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Finding Consensus Bayesian Network Structures

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Abstract

Suppose that multiple experts (or learning algorithms) provide us with alternative Bayesian network (BN) structures over a domain, and that we are interested in combining them into a single consensus BN structure. Specifically, we are interested in that the consensus BN structure only represents independences all the given BN structures agree upon and that it has as few parameters associated as possible. In this paper, we prove that there may exist several non-equivalent consensus BN structures and that finding one of them is NP-hard. Thus, we decide to resort to heuristics to find an approximated consensus BN structure. In this paper, we consider the heuristic proposed by Matzkevich and Abramson, which builds upon two algorithms, called Methods A and B, for efficiently deriving the minimal directed independence map of a BN structure relative to a given node ordering. Methods A and B are claimed to be correct although no proof is provided (a proof is just sketched). In this paper, we show that Methods A and B are not correct and propose a correction of them.

1. Introduction

Bayesian networks (BNs) are a popular graphical formalism for representing probability distributions. A BN consists of structure and parameters. The structure, a directed and acyclic graph (DAG), induces a set of independencies that the represented probability distribution satisfies. The parameters specify the conditional probability distribution of each node given its parents in the structure. The BN represents the probability distribution that results from the product of these conditional probability distributions. Typically, a single expert (or learning algorithm) is consulted to construct a BN of the domain at hand. Therefore, there is a risk that the so-constructed BN is not as accurate as it could be if, for instance, the expert has a bias or overlooks certain details. One way to minimize this risk consists in obtaining multiple BNs of the domain from multiple experts and, then, combining them into a single consensus BN. This approach has received significant attention in the literature (Matzkevich & Abramson, 1992, 1993b; Maynard-Reid II & Chajewska, 2001; Nielsen & Parsons, 2007; Pennock & Wellman, 1999; Richardson & Domingos, 2003; del Sagrado & Moral, 2003). The most relevant of these references is probably the work of Pennock and Wellman (1999), because it shows that even if the experts agree on the BN structure, no method for combining the experts' BNs produces a consensus BN that respects some reasonable assumptions and whose structure is the agreed BN structure. Unfortunately, this problem is often overlooked. To avoid it, we propose to combine the experts' BNs in two steps. First, finding the consensus BN structure and, then, finding the consensus parameters for the consensus BN structure. This paper focuses only on the first step (we briefly discuss the second step in Section 8). Specifically, we assume that multiple experts provide us with alternative DAG models of a domain, and we are interested in combining them into a single consensus DAG. Specifically, we are interested in that the consensus DAG only represents independences all the given DAGs agree upon and as many of them as possible. In other words, the consensus DAG is the DAG that represents the most independences among all the minimal directed independence (MDI) maps of the intersection of the independence models induced by the given DAGs.[1] To our knowledge, whether the consensus DAG can or cannot be found efficiently is still an open problem. See the work of Matzkevich and Abramson (1992, 1993b) for more information. In this paper, we redefine the consensus DAG as the DAG that has the fewest parameters associated among all the MDI maps of the intersection of the independence models induced by the given DAGs. This definition is in line with that of finding a DAG to represent a probability distribution p. The desired DAG is typically defined as the MDI map of p that has the fewest parameters associated rather than as the MDI map of p that represents the most independences. See, for instance, the work of Chickering et al. (2004). The number of parameters associated with a DAG is a measure of the complexity of the DAG, since it is the number of parameters required to specify all the probability distributions that can be represented by the DAG.

In this paper, we prove that there may exist several non-equivalent consensus DAGs and that finding one of them is NP-hard. Thus, we decide to resort to heuristics to find an approximated consensus DAG. In this paper, we consider the following heuristic due to Matzkevich and Abramson (1992, 1993b). See also the work of Matzkevich and Abramson (1993a) for related information. First, let α denote any ordering of the nodes in the given DAGs, which we denote here as $G^1, \dots, G^m$. Then, find the MDI map G^i_α of each G^i relative to α. Finally, let the approximated consensus DAG be the DAG whose arcs are exactly the union of the arcs in $G^1_\alpha, \dots, G^m_\alpha$. It should be mentioned that our formulation of the heuristic differs from that by Matzkevich and Abramson (1992, 1993b) in the following two points. First, the heuristic was introduced under the original definition of consensus DAG. We justify later that the heuristic also makes sense under our definition of consensus DAG. Second, α was originally required to be consistent with one of the given DAGs. We remove this requirement. All in all, a key step in the heuristic is finding the MDI map G^i_α of each G^i. Since this task is not trivial, Matzkevich and Abramson (1993b) present two algorithms, called Methods A and B, for efficiently deriving G^i_α from G^i. Methods A and B are claimed to be correct although no proof is provided (a proof is just sketched). In this paper, we show that Methods A and B are not correct and propose a correction of them.

As said, we are not the first to study the problem of finding the consensus DAG. In addition to the works discussed above by Matzkevich and Abramson (1992, 1993b) and Pennock and Wellman (1999), some other works devoted to this problem are those by Maynard-Reid II and Chajewska (2001); Nielsen and Parsons (2007); Richardson and Domingos (2003);

[1] It is worth mentioning that the term consensus DAG has a different meaning in computational biology (Jackson et al., 2005). There, the consensus DAG of a given set of DAGs $G^1, \dots, G^m$ is defined as the DAG that contains the most of the arcs in $G^1, \dots, G^m$. Therefore, the difficulty lies in keeping as many arcs as possible without creating cycles. Note that, unlike in the present work, a DAG is not interpreted as inducing an independence model by Jackson et al.

del Sagrado and Moral (2003). We elaborate below on the differences between these works and ours. Maynard-Reid II and Chajewska (2001) propose to adapt existing score-based algorithms for learning DAGs from data to the case where the learning data is replaced by the BNs provided by some experts. Their approach suffers the problem pointed out by Pennock and Wellman (1999), because it consists essentially in learning a consensus DAG from a combination of the given BNs. A somehow related approach is proposed by Richardson and Domingos (2003). Specifically, they propose a Bayesian approach to learning DAGs from data, where the prior probability distribution over DAGs is constructed from the DAGs provided by some experts. Since their approach requires data and does not combine the given DAGs into a single DAG, it addresses a problem rather different from the one in this paper. Moreover, the construction of the prior probability distribution over DAGs ignores the fact that some given DAGs may be different but equivalent. That is, unlike in the present work, a DAG is not interpreted as inducing an independence model. A work that is relatively close to ours is that by del Sagrado and Moral (2003). Specifically, they show how to construct a MDI map of the intersection and union of the independence models induced by the DAGs provided by some experts. However, there are three main differences between their work and ours. First, unlike us, they do not assume that the given DAGs are defined over the same set of nodes. Second, unlike us, they assume that there exists a node ordering that is consistent with all the given DAGs. Third, their goal is to find a MDI map whereas ours is to find the MDI map that has the fewest parameters associated among all the MDI maps, i.e. the consensus DAG. Finally, Nielsen and Parsons (2007) develop a general framework to construct the consensus DAG gradually. Their framework is general in the sense that it is not tailored to any particular definition of consensus DAG. Instead, it relies upon a score to be defined by the user and that each expert will use to score different extensions to the current partial consensus DAG. The individual scores are then combined to choose the extension to perform. Unfortunately, we do not see how this framework could be applied to our definition of consensus DAG.

It is worth recalling that this paper deals with the combination of probability distributions expressed as BNs. Those readers interested in the combination of probability distributions expressed in non-graphical numerical forms are referred to, for instance, the work of Genest and Zidek (1986). Note also that we are interested in the combination before any data is observed. Those readers interested in the combination after some data has been observed and each expert has updated her beliefs accordingly are referred to, for instance, the work of Ng and Abramson (1994). Finally, note also that we aim at combining the given DAGs into a DAG, the consensus DAG. Those readers interested in finding not a DAG but graphical features (e.g. arcs or paths) all or a significant number of experts agree upon may want to consult the works of Friedman and Koller (2003); Hartemink et al. (2002); Peña et al. (2004), since these works deal with a similar problem.

The rest of the paper is organized as follows. We start by reviewing some preliminary concepts in Section 2. We analyze the complexity of finding the consensus DAG in Section 3. We discuss the heuristic for finding an approximated consensus DAG in more detail in Section 4. We introduce Methods A and B in Section 5 and show that they are not correct. We correct them in Section 6. We analyze the complexity of the corrected Methods A and B in Section 7 and show that they are more efficient than any other approach we can think of to solve the same problem. We close with some discussion in Section 8.

