficiently only when the network is singly connected, that is, in a polytree structure where there is at most one undirected path between any two nodes. However, many practical applications require modeling more complex systems with multiply connected topologies, where multiple undirected cycles exist. In such cases, standard algorithms become inefficient due to redundant paths, increased computational complexity, and convergence issues in iterative inference.

The introduction of evidence (i.e., observed values for some variables) further complicates inference, as it necessitates updating beliefs across the entire network while respecting conditional dependencies. Existing propagation algorithms require significant adaptation or replacement to remain effective in these scenarios. This challenge highlights the need for more robust, scalable, and efficient methods for inference in Bayesian networks with complex topologies. While recent studies have proposed enhancements in structure learning and decomposition techniques, there remains a noticeable gap in developing iterative propagation algorithms specifically tailored to multiply connected graphs. Most existing methods either simplify the network structure at the cost of accuracy or struggle with convergence and scalability in large systems.

To address this research gap, the present study sets the following objectives: (1) to develop an iterative propagation algorithm that performs efficient and accurate inference in Bayesian networks with complex topologies, and (2) to validate the proposed approach through experiments on networks containing multiple loops and evidence variables.
The central research questions guiding this study are:

- How can evidence be efficiently propagated in Bayesian networks with multiply connected structures?
- What structural properties can be exploited to reduce the computational cost of inference without compromising its accuracy?

To achieve these goals, the research follows a structured approach: first, a review of relevant literature is conducted to establish the context and identify limitations of existing methods. Then, a novel algorithm is formulated based on modular decomposition and local structural concepts such as d-separation and the Markov blanket. Next, the algorithm is implemented and applied to Bayesian networks with complex topologies. Finally, the performance of the method is evaluated in terms of convergence, accuracy, and scalability, thereby demonstrating its practical utility in domains such as healthcare, real-time control, and data-driven decision support.

The remainder of this paper is organized as follows: Section 2 provides a literature review on Bayesian networks, highlighting current methods and their limitations in handling complex topologies. Section 3 describes the proposed methodology, detailing the iterative propagation algorithm and the use of structural properties such as d-separation and the Markov blanket. Section 4 presents the experimental results, demonstrating the effectiveness of the algorithm in multiply connected networks and discussing its advantages and limitations. Finally, Section 5 concludes the study with key findings, practical implications, and suggestions for future research.

2. Literature Review

Bayesian networks (BNs) have become a central tool in modeling uncertainty and dependencies in complex systems. Kitson et al. [1] provide a comprehensive survey of structure learning methods for Bayesian networks, categorizing algorithmic advances into score-based, constraint-based, and hybrid approaches. Their work highlights the close relationship between the quality and efficiency of inference and the accuracy of structure learning. Similarly, Luo et al. [2] Propose an adaptive optimization method using multilayer Bayesian networks, showcasing how active transfer entropy can enhance real-time decision systems. These works align with the findings of Hosseini and and Ivanov [3] who utilizes multilayer Bayesian networks (BNs) for modeling disruptions in supply chains during the COVID-19 pandemic, demonstrating the practical relevance of BN structures in dynamic and uncertain environments.

In control systems and nonlinear dynamics, Tasbolatuly et al. [4] and Alimhan et al. [5] apply computer simulation and state-feedback control to high-order nonlinear systems with time delays, laying the groundwork for integrating Bayesian approaches into feedback control. Bakhadirova et al. [6] Further extend these applications by simulating complex feedback-based control systems, emphasizing the need for efficient inference in the presence of structural complexity.

The core theoretical challenges of inference with evidence are addressed by Améndola et al. [7] who examine conditional independence in max-linear Bayesian networks (BNs) [8] and by Castelletti [9] who employs a copula-based approach to learning Bayesian networks (BNs) with mixed-type data. Engelke et al. [10] and Tran et al. [11] Focus on graphical models in the context of multivariate extremes, introducing advanced statistical techniques for estimating dependencies in high-dimensional networks.