2. Preliminaries

In this section, we review some concepts used in this paper. All the DAGs, probability distributions and independence models in this paper are defined over $\mathbf{V}$, unless otherwise stated. If $A \to B$ is in a DAG G, then we say that A and B are *adjacent* in G. Moreover, we say that A is a *parent* of B and B a *child* of A in G. We denote the parents of B in G by $Pa_G(B)$. A node is called a *sink node* in G if it has no children in G. A *route* between two nodes A and B in G is a sequence of nodes starting with A and ending with B such that every two consecutive nodes in the sequence are adjacent in G. Note that the nodes in a route are not necessarily distinct. The *length* of a route is the number of (not necessarily distinct) arcs in the route. We treat all the nodes in G as routes of length zero. A route between A and B is called *descending* from A to B if all the arcs in the route are directed towards B. If there is a descending route from A to B, then B is called a *descendant* of A. Note that A is a descendant of itself, since we allow routes of length zero. Given a subset $\mathbf{X} \subseteq \mathbf{V}$, a node $A \in \mathbf{X}$ is called *maximal* in G if A is not descendant of any node in $\mathbf{X} \setminus \{A\}$ in G. Given a route ρ between A and B in G and a route ρ' between B and C in G, $\rho \cup \rho'$ denotes the route between A and C in G resulting from appending ρ' to ρ.

The *number of parameters* associated with a DAG G is $\sum_{B \in \mathbf{V}} [\prod_{A \in Pa_G(B)} r_A](r_B - 1)$, where r_A and r_B are the numbers of states of the random variables corresponding to the node A and B. An arc $A \to B$ in G is said to be *covered* if $Pa_G(A) = Pa_G(B) \setminus \{A\}$. By *covering* an arc $A \to B$ in G we mean adding to G the smallest set of arcs so that $A \to B$ becomes covered. We say that a node C is a *collider* in a route in a DAG if there exist two nodes A and B such that $A \to C \leftarrow B$ is a subroute of the route. Note that A and B may coincide. Let $\mathbf{X}$, $\mathbf{Y}$ and $\mathbf{Z}$ denote three disjoint subsets of $\mathbf{V}$. A route in a DAG is said to be $\mathbf{Z}$-*active* when (i) every collider node in the route is in $\mathbf{Z}$, and (ii) every non-collider node in the route is outside $\mathbf{Z}$. When there is no route in a DAG G between a node in $\mathbf{X}$ and a node in $\mathbf{Y}$ that is $\mathbf{Z}$-active, we say that $\mathbf{X}$ is *separated* from $\mathbf{Y}$ given $\mathbf{Z}$ in G and denote it as $\mathbf{X} \perp_G \mathbf{Y} | \mathbf{Z}$. We denote by $\mathbf{X} \not\perp_G \mathbf{Y} | \mathbf{Z}$ that $\mathbf{X} \perp_G \mathbf{Y} | \mathbf{Z}$ does not hold. This definition of separation is equivalent to other more common definitions (Studený, 1998, Section 5.1).

Let $\mathbf{X}$, $\mathbf{Y}$, $\mathbf{Z}$ and $\mathbf{W}$ denote four disjoint subsets of $\mathbf{V}$. Let us abbreviate $\mathbf{X} \cup \mathbf{Y}$ as $\mathbf{XY}$. An *independence model* M is a set of statements of the form $\mathbf{X} \perp_M \mathbf{Y} | \mathbf{Z}$, meaning that $\mathbf{X}$ is independent of $\mathbf{Y}$ given $\mathbf{Z}$. Given a subset $\mathbf{U} \subseteq \mathbf{V}$, we denote by $[M]_{\mathbf{U}}$ all the statements in M such that $\mathbf{X}, \mathbf{Y}, \mathbf{Z} \subseteq \mathbf{U}$. Given two independence models M and N, we denote by $M \subseteq N$ that if $\mathbf{X} \perp_M \mathbf{Y} | \mathbf{Z}$ then $\mathbf{X} \perp_N \mathbf{Y} | \mathbf{Z}$. We say that M is a *graphoid* if it satisfies the following properties: *symmetry* $\mathbf{X} \perp_M \mathbf{Y} | \mathbf{Z} \Rightarrow \mathbf{Y} \perp_M \mathbf{X} | \mathbf{Z}$, *decomposition* $\mathbf{X} \perp_M \mathbf{YW} | \mathbf{Z} \Rightarrow \mathbf{X} \perp_M \mathbf{Y} | \mathbf{Z}$, *weak union* $\mathbf{X} \perp_M \mathbf{YW} | \mathbf{Z} \Rightarrow \mathbf{X} \perp_M \mathbf{Y} | \mathbf{ZW}$, *contraction* $\mathbf{X} \perp_M \mathbf{Y} | \mathbf{ZW} \land \mathbf{X} \perp_M \mathbf{W} | \mathbf{Z} \Rightarrow \mathbf{X} \perp_M \mathbf{YW} | \mathbf{Z}$, and *intersection* $\mathbf{X} \perp_M \mathbf{Y} | \mathbf{ZW} \land \mathbf{X} \perp_M \mathbf{W} | \mathbf{ZY} \Rightarrow \mathbf{X} \perp_M \mathbf{YW} | \mathbf{Z}$. The independence model *induced by a probability distribution* p, denoted as $I(p)$, is the set of probabilistic independences in p. The independence model *induced by a DAG* G, denoted as $I(G)$, is the set of separation statements $\mathbf{X} \perp_G \mathbf{Y} | \mathbf{Z}$. It is known that $I(G)$ is a graphoid (Studený & Bouckaert, 1998, Lemma 3.1). Moreover, $I(G)$ satisfies the *composition* property $\mathbf{X} \perp_G \mathbf{Y} | \mathbf{Z} \land \mathbf{X} \perp_G \mathbf{W} | \mathbf{Z} \Rightarrow \mathbf{X} \perp_G \mathbf{YW} | \mathbf{Z}$ (Chickering & Meek, 2002, Proposition 1). Two DAGs G and H are called *equivalent* if $I(G) = I(H)$.

A DAG G is a *directed independence map* of an independence model M if $I(G) \subseteq M$. Moreover, G is a *minimal* directed independence (MDI) map of M if removing any arc from G makes it cease to be a directed independence map of M. We say that G and an ordering of its nodes are *consistent* when, for every arc $A \rightarrow B$ in G, A precedes B in the node ordering. We say that a DAG G_α is a MDI map of an independence model M *relative to a node ordering* α if G_α is a MDI map of M and G_α is consistent with α. If M is a graphoid, then G_α is unique (Pearl, 1988, Thms. 4 and 9). Specifically, for each node A, $Pa_{G_\alpha}(A)$ is the smallest subset $\mathbf{X}$ of the predecessors of A in α, $Pre_\alpha(A)$, such that $A \perp_M Pre_\alpha(A) \setminus \mathbf{X} | \mathbf{X}$.

3. Finding a Consensus DAG is NP-Hard

Recall that we have defined the consensus DAG of a given set of DAGs $G^1, \ldots, G^m$ as the DAG that has the fewest parameters associated among all the MDI maps of $\cap_{i=1}^m I(G^i)$. A sensible way to start the quest for the consensus DAG is by investigating whether there can exist several non-equivalent consensus DAGs. The following theorem answers this question.

Theorem 1. *There exists a set of DAGs that has two non-equivalent consensus DAGs.*

Proof. Consider the following two DAGs over four random variables with the same number of states each:

$$\begin{array}{ccc} I & \leftarrow & J \\ \downarrow & & \\ K & \rightarrow & L \end{array} \qquad\qquad \begin{array}{ccc} I & \rightarrow & J \\ & & \downarrow \\ K & \leftarrow & L \end{array}$$

Any of the following two non-equivalent DAGs is the consensus DAG of the two DAGs above:

$$\begin{array}{ccc} I & \rightarrow & J \\ \downarrow & \searrow & \uparrow \\ K & \leftarrow & L \end{array} \qquad\qquad \begin{array}{ccc} I & \leftarrow & J \\ \uparrow & \nearrow & \downarrow \\ K & \rightarrow & L \end{array}$$

□

A natural follow-up question to investigate is whether a consensus DAG can be found efficiently. Unfortunately, finding a consensus DAG is NP-hard, as we prove below. Specifically, we prove that the following decision problem is NP-hard:

CONSENSUS

- INSTANCE: A set of DAGs $G^1, \ldots, G^m$ over $\mathbf{V}$, and a positive integer d.
- QUESTION: Does there exist a DAG G over $\mathbf{V}$ such that $I(G) \subseteq \cap_{i=1}^m I(G^i)$ and the number of parameters associated with G is not greater than d ?

Proving that CONSENSUS is NP-hard implies that finding the consensus DAG is also NP-hard, because if there existed an efficient algorithm for finding the consensus DAG, then we could use it to solve CONSENSUS efficiently. Our proof makes use of the following two decision problems:

FEEDBACK ARC SET

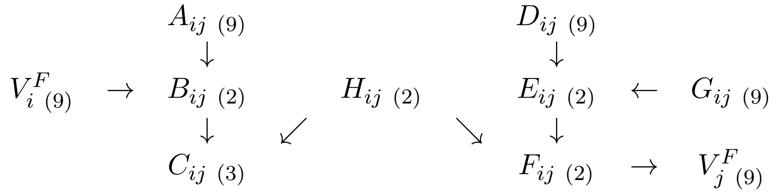
- INSTANCE: A directed graph $G = (\mathbf{V}, \mathbf{A})$ and a positive integer k.
- QUESTION: Does there exist a subset $\mathbf{B} \subset \mathbf{A}$ such that $|\mathbf{B}| \leq k$ and $\mathbf{B}$ has at least one arc from every directed cycle in G ?