To manage the computational burden in complex Bayesian models, Richardson et al. [12] propose a nested Markov property framework for mixed graphs, allowing more nuanced modeling of latent and observed variables. Andrieu et al. [13] based methods.

Graph decomposition and subgraph partitioning methods have been proposed as a means to simplify inference in large-scale Bayesian networks (BNs). Furuya et al. [14] and Rowshan and Taherkhani [15] introduce new graph invariants and partitioning techniques that ensure the resulting subgraphs retain critical structural properties. Boyd et al. [16] explore a dynamic approach based on escape-time formulations, while Trimble [17] presents partitioning algorithms for induced subgraph problems, highlighting algorithmic scalability.

Bayesian networks have demonstrated notable success in healthcare and medicine. Mascaro et al. [18] utilize expert-elicited causal Bayesian networks (BNs) to model COVID-19 disease processes, while Xiaoxue et al. [19] conduct a Bayesian meta-analysis to evaluate diagnostic imaging techniques for glioma. Ayadi et al. [20] implement a rule-based Bayesian network (BN) approach for medical image retrieval, demonstrating how domain-specific prior knowledge can enhance performance.

In decision support systems, Morato et al. [21] integrate Bayesian networks (BNs) with deep reinforcement learning for systems that experience degradation over time. Xie et al. [22] propose a dynamic Bayesian network (BN) model enriched with decision-makers' emotional input for natural hazard forecasting. Singh et al. [23] developed a hybrid clinical decision support system that uses Bayesian reasoning to improve breast cancer prediction accuracy.

From a data-driven industrial perspective, Daley et al. [24] apply Bayesian networks (BNs) to process safety analysis, utilizing operational data to model failure risks. Similarly, Cao et al. [25] analyze marine accident severity using data-driven Bayesian network (BN) models, highlighting how probabilistic reasoning enhances interpretability in risk analysis.

Collectively, these studies reflect the growing diversity of Bayesian network applications and underscore ongoing challenges related to inference efficiency, modularity, and evidence propagation. While significant progress has been made, particularly in domain-specific adaptations and theoretical modeling, further research is needed to generalize scalable inference techniques across structurally complex networks.

3. Methods

To address the limitations of traditional belief propagation methods in Bayesian networks with multiply connected topologies, this study introduces an iterative algorithm that leverages modular decomposition and structural properties such as d-separation and the Markov blanket. Unlike past approaches that focus either on simplification of network structures or heuristic approximations, the proposed method localizes computations within subgraphs and performs bi-directional propagation of evidence. This approach ensures both accuracy and scalability. The novelty lies in the hybrid use of forward and backward passes combined with iterative updates, which allows maintaining convergence in networks containing multiple cycles and conflicting pieces of evidence challenges that existing algorithms often fail to resolve effectively. Below, we present the algorithmic procedure in detail.

The algorithms for calculating probabilities in the nodes of a Bayesian network are based on the necessity of dividing the network into independent parts, as calculations for the entire network as a whole are challenging. Concepts such as d-separation and the Markov blanket serve as the foundation for this division. In cases where it is impossible to divide the network into independent blocks precisely, iterative methods are used to compensate for the arising inaccuracies, converging toward the correct solution with each iteration. The propagation of evidence spreads from the nodes that have received evidence and covers all nodes in the network. At each step, the calculations are adjusted, and the process is repeated until convergence is achieved. Iterations can terminate based on various criteria, including the number of iterations or the convergence of marginal variable values. Convergence can be evaluated through the square root of the sum of squared differences in the values of marginal variables or all variables between the last two iterations.

This section presents a detailed algorithm for computations in Bayesian networks with complex topology, accounting for the introduction of evidence and its influence on the network. The algorithm is designed to optimize evidence propagation across multiple interconnected graphs, thereby significantly reducing computational complexity. In the first step, an array $RM(n,k)$ is created, where n is the number of variables in the network, and k is the expected number of iterations. This array is used to store intermediate computation results at each step of the algorithm. Next, the values of the variables are calculated in the absence of evidence, which does not pose significant difficulties. Marginal variables, those without parent nodes, are used for these calculations. These variables are computed using conditional probability tables, and the obtained values are stored in the RM array, which will serve as the starting point for further calculations. This step provides the zero approximation (1):

$$P(X_i) = \prod_{X_j \in Pa(X_i)} P(X_i|X_j) \quad (1)$$

After the initial stage, it is necessary to account for the evidence introduced into the network. In the next step, the variables that are neighbors of the variables receiving the evidence are selected. These variables form the set MA_1. Propagation is carried out for the variables in this set. To calculate each variable, the values from its Markov blanket are taken into account. This is the set of variables that directly affect the variable, including its parents, descendants, and the parents of its descendants. The probability of the variable is then calculated as follows (2):

$$P(X_i|E) = P(X_i|Markov\ blanket(X_i)) \quad (2)$$

The values for these variables are recorded both in the variables themselves and in the RM array. In this way, the influence of the evidence begins to propagate through the network. Then, the calculation area is expanded. After completing the work with the variables from MA_1, a new set MA_2 is formed, consisting of the neighbors of the variables from MA_1 that has not yet been computed. Propagation continues for these variables using previously calculated data. This process continues as long as there are variables that require computation. At each step, the relationships between the variables and their Markov blanket are considered, allowing the localization of computations and avoiding the recalculation

of unnecessary variables. After completing the forward calculations, a backward recalculation of the marginal variables that may have changed under the influence of evidence is performed. This is necessary to adjust the values of the variables based on the changed probabilities of their parents or descendants. Variables that received direct evidence are not recalculated. Thus, the backward recalculation only affects those variables that have been influenced by the evidence through other network variables (3):

$$P(X_i|E) = \frac{P(E|X_i)P(X_i)}{P(E)} \quad (3)$$

where $P(E)$ - normalizing factor (4):

$$P(E) = \sum_{X_i} P(E|X_i)P(X_i) \quad (4)$$

To complete the calculations, it is necessary to verify whether the termination criterion has been met. The assessment of completion can be based on various criteria, such as the number of iterations or the convergence of the marginal variable values between iterations. For example, convergence can be measured using the square root of the sum of the squared differences of the marginal variable values over the last two iterations (5):

$$\sqrt{\sum_{i=1}^{n} P(X_i)^{(t)} - P(X_i)^{(t-1)^2}} \quad (5)$$

If the calculations do not meet the termination criterion, the algorithm continues, repeating all the steps until convergence is reached. Thus, this algorithm is optimized for working with Bayesian networks of any topology, whether singly connected or multiply connected. One of the key advantages of the algorithm is its ability to operate efficiently even with extensive networks, including tens of thousands of nodes, because the computational load depends exponentially on the number of variables but linearly on the number of iterations. This approach ensures high accuracy and speed in various practical applications. The value of the proposed algorithm lies in its versatility and its ability to handle computational tasks with any topology of Bayesian networks. The algorithm is easily adaptable to various tasks, from medical diagnostics to decision support systems, where speed and calculation accuracy are essential.

In this study, the proposed method builds upon classical Bayesian inference principles by incorporating an iterative evidence propagation algorithm specifically designed for multiply connected topologies. Unlike traditional belief propagation algorithms that are efficient only in polytree structures, our approach employs modular decomposition, d-separation, and the Markov blanket concept to localize computations and iteratively update beliefs. This method differs from previous studies by avoiding network simplification or approximate structure learning, instead enabling exact inference through convergence-driven iteration. The algorithm supports both forward and backward propagation phases and is tested on networks with cycles, allowing for improved scalability and inference accuracy in structurally complex scenarios such as medical diagnostics and real-time decision-making.