LEARN

- INSTANCE: A probability distribution p over $\mathbf{V}$, and a positive integer d.
- QUESTION: Does there exist a DAG G over $\mathbf{V}$ such that $I(G) \subseteq I(p)$ and the number of parameters associated with G is not greater than d ?

FEEDBACK ARC SET is NP-complete (Garey & Johnson, 1979). FEEDBACK ARC SET remains NP-complete for directed graphs in which the total degree of each vertex is at most three (Gavril, 1977). This degree-bounded FEEDBACK ARC SET problem is used by Chickering et al. (2004) to prove that LEARN is NP-hard. In their proof, Chickering et al. (2004) use the following polynomial reduction of any instance of the degree-bounded FEEDBACK ARC SET into an instance of LEARN:

- Let the instance of the degree-bounded FEEDBACK ARC SET consist of the directed graph $F = (\mathbf{V}^F, \mathbf{A}^F)$ and the positive integer k.
- Let L denote a DAG whose nodes and arcs are determined from F as follows. For every arc $V_i^F \to V_j^F$ in $\mathbf{A}^F$, create the following nodes and arcs in L:



  The number in parenthesis besides each node is the number of states of the corresponding random variable. Let $\mathbf{H}^L$ denote all the nodes H_{ij} in L, and let $\mathbf{V}^L$ denote the rest of the nodes in L.

- Specify a (join) probability distribution $p(\mathbf{H}^L, \mathbf{V}^L)$ such that $I(p(\mathbf{H}^L, \mathbf{V}^L)) = I(L)$.
- Let the instance of LEARN consist of the (marginal) probability distribution $p(\mathbf{V}^L)$ and the positive integer d, where d is computed from F and k as shown in the work of Chickering et al. (2004, Equation 2).

We now describe how the instance of LEARN resulting from the reduction above can be further reduced into an instance of CONSENSUS in polynomial time:

- Let C^1 denote the DAG over $\mathbf{V}^L$ that has all and only the arcs in L whose both endpoints are in $\mathbf{V}^L$.

- Let C^2 denote the DAG over $\mathbf{V}^L$ that only has the arcs $B_{ij} \rightarrow C_{ij} \leftarrow F_{ij}$ for all i and j.
- Let C^3 denote the DAG over $\mathbf{V}^L$ that only has the arcs $C_{ij} \rightarrow F_{ij} \leftarrow E_{ij}$ for all i and j.
- Let the instance of CONSENSUS consist of the DAGs C^1, C^2 and C^3, and the positive integer d.

Theorem 2. *CONSENSUS is NP-hard.*

Proof. We start by proving that there is a polynomial reduction of any instance $\mathcal{F}$ of the degree-bounded FEEDBACK ARC SET into an instance $\mathcal{C}$ of CONSENSUS. First, reduce $\mathcal{F}$ into an instance $\mathcal{L}$ of LEARN as shown in the work of Chickering et al. (2004) and, then, reduce $\mathcal{L}$ into $\mathcal{C}$ as shown above.

We now prove that there is a solution to $\mathcal{F}$ iff there is a solution to $\mathcal{C}$. Chickering et al. (2004, Thms. 8 and 9) prove that there is a solution to $\mathcal{F}$ iff there is a solution to $\mathcal{L}$. Therefore, it only remains to prove that there is a solution to $\mathcal{L}$ iff there is a solution to $\mathcal{C}$ (note that the parameter d of $\mathcal{L}$ and the parameter d of $\mathcal{C}$ are the same). Let L and $p(\mathbf{H}^L, \mathbf{V}^L)$ denote the DAG and the probability distribution constructed in the reduction of $\mathcal{F}$ into $\mathcal{L}$. Recall that $I(p(\mathbf{H}^L, \mathbf{V}^L)) = I(L)$. Moreover:

- Let L^1 denote the DAG over $(\mathbf{H}^L, \mathbf{V}^L)$ that has all and only the arcs in L whose both endpoints are in $\mathbf{V}^L$.
- Let L^2 denote the DAG over $(\mathbf{H}^L, \mathbf{V}^L)$ that only has the arcs $B_{ij} \rightarrow C_{ij} \leftarrow H_{ij} \rightarrow F_{ij}$ for all i and j.
- Let L^3 denote the DAG over $(\mathbf{H}^L, \mathbf{V}^L)$ that only has the arcs $C_{ij} \leftarrow H_{ij} \rightarrow F_{ij} \leftarrow E_{ij}$ for all i and j.

Note that any separation statement that holds in L also holds in L^1, L^2 and L^3. Then, $I(p(\mathbf{H}^L, \mathbf{V}^L)) = I(L) \subseteq \cap_{i=1}^3 I(L^i)$ and, thus, $I(p(\mathbf{V}^L)) \subseteq [\cap_{i=1}^3 I(L^i)]_{\mathbf{V}^L} = \cap_{i=1}^3 [I(L^i)]_{\mathbf{V}^L}$. Let C^1, C^2 and C^3 denote the DAGs constructed in the reduction of $\mathcal{L}$ into $\mathcal{C}$. Note that $[I(L^i)]_{\mathbf{V}^L} = I(C^i)$ for all i. Then, $I(p(\mathbf{V}^L)) \subseteq \cap_{i=1}^3 I(C^i)$ and, thus, if there is a solution to $\mathcal{L}$ then there is a solution to $\mathcal{C}$. We now prove the opposite. The proof is essentially the same as that in the work of Chickering et al. (2004, Thm. 9). Let us define the (V_i, V_j) edge component of a DAG G over $\mathbf{V}^L$ as the subgraph of G that has all and only the arcs in G whose both endpoints are in $\{V_i, A_{ij}, B_{ij}, C_{ij}, D_{ij}, E_{ij}, F_{ij}, G_{ij}, V_j\}$. Given a solution C to $\mathcal{C}$, we create another solution C' to $\mathcal{C}$ as follows:

- Initialize C' to C^1.
- For every (V_i, V_j) edge component of C, if there is no directed path in C from V_i to V_j, then add to C' the arcs $E_{ij} \rightarrow C_{ij} \leftarrow F_{ij}$.
- For every (V_i, V_j) edge component of C, if there is a directed path in C from V_i to V_j, then add to C' the arcs $B_{ij} \rightarrow F_{ij} \leftarrow C_{ij}$.

Note that C' is acyclic because C is acyclic. Moreover, $I(C') \subseteq \cap_{i=1}^{3} I(C^i)$ because $I(C') \subseteq I(C^i)$ for all i. In order to be able to conclude that C' is a solution to $\mathcal{C}$, it only remains to prove that the number of parameters associated with C' is not greater than d. Specifically, we prove below that C' does not have more parameters associated than C, which has less than d parameters associated because it is a solution to $\mathcal{C}$.

As seen before, $I(C') \subseteq I(C^1)$. Likewise, $I(C) \subseteq I(C^1)$ because C is a solution to $\mathcal{C}$. Thus, there exists a sequence S (resp. S') of covered arc reversals and arc additions that transforms C^1 into C (resp. C') (Chickering, 2002, Thm. 4). Note that a covered arc reversal does not modify the number of parameters associated with a DAG, whereas an arc addition increases it (Chickering, 1995, Thm. 3). Thus, S and S' monotonically increase the number of parameters associated with C^1 as they transform it. Recall that C^1 consists of a series of edge components of the form

$$\begin{tikzcd}
 & A_{ij\ (9)} \arrow[d] & D_{ij\ (9)} \arrow[d] & \\
V^F_{i\ (9)} \arrow[r] & B_{ij\ (2)} \arrow[d] & E_{ij\ (2)} \arrow[d] & G_{ij\ (9)} \arrow[l] \\
 & C_{ij\ (3)} & F_{ij\ (2)} \arrow[r] & V^F_{j\ (9)}
\end{tikzcd}$$