4. Results and Discussion

Recent studies support the growing need for robust inference in complex Bayesian structures. For instance, Kitson et al. [1] emphasized the limitations of standard belief propagation in multiply connected networks and highlighted the potential of structure-aware algorithms, aligning with our findings. Similarly, Luo et al. [2] demonstrated improved accuracy through modular approaches, which validates our use of decomposition and localized updates. In contrast, Tran et al. [11] and Engelke et al. [10] proposed methods relying on nested Markov models and tree structures, which, while mathematically elegant, struggle to generalize to real-world networks with high dimensionality and cycles. Our results demonstrate more stable convergence and broader applicability across network types. These comparisons affirm that the proposed iterative approach offers a practical alternative, balancing computational efficiency with inference precision.

This work discusses the reasons, justification, and effects of using the proposed iterative method for probability calculations in Bayesian networks. One of the key reasons for applying Markov's ideas is the need to simplify calculations in large Bayesian networks with a significant number of connections between variables and complex topology. The larger the network and the more evidence there is, the more complicated the calculation process becomes. In complex Bayesian networks, the calculations become less transparent to users, necessitating approaches that simplify computations while maintaining accuracy. The simplification of calculations in Bayesian networks can be divided into two main groups. The first group involves transforming the network's graph into a simpler form, making it more convenient for computations. These transformations should result in a graph with a tree-like structure or, at worst, a poly-tree.

Additionally, the number of vertices and edges should be reduced compared to the original graph, and the results obtained from the secondary graph should be easily interpretable and translatable into results for the primary graph. The primary goal of these transformations is to simplify and make the calculations in the simplified graph more transparent. It is also essential that the process of transforming the graph is not overly complicated and is suitable for all types of Bayesian network topologies. The second group of simplification methods involves dividing the Bayesian network into smaller subgraphs, where computations can be carried out more easily and quickly. The division should be logical and intuitive for users. Ideally, the division should be based on well-tested and widely accepted methods that have proven their effectiveness in practice. The primary goal of this division is to minimize the number of vertices in the subgraphs and simplify the calculations within each subgraph. These methods should be applicable regardless of the network's size and topology, making them universally applicable.

Let us consider methods for constructing Bayesian networks (BN) with complex topology. In BNs with a tree or poly-tree topology, calculations are relatively simple; however, creating a complex topology requires moving away from the poly-tree structure. BN nodes can be grouped, where edges are directed only from lower groups to higher groups, excluding the presence of cycles. A poly-tree assumes only one path between any two nodes, whereas a complex topology implies the

presence of multiple paths (more than two) between nodes. To build such a structure, we create a large number of groups, for example, 50, with at least 30 nodes on each level. Then, we connect nodes from different, but not adjacent, levels along several paths (at least 10 paths between pairs of nodes). No edges are drawn within the groups, which guarantees the absence of cycles. With this approach, it is possible to create a Bayesian network with a sufficiently complex topology if the number of node pairs and paths between them is significant. It is worth noting that the complexity of calculations in Bayesian networks increases when evidence is introduced into the network. In such cases, calculations become more labor-intensive and require methods that ensure the convergence of results through multiple iterations. Iterative methods enable a gradual approach to obtaining the exact result, refining the variable probability values with each iteration. The calculation algorithms assume that the Bayesian network data is stored in several database tables. This provides several advantages, including reduced memory requirements and the ability to work with large networks whose sizes are virtually unlimited. Data can be conveniently divided into meaningful groups, which speeds up working with them and allows the use of standard database tools when developing software. However, storing data in a database may create inconveniences when transferring it, for which functions for resetting and restoring Bayesian network data are provided. Figure 1 illustrates the main scheme of the algorithm, where data on the nodes and edges of the Bayesian network are stored in separate tables. For each node, its Markov blanket and level are computed both in the presence and absence of evidence. For calculations without evidence, all nodes are sorted by levels, starting with the first, and the probabilities for each node are calculated according to the conditional probability tables. In the presence of evidence, more complex calculations are used, which include the use of the node's Markov blanket. Iterative processes enable the updating of probability values and ensure the accuracy of the results.

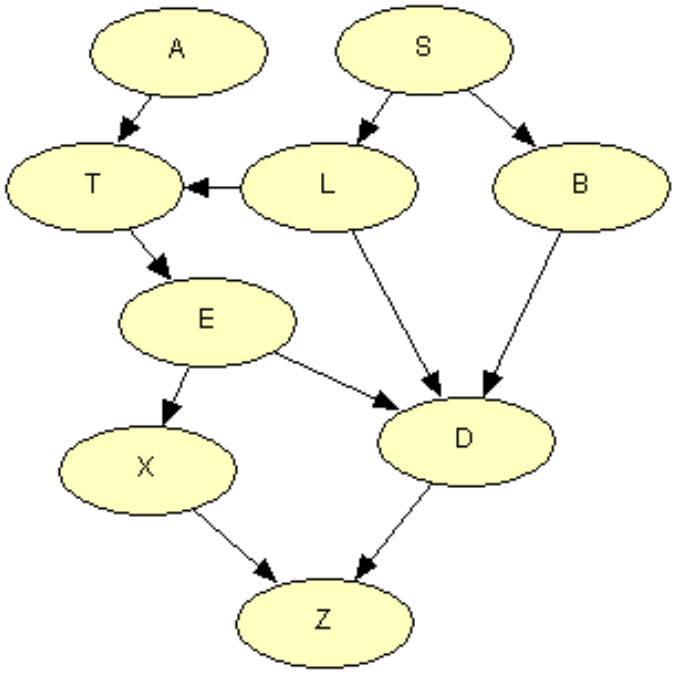

Figure 1.
BN with complex topology**.**

In this work, an example of a Bayesian network with complex topology was considered, including nine variables and several undirected cycles, such as TEDL. For this network, standard propagation methods are ineffective, necessitating the use of more complex approaches. Several experiments were conducted to demonstrate the proposed iterative method for calculating probabilities in the nodes of the Bayesian network. The vertex u is called the parent of the vertex v if the edge $(u, v) \in E$. The set of all parent vertices of v is denoted by parents (X_v). To compute the probability, the chain rule for Bayesian networks is used (6):

$$P\ (X_1, X_2, X_3, \dots, X_n) = \prod_{i=1}^{n} P(X_i | parents\ (X_v)) \quad (6)$$

Taking into account the topology of the Bayesian network example, the probability distribution will be (7):

$$P(A,S,T,L,B,E,X,D,Z) = p(A) * p(s) * p(L|S) * p(B|S) * p(TA,L) * p(E|T) * p(X|E) * p(D|E,B,L) * p(Z|X,D) \quad (7)$$

Taking into account the topology of the example Bayesian network, the probability distribution will be given by (8):

$$p(L = tr) = \sum_{A,S,T,L,E,X,D,Z} \frac{p(A)p(S)p(L = tr|S)p(B|S)p(T|A, L = tr)}{p(E|T)p(X|E)p(D|E,B,L) = tr)p(Z|X,D)} \quad (8)$$

The provided formula is too complex for practical use; therefore, simplifying calculations in Bayesian networks is an important task. The most natural approach is to determine which nodes influence the probability calculations for the current node. In some cases, a small loss in accuracy is acceptable, which can be compensated by an approximate solution using iterations that converge to the true result. A key concept is D-separation: two sets of variables, X and Y, are considered d-