The number in parenthesis besides each node is the number of states of the corresponding random variable. Let us study how the sequences S and S' modify each edge component of C^1. S' simply adds the arcs $B_{ij} \to F_{ij} \leftarrow C_{ij}$ or the arcs $E_{ij} \to C_{ij} \leftarrow F_{ij}$. Note that adding the first pair of arcs results in an increase of 10 parameters, whereas adding the second pair of arcs results in an increase of 12 parameters. Unlike S', S may reverse some arc in the edge component. If that is the case, then S must cover the arc first, which implies an increase of at least 16 parameters (covering $F_{ij} \to V_j$ by adding $E_{ij} \to V_j$ implies an increase of exactly 16 parameters, whereas any other arc covering implies a larger increase). Then, S implies a larger increase in the number of parameters than S'. On the other hand, if S does not reverse any arc in the edge component, then S simply adds the arcs that are in C but not in C^1. Note that either $C_{ij} \to F_{ij}$ or $C_{ij} \leftarrow F_{ij}$ is in C, because otherwise $C_{ij} \perp_C F_{ij} | \mathbf{Z}$ for some $\mathbf{Z} \subset \mathbf{V}^L$ which contradicts the fact that C is a solution to $\mathcal{C}$ since $C_{ij} \not\perp_{C^2} F_{ij} | \mathbf{Z}$. If $C_{ij} \to F_{ij}$ is in C, then either $B_{ij} \to F_{ij}$ or $B_{ij} \leftarrow F_{ij}$ is in C because otherwise $B_{ij} \perp_C F_{ij} | \mathbf{Z}$ for some $\mathbf{Z} \subset \mathbf{V}^L$ such that $C_{ij} \in \mathbf{Z}$, which contradicts the fact that C is a solution to $\mathcal{C}$ since $B_{ij} \not\perp_{C^2} F_{ij} | \mathbf{Z}$. As $B_{ij} \leftarrow F_{ij}$ would create a cycle in C, $B_{ij} \to F_{ij}$ is in C. Therefore, S adds the arcs $B_{ij} \to F_{ij} \leftarrow C_{ij}$ and, by construction of C', S' also adds them. Thus, S implies an increase of at least as many parameters as S'. On the other hand, if $C_{ij} \leftarrow F_{ij}$ is in C, then either $C_{ij} \to E_{ij}$ or $C_{ij} \leftarrow E_{ij}$ is in C because otherwise $C_{ij} \perp_C E_{ij} | \mathbf{Z}$ for some $\mathbf{Z} \subset \mathbf{V}^L$ such that $F_{ij} \in \mathbf{Z}$, which contradicts the fact that C is a solution to $\mathcal{C}$ since $C_{ij} \not\perp_{C^3} E_{ij} | \mathbf{Z}$. As $C_{ij} \to E_{ij}$ would create a cycle in C, $C_{ij} \leftarrow E_{ij}$ is in C. Therefore, S adds the arcs $E_{ij} \to C_{ij} \leftarrow F_{ij}$ and, by construction of C', S' adds either the arcs $E_{ij} \to C_{ij} \leftarrow F_{ij}$ or the arcs $B_{ij} \to F_{ij} \leftarrow C_{ij}$. In any case, S implies an increase of at least as many parameters as S'. Consequently, C' does not have more parameters associated than C.

Finally, note that $I(p(\mathbf{V}^L)) \subseteq I(C')$ by Chickering et al. (2004, Lemma 7). Thus, if there is a solution to $\mathcal{C}$ then there is a solution to $\mathcal{L}$.

□

It is worth noting that our proof above contains two restrictions. First, the number of DAGs to consensuate is three. Second, the number of states of each random variable in $\mathbf{V}^L$ is not arbitrary but prescribed. The first restriction is easy to relax: Our proof can be extended to consensuate more than three DAGs by simply letting C^i be a DAG over $\mathbf{V}^L$ with no arcs for all $i > 3$. However, it is an open question whether CONSENSUS remains NP-hard when the number of DAGs to consensuate is two and/or the number of states of each random variable in $\mathbf{V}^L$ is arbitrary.

The following theorem strengthens the previous one.

Theorem 3. *CONSENSUS is NP-complete.*

Proof. By Theorem 2, all that remains to prove is that CONSENSUS is in NP, i.e. that we can verify in polynomial time if a given DAG G is a solution to a given instance of CONSENSUS.

Let α denote any node ordering that is consistent with G. The causal list of G relative to α is the set of separation statements $A \perp_G Pre_\alpha(A) \setminus Pa_G(A) | Pa_G(A)$ for all node A. It is known that $I(G)$ coincides with the closure with respect to the graphoid properties of the causal list of G relative to α (Pearl, 1988, Corollary 7). Therefore, $I(G) \subseteq \cap_{i=1}^m I(G^i)$ iff $A \perp_{G^i} Pre_\alpha(A) \setminus Pa_G(A) | Pa_G(A)$ for all $1 \leq i \leq m$, because $\cap_{i=1}^m I(G^i)$ is a graphoid (del Sagrado & Moral, 2003, Corollary 1). Let n, a and a_i denote, respectively, the number of nodes in G, the number of arcs in G, and the number of arcs in G^i. Let $b = \max_{1 \leq i \leq m} a_i$. Checking a separation statement in G^i takes $O(a_i)$ time (Geiger et al., 1990, p. 530). Then, checking whether $I(G) \subseteq \cap_{i=1}^m I(G^i)$ takes $O(mnb)$ time. Finally, note that computing the number of parameters associated with G takes $O(a)$.

□

4. Finding an Approximated Consensus DAG

Since finding a consensus DAG of some given DAGs is NP-hard, we decide to resort to heuristics to find an approximated consensus DAG. This does not mean that we discard the existence of fast super-polynomial algorithms. It simply means that we do not pursue that possibility in this paper. Specifically, in this paper we consider the following heuristic due to Matzkevich and Abramson (1992, 1993b). See also the work of Matzkevich and Abramson (1993a) for related information. First, let α denote any ordering of the nodes in the given DAGs, which we denote here as $G^1, \ldots, G^m$. Then, find the MDI map G^i_α of each G^i relative to α. Finally, let the approximated consensus DAG be the DAG whose arcs are exactly the union of the arcs in $G^1_\alpha, \ldots, G^m_\alpha$. The following theorem justifies taking the union of the arcs. Specifically, it proves that the DAG returned by the heuristic is the consensus DAG if this was required to be consistent with α.

Theorem 4. *The DAG H returned by the heuristic above is the DAG that has the fewest parameters associated among all the MDI maps of $\cap_{i=1}^m I(G^i)$ relative to α.*

Proof. We start by proving that H is a MDI map of $\cap_{i=1}^m I(G^i)$. First, we show that $I(H) \subseteq \cap_{i=1}^m I(G^i)$. It suffices to note that $I(H) \subseteq \cap_{i=1}^m I(G^i_\alpha)$ because each G^i_α is a subgraph of H, and that $\cap_{i=1}^m I(G^i_\alpha) \subseteq \cap_{i=1}^m I(G^i)$ because $I(G^i_\alpha) \subseteq I(G^i)$ for all i. Now, assume to the contrary that the DAG H' resulting from removing an arc $A \rightarrow B$ from H satisfies that $I(H') \subseteq \cap_{i=1}^{m} I(G^i)$. By construction of H, $A \rightarrow B$ is in G_α^i for some i, say $i = j$. Note that $B \perp_{H'} Pre_\alpha(B) \setminus Pa_{H'}(B) | Pa_{H'}(B)$, which implies $B \perp_{G^j} Pre_\alpha(B) \setminus ((\cup_{i=1}^{m} Pa_{G_\alpha^i}(B)) \setminus \{A\}) | (\cup_{i=1}^{m} Pa_{G_\alpha^i}(B)) \setminus \{A\}$ because $Pa_{H'}(B) = (\cup_{i=1}^{m} Pa_{G_\alpha^i}(B)) \setminus \{A\}$ and $I(H') \subseteq \cap_{i=1}^{m} I(G^i)$. Note also that $B \perp_{G_\alpha^j} Pre_\alpha(B) \setminus Pa_{G_\alpha^j}(B) | Pa_{G_\alpha^j}(B)$, which implies $B \perp_{G^j} Pre_\alpha(B) \setminus Pa_{G_\alpha^j}(B) | Pa_{G_\alpha^j}(B)$ because $I(G_\alpha^j) \subseteq I(G^j)$. Therefore, $B \perp_{G^j} Pre_\alpha(B) \setminus (Pa_{G_\alpha^j}(B) \setminus \{A\}) | Pa_{G_\alpha^j}(B) \setminus \{A\}$ by intersection. However, this contradicts the fact that G_α^j is the MDI map of G^j relative to α. Then, H is a MDI map of $\cap_{i=1}^{m} I(G^i)$ relative to α.

Finally, note that $\cap_{i=1}^{m} I(G^i)$ is a graphoid (del Sagrado & Moral, 2003, Corollary 1). Consequently, H is the only MDI map of $\cap_{i=1}^{m} I(G^i)$ relative to α.

□

A key step in the heuristic above is, of course, choosing a good node ordering α. Unfortunately, the fact that CONSENSUS is NP-hard implies that it is also NP-hard to find the best node ordering α, i.e. the node ordering that makes the heuristic to return the MDI map of $\cap_{i=1}^{m} I(G^i)$ that has the fewest parameters associated. To see it, note that if there existed an efficient algorithm for finding the best node ordering, then Theorem 4 would imply that we could solve CONSENSUS efficiently by running the heuristic with the best node ordering.

In the last sentence, we have implicitly assumed that the heuristic is efficient, which implies that we have implicitly assumed that we can efficiently find the MDI map G_α^i of each G^i. The rest of this paper shows that this assumption is correct.

5. Methods A and B are not Correct

Matzkevich and Abramson (1993b) do not only propose the heuristic discussed in the previous section, but they also present two algorithms, called Methods A and B, for efficiently deriving the MDI map G_α of a DAG G relative to a node ordering α. The algorithms work iteratively by covering and reversing an arc in G until the resulting DAG is consistent with α. It is obvious that such a way of working produces a directed independence map of G. However, in order to arrive at G_α, the arc to cover and reverse in each iteration must be carefully chosen. The pseudocode of Methods A and B can be seen in Figure 1. Method A starts by calling Construct β to derive a node ordering β that is consistent with G and as close to α as possible (line 6). By β being as close to α as possible, we mean that the number of arcs Methods A and B will later cover and reverse is kept at a minimum, because Methods A and B will use β to choose the arc to cover and reverse in each iteration. In particular, Method A finds the leftmost node in β that should be interchanged with its left neighbor (line 2) and it repeatedly interchanges this node with its left neighbor (lines 3-4 and 6-7). Each of these interchanges is preceded by covering and reversing the corresponding arc in G (line 5). Method B is essentially identical to Method A. The only differences between them are that the word "right" is replaced by the word "left" and vice versa in lines 2-4, and that the arcs point in opposite directions in line 5. Note that Methods A and B do not reverse an arc more than once.

```
     Construct $\beta(G, \alpha)$

     /* Given a DAG $G$ and a node ordering $\alpha$, the algorithm returns a node ordering $\beta$ that
     is consistent with $G$ and as close to $\alpha$ as possible */

  1  $\beta = \emptyset$
  2  $G' = G$
  3  Let $A$ denote a sink node in $G'$
/* 3  Let $A$ denote the rightmost node in $\alpha$ that is a sink node in $G'$ */
  4  Add $A$ as the leftmost node in $\beta$
  5  Let $B$ denote the right neighbor of $A$ in $\beta$
  6  If $B \neq \emptyset$ and $A \notin Pa_G(B)$ and $A$ is to the right of $B$ in $\alpha$ then
  7    Interchange $A$ and $B$ in $\beta$
  8    Go to line 5
  9  Remove $A$ and all its incoming arcs from $G'$
 10  If $G' \neq \emptyset$ then go to line 3
 11  Return $\beta$

     Method A$(G, \alpha)$

     /* Given a DAG $G$ and a node ordering $\alpha$, the algorithm returns $G_\alpha$ */

  1  $\beta$=Construct $\beta(G, \alpha)$
  2  Let $Y$ denote the leftmost node in $\beta$ whose left neighbor in $\beta$ is to its right in $\alpha$
  3  Let $Z$ denote the left neighbor of $Y$ in $\beta$
  4  If $Z$ is to the right of $Y$ in $\alpha$ then
  5    If $Z \rightarrow Y$ is in $G$ then cover and reverse $Z \rightarrow Y$ in $G$
  6    Interchange $Y$ and $Z$ in $\beta$
  7    Go to line 3
  8  If $\beta \neq \alpha$ then go to line 2
  9  Return $G$

     Method B$(G, \alpha)$

     /* Given a DAG $G$ and a node ordering $\alpha$, the algorithm returns $G_\alpha$ */

  1  $\beta$=Construct $\beta(G, \alpha)$
  2  Let $Y$ denote the leftmost node in $\beta$ whose right neighbor in $\beta$ is to its left in $\alpha$
  3  Let $Z$ denote the right neighbor of $Y$ in $\beta$
  4  If $Z$ is to the left of $Y$ in $\alpha$ then
  5    If $Y \rightarrow Z$ is in $G$ then cover and reverse $Y \rightarrow Z$ in $G$
  6    Interchange $Y$ and $Z$ in $\beta$
  7    Go to line 3
  8  If $\beta \neq \alpha$ then go to line 2
  9  Return $G$
```

Figure 1: Construct β, and Methods A and B. Our correction of Construct β consists in (i) replacing line 3 with the line in comments under it, and (ii) removing lines 5-8.

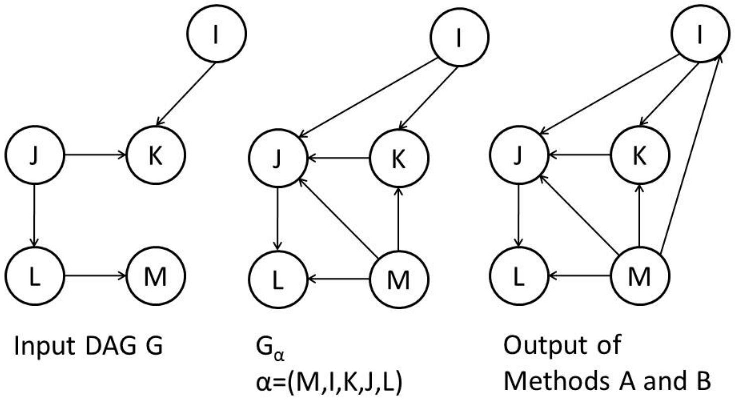


Figure 2: A counterexample to the correctness of Methods A and B.

Methods A and B are claimed to be correct in the work of Matzkevich and Abramson (1993b, Thm. 4 and Corollary 2) although no proof is provided (a proof is just sketched). The following counterexample shows that Methods A and B are actually not correct. Let G be the DAG in the left-hand side of Figure 2. Let $\alpha = (M, I, K, J, L)$. Then, we can make use of the characterization introduced in Section 2 to see that G_α is the DAG in the center of Figure 2. However, Methods A and B return the DAG in the right-hand side of Figure 2. To see it, we follow the execution of Methods A and B step by step. First, Methods A and B construct β by calling Construct β, which runs as follows:

1. Initially, $\beta = \emptyset$ and $G' = G$.

2. Select the sink node M in G'. Then, $\beta = (M)$. Remove M and its incoming arcs from G'.

3. Select the sink node L in G'. Then, $\beta = (L, M)$. No interchange in β is performed because $L \in Pa_G(M)$. Remove L and its incoming arcs from G'.

4. Select the sink node K in G'. Then, $\beta = (K, L, M)$. No interchange in β is performed because K is to the left of L in α. Remove K and its incoming arcs from G'.

5. Select the sink node J in G'. Then, $\beta = (J, K, L, M)$. No interchange in β is performed because $J \in Pa_G(K)$.

6. Select the sink node I in G'. Then, $\beta = (I, J, K, L, M)$. No interchange in β is performed because I is to the left of J in α.

When Construct β ends, Methods A and B continue as follows:

7. Initially, $\beta = (I, J, K, L, M)$.

8. Add the arc $I \to J$ and reverse the arc $J \to K$ in G. Interchange J and K in β. Then, $\beta = (I, K, J, L, M)$.

9. Add the arc $J \to M$ and reverse the arc $L \to M$ in G. Interchange L and M in β. Then, $\beta = (I, K, J, M, L)$.

10. Add the arcs $I \to M$ and $K \to M$, and reverse the arc $J \to M$ in G. Interchange J and M in β. Then, $\beta = (I, K, M, J, L)$.

11. Reverse the arc $K \to M$ in G. Interchange K and M in β. Then, $\beta = (I, M, K, J, L)$.

12. Reverse the arc $I \to M$ in G. Interchange I and M in β. Then, $\beta = (M, I, K, J, L) = \alpha$.

As a matter of fact, one can see as early as in step 8 above that Methods A and B will fail: One can see that I and M are not separated in the DAG resulting from step 8, which implies that I and M will not be separated in the DAG returned by Methods A and B, because covering and reversing arcs never introduces new separation statements. However, I and M are separated in G_α.

Note that we constructed β by selecting first M, then L, then K, then J, and finally I. However, we could have selected first K, then I, then M, then L, and finally J, which would have resulted in $\beta = (J, L, M, I, K)$. With this β, Methods A and B return G_α. Therefore, it makes a difference which sink node is selected in line 3 of Construct β. However, Construct β overlooks this detail. We propose correcting Construct β by (i) replacing line 3 by "Let A denote the rightmost node in α that is a sink node in G'", and (ii) removing lines 5-8 since they will never be executed. Hereinafter, we assume that any call to Construct β is a call to the corrected version thereof. The rest of this paper is devoted to prove that Methods A and B now do return G_α.

6. The Corrected Methods A and B are Correct

Before proving that Methods A and B are correct, we introduce some auxiliary lemmas. Their proof can be found in Appendix A. Let us call *percolating Y right-to-left in β* to iterating through lines 3-7 in Method A while possible. Let us modify Method A by replacing line 2 by "Let Y denote the leftmost node in β that has not been considered before" and by adding the check $Z \neq \emptyset$ to line 4. The pseudocode of the resulting algorithm, which we call Method A2, can be seen in Figure 3. Method A2 percolates right-to-left in β one by one all the nodes in the order in which they appear in β.