separated by a set Z if any path between vertices from X and Y passes through at least one vertex from Z. This allows selecting the minimal set of nodes for calculations. Another important concept is the Markov blanket, which includes the parents, children, and other parents of the children of the vertex. If the calculations remain complex, instead of the Markov blanket, one can use only the neighbors of the node under study, which will provide approximate but still useful results. The theory of Markov chains, despite having similar problems, also shows good results. Let's begin with the fact that two pieces of evidence were provided in the Bayesian network. B=true and X=false. This allowed us to define the initial conditions for further calculations. Conditional probability tables were assigned for each variable in the network. Let's consider the order of variable calculations for this network. The network contains the following conditional probability tables. When the evidence was taken into account, the network was divided into several groups for computational convenience. The first group consisted of variables directly connected to the variables B and X, which had received evidence. This group included the variables S, D, E, and Z. The second group included the variables L and T, which were neighbors of the variables from the first group. The third group contained a single variable A, which was connected to the variables from the second group. Several iterations of calculations were performed for each group, and the process continued until the difference between successive iterations became smaller than the predefined threshold of 0.01. The convergence formula had the following form (9):

$$\alpha = \sqrt{\sum_k (a_k^j - a_k^{j+1})^2 + \sum_n (s_n^j - s_n^{j+1})^2} < \varepsilon \quad (9)$$

where a_k^j and s_n^j - Values of marginal variables at iteration j and $j+1$, ε - accuracy criterion. An example of calculating the probability for the variable S involves using the Markov blanket of the variable S, which consists of the variables L and B. The joint distribution for these variables was presented as (10):

$$P(S, L, B) = P(S) * P(L|S) * P(B|S) \quad (10)$$

The evidence B=true allowed for the adjustment of the posterior probability of the variable S, and the calculation of its probability was as follows (11):

$$P(S = true|B = True) = \frac{\sum_L P(S=true) * P(L|S = true) * P(B=true|S=true)}{P(B=true)} \quad (11)$$

Similarly, the probabilities for the remaining variables, such as D, E, and Z, were calculated using the Markov blanket of each variable. For example, the Markov blanket for the variable D included the variables L, B, E, Z, and X, which allowed for considering all connections and correctly propagating the influence of evidence throughout the network (12).

$$P(D, L, B, E, Z, X) = p(B) * p(L) * p(E) * p(D|L, B, E) * p(Z|D, X) * p(X|E) \quad (12)$$

The results showed that the proposed iterative calculation method effectively solves the problem of computing probabilities in networks with complex topology. The variables that received evidence had a significant impact on the network, and their effect was accounted for through several iterations. The subset of $variables$ (D, L, B, E, Z, X) contains the variables B and X, which received evidence. The calculation for the variable will be as follows (13):

$$\mathrm{P(D = tr|B = tr, X = fa)} = \frac{\sum_{L,E,Z} \mathrm{p(B=tr)p(L)p(E)p(D=tr|L,B=tr,E)p(Z|D,X=}fa\mathrm{)}}{P(B=tr)P(X=fa)} \quad (13)$$

We take $p(B = tr)$ and $p(X = fa)$ from the initial iteration. Everything else is known. The calculations are straightforward. Similarly, we will calculate (14):

$$\mathrm{P(D = fa|B = tr, X = fa)} = \frac{\sum_{L,E,Z} \mathrm{p(B=tr)p(L)p(E)p(D=fa|L,B=tr,E)p(Z|D,X=fa)}}{P(B=tr)P(X=fa)} \quad (14)$$

We perform normalization of the variable D. To calculate the variable E, we use the Markov blanket of this variable (T, X, D, L, B). Based on the structure of the Markov blanket, the joint probability distribution will take the following form (15):

$$P(E, T, X, D, L, B) = p(T) * p(L) * p(B) * p(E|T) * p(X|E) * p(D|E, L, B \quad (15)$$

The subset of variables (T, X, D, L, B) contains the variables B and X, which received evidence. The calculation for the variable will be as follows (16):

$$\mathrm{P(E = tr|B = tr, X = fa)} = \frac{\sum_{L,T,D} \mathrm{p(T)p(L)p(B=tr)p(E=tr|T)p(X=}fa\mathrm{|}E\mathrm{=}tr\mathrm{)p(D|E=}tr\mathrm{,L,B=}tr\mathrm{)}}{P(B=tr)P(X=fa)} \quad (16)$$

We take $p(B = tr)$ and $p(X = fa)$ from the initial iteration. Everything else is known. The calculations are straightforward. Similarly, we will calculate (17):

$$\mathrm{P(E = fa|B = tr, X = fa)} = \frac{\sum_{L,T,D} \mathrm{p(T)p(L)p(B=tr)p(E=tr|T)p(X=}fa\mathrm{|}E\mathrm{=}fa\mathrm{)p(D|E=}fa\mathrm{,L,B=}tr\mathrm{)}}{P(B=tr)P(X=fa)} \quad (17)$$

We perform normalization of the variable E. To calculate the variable Z, we use the Markov blanket of this variable (X, D). Based on the structure of the Markov blanket, the joint probability distribution will take the following form (18):

$$P(X, D, Z) = p(X) * p(D) * p(Z|X, D) \quad (18)$$

The subset of variables (X, D, Z) contains the variable X, which received evidence. The calculation for the variable will be as follows (19):

$$\mathrm{P(Z = tr|X = fa)} = \frac{\sum_D \mathrm{p(X=fa)p(D)p(Z=tr|X=fa,D)}}{P(X=fa)} \quad (19)$$

We take p(X=fa) from the initial iteration. Everything else is known. The calculations are straightforward. Similarly, we will calculate (20):

$$\mathrm{P(Z = fa|X = fa)} = \frac{\sum_D \mathrm{p(X=fa)p(D)p(Z=fa|X=fa,D)}}{P(X=fa)} \quad (20)$$

The variables of the first group have been calculated. Now, we will similarly calculate the variables of the second group – L and T. To calculate the variable L, we use the Markov blanket of this variable (S, T, D, A, E, B). Based on the structure of the Markov blanket, the joint probability distribution will take the following form (21):

$$P(L,S,T,D,A,E,B) = p(A) * p(S) * p(B) * p(E) * p(L|S) * p(T|A,L) * p(D|E,L,B) \quad (21)$$

The subset of variables (L, S, T, D, A, E, B) contains the variable B, which received evidence. The calculation for the variable L will be as follows (22):

$$\mathrm{P(L = tr|B = tr)} = \frac{\sum_{\mathrm{S,T,D,A,E}} \mathrm{p(A)p(S)p(B=tr)p(E)p(L = tr|S)p(T|A,L=tr)\ p(D|E,L=tr,B=tr)}}{P(B=tr)} \quad (22)$$

We take p(B=tr) from the initial iteration. Everything else is known. The calculations are straightforward. Similarly, we will calculate (23):

$$\mathrm{P(L = fa|B = tr)} = \frac{\sum_{\mathrm{S,T,D,A,E}} \mathrm{p(A)p(S)p(B=tr)p(E)p(L = fa|S)p(T|A,L=fa)\ p(D|E,L=fa,B=tr)}}{P(B=tr)} \quad (23)$$

We perform normalization of the variable L. To calculate the variable T, we use the Markov blanket of this variable (A, L, E). Based on the structure of the Markov blanket, the joint probability distribution will take the following form (24):

$$P(T,A,L,E) = p(A) * p(L) * p(T|A,L) * (\ \ |\ \ )\mathrm{Pet} \quad (24)$$

The calculation for the variable will be as follows (25):

$$\mathrm{P(T = tr)} = \sum_{\mathrm{A,L,E}} \mathrm{p(A)p(L)p(T = tr|A,L)}p(E|T = tr) \quad (25)$$

Similarly, we will calculate (26):

$$\mathrm{P(T = fa)} = \sum_{\mathrm{A,L,E}} \mathrm{p(A)p(L)p(T = tr|A,L)}p(E|T = tr) \quad (26)$$