Lemma 1. *Method A(G, α) and Method A2(G, α) return the same DAG.*

Lemma 2. *Method A2(G, α) and Method B(G, α) return the same DAG.*

Let us call *percolating Y left-to-right in β* to iterating through lines 3-7 in Method B while possible. Let us modify Method B by replacing line 2 by "Let Y denote the rightmost node in α that has not been considered before" and by adding the check $Z \neq \emptyset$ to line 4. The pseudocode of the resulting algorithm, which we call Method B2, can be seen in Figure

```
Method A2($G$, $\alpha$)

/* Given a DAG $G$ and a node ordering $\alpha$, the algorithm returns $G_\alpha$ */

1  $\beta$=Construct $\beta(G, \alpha)$
2  Let $Y$ denote the leftmost node in $\beta$ that has not been considered before
3  Let $Z$ denote the left neighbor of $Y$ in $\beta$
4  If $Z \neq \emptyset$ and $Z$ is to the right of $Y$ in $\alpha$ then
5    If $Z \to Y$ is in $G$ then cover and reverse $Z \to Y$ in $G$
6    Interchange $Y$ and $Z$ in $\beta$
7    Go to line 3
8  If $\beta \neq \alpha$ then go to line 2
9  Return $G$

Method B2($G$, $\alpha$)

/* Given a DAG $G$ and a node ordering $\alpha$, the algorithm returns $G_\alpha$ */

1  $\beta$=Construct $\beta(G, \alpha)$
2  Let $Y$ denote the rightmost node in $\alpha$ that has not been considered before
3  Let $Z$ denote the right neighbor of $Y$ in $\beta$
4  If $Z \neq \emptyset$ and $Z$ is to the left of $Y$ in $\alpha$ then
5    If $Y \to Z$ is in $G$ then cover and reverse $Y \to Z$ in $G$
6    Interchange $Y$ and $Z$ in $\beta$
7    Go to line 3
8  If $\beta \neq \alpha$ then go to line 2
9  Return $G$
```

Figure 3: Methods A2 and B2.

3. Method B2 percolates left-to-right in β one by one all the nodes in the reverse order in which they appear in α.

Lemma 3. *Method B(G, α) and Method B2(G, α) return the same DAG.*

We are now ready to prove the main result of this paper.

Theorem 5. *Let G_α denote the MDI map of a DAG G relative to a node ordering α. Then, Method A(G, α) and Method B(G, α) return G_α.*

Proof. By Lemmas 1-3, it suffices to prove that Method B2(G, α) returns G_α. It is evident that Method B2 transforms β into α and, thus, that it halts at some point. Therefore, Method B2 performs a finite sequence of n modifications (arc additions and covered arc reversals) to G. Let G_i denote the DAG resulting from the first i modifications to G, and let $G_0 = G$. Specifically, Method B2 constructs G_{i+1} from G_i by either (i) reversing the covered arc $Y \to Z$, or (ii) adding the arc $X \to Z$ for some $X \in Pa_{G_i}(Y) \setminus Pa_{G_i}(Z)$, or (iii) adding the arc $X \to Y$ for some $X \in Pa_{G_i}(Z) \setminus Pa_{G_i}(Y)$. Note that $I(G_{i+1}) \subseteq I(G_i)$ for all $0 \leq i < n$ and, thus, that $I(G_n) \subseteq I(G_0)$.

We start by proving that G_i is a DAG that is consistent with β for all $0 \leq i \leq n$. Since this is true for G_0 due to line 1, it suffices to prove that if G_i is a DAG that is consistent with β then so is G_{i+1} for all $0 \leq i < n$. We consider the following four cases.

Case 1 Method B2 constructs G_{i+1} from G_i by reversing the covered arc $Y \to Z$. Then, G_{i+1} is a DAG because reversing a covered arc does not create any cycle (Chickering, 1995, Lemma 1). Moreover, note that Y and Z are interchanged in β immediately after the covered arc reversal. Thus, G_{i+1} is consistent with β.

Case 2 Method B2 constructs G_{i+1} from G_i by adding the arc $X \to Z$ for some $X \in Pa_{G_i}(Y) \setminus Pa_{G_i}(Z)$. Note that X is to the left of Y and Y to the left of Z in β, because G_i is consistent with β. Then, X is to the left of Z in β and, thus, G_{i+1} is a DAG that is consistent with β.

Case 3 Method B2 constructs G_{i+1} from G_i by adding the arc $X \to Y$ for some $X \in Pa_{G_i}(Z) \setminus Pa_{G_i}(Y)$. Note that X is to the left of Z in β because G_i is consistent with β, and Y is the left neighbor of Z in β (recall line 3). Then, X is to the left of Y in β and, thus, G_{i+1} is a DAG that is consistent with β.

Case 4 Note that β may get modified before Method B2 constructs G_{i+1} from G_i. Specifically, this happens when Method B2 executes lines 5-6 but there is no arc between Y and Z in G_i. However, the fact that G_i is consistent with β before Y and Z are interchanged in β and the fact that Y and Z are neighbors in β (recall line 3) imply that G_i is consistent with β after Y and Z have been interchanged.

Since Method B2 transforms β into α, it follows from the result proven above that G_n is a DAG that is consistent with α. In order to prove the theorem, i.e. that $G_n = G_\alpha$, all that remains to prove is that $I(G_\alpha) \subseteq I(G_n)$. To see it, note that $G_n = G_\alpha$ follows from $I(G_\alpha) \subseteq I(G_n)$, $I(G_n) \subseteq I(G_0)$, the fact that G_n is a DAG that is consistent with α, and the fact that G_α is the unique MDI map of G_0 relative to α. Recall that G_α is guaranteed to be unique because $I(G_0)$ is a graphoid.

The rest of the proof is devoted to prove that $I(G_\alpha) \subseteq I(G_n)$. Specifically, we prove that if $I(G_\alpha) \subseteq I(G_i)$ then $I(G_\alpha) \subseteq I(G_{i+1})$ for all $0 \leq i < n$. Note that this implies that $I(G_\alpha) \subseteq I(G_n)$ because $I(G_\alpha) \subseteq I(G_0)$ by definition of MDI map. First, we prove it when Method B2 constructs G_{i+1} from G_i by reversing the covered arc $Y \to Z$. That the arc reversed is covered implies that $I(G_{i+1}) = I(G_i)$ (Chickering, 1995, Lemma 1). Thus, $I(G_\alpha) \subseteq I(G_{i+1})$ because $I(G_\alpha) \subseteq I(G_i)$.

Now, we prove that if $I(G_\alpha) \subseteq I(G_i)$ then $I(G_\alpha) \subseteq I(G_{i+1})$ for all $0 \leq i < n$ when Method B2 constructs G_{i+1} from G_i by adding an arc. Specifically, we prove that if there is an $\mathbf{S}$-active route ($\mathbf{S} \subseteq \mathbf{V}$) ρ^{AB}_{i+1} between two nodes A and B in G_{i+1}, then there is an $\mathbf{S}$-active route between A and B in G_α. We prove this result by induction on the number of occurrences of the added arc in ρ^{AB}_{i+1}. We assume without loss of generality that the added arc occurs in ρ^{AB}_{i+1} as few or fewer times than in any other $\mathbf{S}$-active route between A and B in G_{i+1}. We call this the minimality property of ρ^{AB}_{i+1}.[2] If the number of occurrences of the

[2] It is not difficult to show that the number of occurrences of the added arc in ρ^{AB}_{i+1} is then at most two (see Case 2.1 for some intuition). However, the proof of the theorem is simpler if we ignore this fact.

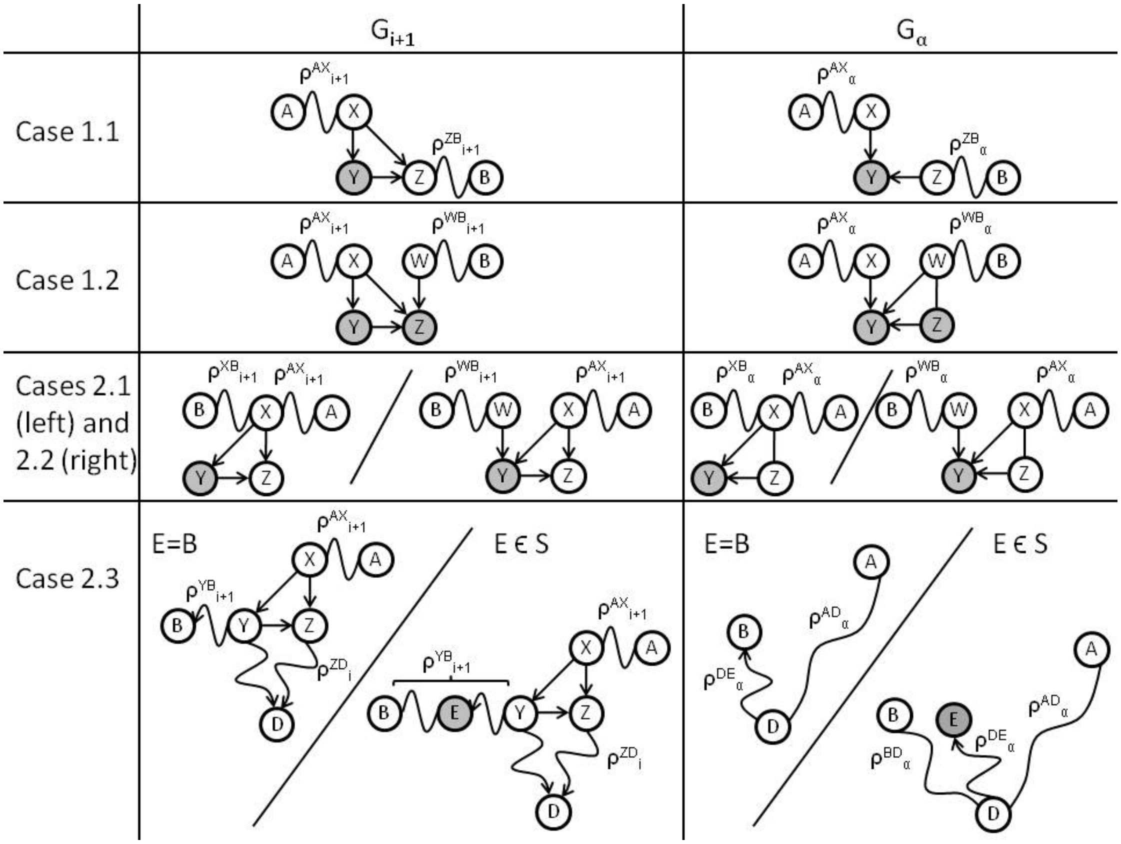


Figure 4: Different cases in the proof of Theorem 5. Only the relevant subgraphs of G_{i+1} and G_α are depicted. An undirected edge between two nodes denotes that the nodes are adjacent. A curved edge between two nodes denotes an **S**-active route between the two nodes. If the curved edge is directed, then the route is descending. A grey node denotes a node that is in **S**.