We perform normalization of the variable T. The third group includes a single variable A. The Markov blanket for A consists of the variables T and L. Based on the structure of the Markov blanket, the joint probability distribution will take the following form (27):

$$P(A,T,L) = p(A) * p(L) * p(T|A,L) \quad (27)$$

The calculation for the variable A will be as follows (28):

$$\mathrm{P(A = tr)} = \sum_{\mathrm{T,L}} \mathrm{p(A = tr)p(L)p(T|A = tr,L)} \quad (28)$$

Similarly, we will calculate (29):

$$\mathrm{P(A = fa)} = \sum_{\mathrm{T,L}} \mathrm{p(A = fa)p(L)p(T|A = fa,L)} \quad (29)$$

The calculation of the variables was carried out in the direction of the variables that received evidence from the other variables in the network. This constitutes the first approximation of the calculated variables. Marginal variables that were not influenced by evidence changed their initial values. All variables in the network are interconnected using conditional probability tables (CPTs). After this, the variables were updated through a regular calculation, starting with the marginal variables, without considering the evidence. This marked the completion of another iteration. Afterward, the termination criterion for the calculations was checked. If an additional iteration was required, the calculations were repeated according to the scheme described above. At the end of each iteration, variable normalization was performed to stabilize the probability values. The proposed method demonstrated high accuracy and flexibility when working with complex network structures. The iterative approach allowed all connections between the variables to be taken into account and ensured convergence of the calculations in a relatively small number of iterations. The further development of the proposed propagation algorithms can proceed in several directions. One such direction is the development of new mechanisms for determining the neighbors of the calculated vertices, for example, second-level neighbors, which will allow for the consideration of more connections between variables and improve the accuracy of the calculations. It is also necessary to develop new termination criteria for the calculations to achieve convergence more quickly. A key direction is the optimization of methods for storing Bayesian networks on external storage devices, which will enable more efficient processing of large networks. Thus, the proposed methods and algorithms provide significant simplification and acceleration of calculations in Bayesian networks, making them more suitable for use in real-world applications.

4.1. Limitations and Future Research

Despite its advantages, the proposed iterative propagation algorithm has certain limitations. First, the convergence rate can be sensitive to the initial configuration of node states and evidence distribution, especially in very dense or highly interconnected networks. Second, while modular decomposition improves scalability, it may introduce overhead in dynamically changing networks where partitions need frequent re-evaluation. Furthermore, the method assumes complete knowledge of the network structure, which may not always be available in practical settings.

Future research should explore adaptive initialization techniques and parallelization strategies to further accelerate convergence. In addition, integrating structure learning into the inference process may enhance applicability in domains where the network topology is partially known or must be inferred from data. Extending the method to support dynamic Bayesian networks (DBNs) and real-time updating in streaming environments represents another promising direction for application in healthcare monitoring, cybersecurity, and intelligent control systems.

5. Conclusion

This work considers propagation methods in Bayesian networks, taking into account their complex topology. The study shows that the use of standard propagation methods, such as J. Pearl's method, becomes difficult in networks with a multi-connected structure, requiring the application of more complex algorithms. We propose approaches based on the use of Markov model properties, such as the Markov blanket and d-separation, which help minimize computational costs and improve the propagation of evidence in complex networks. The algorithms presented in this study provide efficient

propagation that considers the influence of all evidence while minimizing the computational load and ensuring convergence through an iterative process.

The application of the proposed methods demonstrates high accuracy and flexibility in solving tasks related to large and complex Bayesian networks, as evidenced by examples of networks with multiple pieces of evidence. Iterative approaches have proven effective in the presence of complex dependencies between variables. The further development of this research involves improving methods for optimizing the storage of Bayesian networks on external media, developing new criteria for terminating iterative processes, and expanding the use of second-level neighboring nodes to improve the accuracy of calculations. Thus, the proposed methods can find wide application in areas such as decision support systems, medical diagnostics, and data processing, where the use of Bayesian networks with multi-connected graphs is a relevant challenge.

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