added arc in ρ^{AB}_{i+1} is zero, then ρ^{AB}_{i+1} is an **S**-active route between A and B in G_i too and, thus, there is an **S**-active route between A and B in G_α since $I(G_\alpha) \subseteq I(G_i)$. Assume as induction hypothesis that the result holds for up to k occurrences of the added arc in ρ^{AB}_{i+1}. We now prove it for $k+1$ occurrences. We consider the following two cases. Each case is illustrated in Figure 4.

Case 1 Method B2 constructs G_{i+1} from G_i by adding the arc $X \rightarrow Z$ for some $X \in Pa_{G_i}(Y) \setminus Pa_{G_i}(Z)$. Note that $X \rightarrow Z$ occurs in ρ^{AB}_{i+1}.[3] Let $\rho^{AB}_{i+1} = \rho^{AX}_{i+1} \cup X \rightarrow Z \cup \rho^{ZB}_{i+1}$. Note that $X \notin \mathbf{S}$ and ρ^{AX}_{i+1} is **S**-active in G_{i+1} because, otherwise, ρ^{AB}_{i+1} would not be

[3] Note that maybe $A = X$ and/or $B = Z$.

$\mathbf{S}$-active in G_{i+1}. Then, there is an $\mathbf{S}$-active route ρ_α^{AX} between A and X in G_α by the induction hypothesis. Moreover, $Y \in \mathbf{S}$ because, otherwise, $\rho_{i+1}^{AX} \cup X \to Y \to Z \cup \rho_{i+1}^{ZB}$ would be an $\mathbf{S}$-active route between A and B in G_{i+1} that would violate the minimality property of ρ_{i+1}^{AB}. Note that $Y \leftarrow Z$ is in G_α because (i) Y and Z are adjacent in G_α since $I(G_\alpha) \subseteq I(G_i)$, and (ii) Z is to the left of Y in α (recall line 4). Note also that $X \to Y$ is in G_α. To see it, note that X and Y are adjacent in G_α since $I(G_\alpha) \subseteq I(G_i)$. Recall that Method B2 percolates left-to-right in β one by one all the nodes in the reverse order in which they appear in α. Method B2 is currently percolating Y and, thus, the nodes to the right of Y in α are to the right of Y in β too. If $X \leftarrow Y$ were in G_α then X would be to the right of Y in α and, thus, X would be to the right of Y in β. However, this would contradict the fact that X is to the left of Y in β, which follows from the fact that G_i is consistent with β. Thus, $X \to Y$ is in G_α. We now consider two cases.

Case 1.1 Assume that $Z \notin \mathbf{S}$. Then, ρ_{i+1}^{ZB} is $\mathbf{S}$-active in G_{i+1} because, otherwise, ρ_{i+1}^{AB} would not be $\mathbf{S}$-active in G_{i+1}. Then, there is an $\mathbf{S}$-active route ρ_α^{ZB} between Z and B in G_α by the induction hypothesis. Then, $\rho_\alpha^{AX} \cup X \to Y \leftarrow Z \cup \rho_\alpha^{ZB}$ is an $\mathbf{S}$-active route between A and B in G_α.

Case 1.2 Assume that $Z \in \mathbf{S}$. Then, $\rho_{i+1}^{ZB} = Z \leftarrow W \cup \rho_{i+1}^{WB}$.[4] Note that $W \notin \mathbf{S}$ and ρ_{i+1}^{WB} is $\mathbf{S}$-active in G_{i+1} because, otherwise, ρ_{i+1}^{AB} would not be $\mathbf{S}$-active in G_{i+1}. Then, there is an $\mathbf{S}$-active route ρ_α^{WB} between W and B in G_α by the induction hypothesis. Note that W and Z are adjacent in G_α since $I(G_\alpha) \subseteq I(G_i)$. This and the fact proven above that $Y \leftarrow Z$ is in G_α imply that Y and W are adjacent in G_α because, otherwise, $Y \not\perp_{G_i} W|\mathbf{U}$ but $Y \perp_{G_\alpha} W|\mathbf{U}$ for some $\mathbf{U} \subseteq \mathbf{V}$ such that $Z \in \mathbf{U}$, which would contradict that $I(G_\alpha) \subseteq I(G_i)$. In fact, $Y \leftarrow W$ is in G_α. To see it, recall that the nodes to the right of Y in α are to the right of Y in β too. If $Y \to W$ were in G_α then W would be to the right of Y in α and, thus, W would be to the right of Y in β too. However, this would contradict the fact that W is to the left of Y in β, which follows from the fact that W is to the left of Z in β because G_i is consistent with β, and the fact that Y is the left neighbor of Z in β (recall line 3). Thus, $Y \leftarrow W$ is in G_α. Then, $\rho_\alpha^{AX} \cup X \to Y \leftarrow W \cup \rho_\alpha^{WB}$ is an $\mathbf{S}$-active route between A and B in G_α.

Case 2 Method B2 constructs G_{i+1} from G_i by adding the arc $X \to Y$ for some $X \in Pa_{G_i}(Z) \setminus Pa_{G_i}(Y)$. Note that $X \to Y$ occurs in ρ_{i+1}^{AB}.[5] Let $\rho_{i+1}^{AB} = \rho_{i+1}^{AX} \cup X \to Y \cup \rho_{i+1}^{YB}$. Note that $X \notin \mathbf{S}$ and ρ_{i+1}^{AX} is $\mathbf{S}$-active in G_{i+1} because, otherwise, ρ_{i+1}^{AB} would not be $\mathbf{S}$-active in G_{i+1}. Then, there is an $\mathbf{S}$-active route ρ_α^{AX} between A and X in G_α by the induction hypothesis. Note that $Y \leftarrow Z$ is in G_α because (i) Y and Z are adjacent in G_α since $I(G_\alpha) \subseteq I(G_i)$, and (ii) Z is to the left of Y in α (recall line 4). Note also that X and Z are adjacent in G_α since $I(G_\alpha) \subseteq I(G_i)$. This and the fact that $Y \leftarrow Z$ is in G_α imply that X and Y are adjacent in G_α because, otherwise, $X \not\perp_{G_i} Y|\mathbf{U}$ but $X \perp_{G_\alpha} Y|\mathbf{U}$ for some $\mathbf{U} \subseteq \mathbf{V}$ such that $Z \in \mathbf{U}$, which would contradict that

[4] Note that maybe $W = B$. Note also that $W \neq X$ because, otherwise, $\rho_{i+1}^{AX} \cup X \to Y \leftarrow X \cup \rho_{i+1}^{WB}$ would be an $\mathbf{S}$-active route between A and B in G_{i+1} that would violate the minimality property of ρ_{i+1}^{AB}.

[5] Note that maybe $A = X$ and/or $B = Y$.

$I(G_\alpha) \subseteq I(G_i)$. In fact, $X \rightarrow Y$ is in G_α. To see it, recall that Method B2 percolates left-to-right in β one by one all the nodes in the reverse order in which they appear in α. Method B2 is currently percolating Y and, thus, the nodes to the right of Y in α are to the right of Y in β too. If $X \leftarrow Y$ were in G_α then X would be to the right of Y in α and, thus, X would be to the right of Y in β too. However, this would contradict the fact that X is to the left of Y in β, which follows from the fact that X is to the left of Z in β because G_i is consistent with β, and the fact that Y is the left neighbor of Z in β (recall line 3). Thus, $X \rightarrow Y$ is in G_α. We now consider three cases.

Case 2.1 Assume that $Y \in \mathbf{S}$ and $\rho_{i+1}^{YB} = Y \leftarrow X \cup \rho_{i+1}^{XB}$. Note that ρ_{i+1}^{XB} is $\mathbf{S}$-active in G_{i+1} because, otherwise, ρ_{i+1}^{AB} would not be $\mathbf{S}$-active in G_{i+1}. Then, there is an $\mathbf{S}$-active route ρ_α^{XB} between X and B in G_α by the induction hypothesis. Then, $\rho_\alpha^{AX} \cup X \rightarrow Y \leftarrow X \cup \rho_\alpha^{XB}$ is an $\mathbf{S}$-active route between A and B in G_α.

Case 2.2 Assume that $Y \in \mathbf{S}$ and $\rho_{i+1}^{YB} = Y \leftarrow W \cup \rho_{i+1}^{WB}$.[6] Note that $W \notin \mathbf{S}$ and ρ_{i+1}^{WB} is $\mathbf{S}$-active in G_{i+1} because, otherwise, ρ_{i+1}^{AB} would not be $\mathbf{S}$-active in G_{i+1}. Then, there is an $\mathbf{S}$-active route ρ_α^{WB} between W and B in G_α by the induction hypothesis. Note also that $Y \leftarrow W$ is in G_α. To see it, note that Y and W are adjacent in G_α since $I(G_\alpha) \subseteq I(G_i)$. Recall that the nodes to the right of Y in α are to the right of Y in β too. If $Y \rightarrow W$ were in G_α then W would be to the right of Y in α and, thus, W would be to the right of Y in β too. However, this would contradict the fact that W is to the left of Y in β, which follows from the fact that G_i is consistent with β. Thus, $Y \leftarrow W$ is in G_α. Then, $\rho_\alpha^{AX} \cup X \rightarrow Y \leftarrow W \cup \rho_\alpha^{WB}$ is an $\mathbf{S}$-active route between A and B in G_α.

Case 2.3 Assume that $Y \notin \mathbf{S}$. The proof of this case is based on that of step 8 in the work of Chickering (2002, Lemma 30). Let D denote the node that is maximal in G_α from the set of descendants of Y in G_i. Note that D is guaranteed to be unique by Chickering (2002, Lemma 29), because $I(G_\alpha) \subseteq I(G_i)$. Note also that $D \neq Y$, because Z is a descendant of Y in G_i and, as shown above, $Y \leftarrow Z$ is in G_α. We now show that D is a descendant of Z in G_i. We consider three cases.

Case 2.3.1 Assume that $D = Z$. Then, D is a descendant of Z in G_i.

Case 2.3.2 Assume that $D \neq Z$ and D was a descendant of Z in G_0. Recall that Method B2 percolates left-to-right in β one by one all the nodes in the reverse order in which they appear in α. Method B2 is currently percolating Y and, thus, it has not yet percolated Z because Z is to the left of Y in α (recall line 4). Therefore, none of the descendants of Z in G_0 (among which is D) is to the left of Z in β. This and the fact that β is consistent with G_i imply that Z is a node that is maximal in G_i from the set of descendants of Z in G_0. Actually, Z is the only such node by Chickering (2002, Lemma 29), because $I(G_i) \subseteq I(G_0)$. Then, the descendants of Z in G_0 are descendants of Z in G_i too. Thus, D is a descendant of Z in G_i.

[6] Note that maybe $W = B$. Note also that $W \neq X$, because the case where $W = X$ is covered by Case 2.1.

Case 2.3.3 Assume that $D \neq Z$ and D was not a descendant of Z in G_0. As shown in Case 2.3.2, the descendants of Z in G_0 are descendants of Z in G_i too. Therefore, none of the descendants of Z in G_0 was to the left of D in α because, otherwise, some descendant of Z and thus of Y in G_i would be to the left of D in α, which would contradict the definition of D. This and the fact that D was not a descendant of Z in G_0 imply that D was still in G' when Z became a sink node of G' in Construct β (recall Figure 1). Therefore, Construct β added D to β after having added Z (recall lines 3-4), because D is to the left of Z in α by definition of D.[7] For the same reason, Method B2 has not interchanged D and Z in β (recall line 4). Thus, D is currently still to the left of Z in β, which implies that D is to the left of Y in β, because Y is the left neighbor of Z in β (recall line 3). However, this contradicts the fact that G_i is consistent with β, because D is a descendant of Y in G_i. Thus, this case never occurs.

We continue with the proof of Case 2.3. Note that $Y \notin \mathbf{S}$ implies that ρ^{YB}_{i+1} is $\mathbf{S}$-active in G_{i+1} because, otherwise, ρ^{AB}_{i+1} would not be $\mathbf{S}$-active in G_{i+1}. Note also that no descendant of Z in G_i is in $\mathbf{S}$ because, otherwise, there would be an $\mathbf{S}$-active route ρ^{XY}_i between X and Y in G_i and, thus, $\rho^{AX}_{i+1} \cup \rho^{XY}_i \cup \rho^{YB}_{i+1}$ would be an $\mathbf{S}$-active route between A and B in G_{i+1} that would violate the minimality property of ρ^{AB}_{i+1}. This implies that $D \notin \mathbf{S}$ because, as shown above, D is a descendant of Z in G_i. It also implies that there is an $\mathbf{S}$-active descending route ρ^{ZD}_i from Z to D in G_i. Then, $\rho^{AX}_{i+1} \cup X \to Z \cup \rho^{ZD}_i$ is an $\mathbf{S}$-active route between A and D in G_{i+1}. Likewise, $\rho^{BY}_{i+1} \cup Y \to Z \cup \rho^{ZD}_i$ is an $\mathbf{S}$-active route between B and D in G_{i+1}, where ρ^{BY}_{i+1} denotes the route resulting from reversing ρ^{YB}_{i+1}. Therefore, there are $\mathbf{S}$-active routes ρ^{AD}_α and ρ^{BD}_α between A and D and between B and D in G_α by the induction hypothesis.

Consider the subroute of ρ^{AB}_{i+1} that starts with the arc $X \to Y$ and continues in the direction of this arc until it reaches a node E such that $E = B$ or $E \in \mathbf{S}$. Note that E is a descendant of Y in G_i and, thus, E is a descendant of D in G_α by definition of D. Let ρ^{DE}_α denote the descending route from D to E in G_α. Assume without loss of generality that G_α has no descending route from D to B or to a node in $\mathbf{S}$ that is shorter than ρ^{DE}_α. This implies that if $E = B$ then ρ^{DE}_α is $\mathbf{S}$-active in G_α because, as shown above, $D \notin \mathbf{S}$. Thus, $\rho^{AD}_\alpha \cup \rho^{DE}_\alpha$ is an $\mathbf{S}$-active route between A and B in G_α. On the other hand, if $E \in \mathbf{S}$ then $E \neq D$ because $D \notin \mathbf{S}$. Thus, $\rho^{AD}_\alpha \cup \rho^{DE}_\alpha \cup \rho^{ED}_\alpha \cup \rho^{DB}_\alpha$ is an $\mathbf{S}$-active route between A and B in G_α, where ρ^{ED}_α and ρ^{DB}_α denote the routes resulting from reversing ρ^{DE}_α and ρ^{BD}_α.

□

Finally, we show how the correctness of Method B2 leads to an alternative proof of the so-called Meek's conjecture (1997). Given two DAGs G and H such that $I(H) \subseteq I(G)$, Meek's conjecture states that we can transform G into H by a sequence of arc additions and covered arc reversals such that after each operation in the sequence G is a DAG and

[7] Note that this statement is true thanks to our correction of Construct β.

```
Method G2H($G$, $H$)

/* Given two DAGs $G$ and $H$ such that $I(H) \subseteq I(G)$, the algorithm transforms
$G$ into $H$ by a sequence of arc additions and covered arc reversals such that
after each operation in the sequence $G$ is a DAG and $I(H) \subseteq I(G)$ */

1   Let $\alpha$ denote a node ordering that is consistent with $H$
2   $G$=Method B2($G$, $\alpha$)
3   Add to $G$ the arcs that are in $H$ but not in $G$
```

Figure 5: Method G2H.

$I(H) \subseteq I(G)$. The importance of Meek's conjecture lies in that it allows to develop efficient and asymptotically correct algorithms for learning BNs from data under mild assumptions (Chickering, 2002; Chickering & Meek, 2002; Meek, 1997; Nielsen et al., 2003). Meek's conjecture was proven to be true in the work of Chickering (2002, Thm. 4) by developing an algorithm that constructs a valid sequence of arc additions and covered arc reversals. We propose an alternative algorithm to construct such a sequence. The pseudocode of our algorithm, called Method G2H, can be seen in Figure 5. The following corollary proves that Method G2H is correct.

Corollary 1. *Given two DAGs G and H such that $I(H) \subseteq I(G)$, Method G2H(G, H) transforms G into H by a sequence of arc additions and covered arc reversals such that after each operation in the sequence G is a DAG and $I(H) \subseteq I(G)$.*

Proof. Note from Method G2H's line 1 that α denotes a node ordering that is consistent with H. Let G_α denote the MDI map of G relative to α. Recall that G_α is guaranteed to be unique because $I(G)$ is a graphoid. Note that $I(H) \subseteq I(G)$ implies that G_α is a subgraph of H. To see it, note that $I(H) \subseteq I(G)$ implies that we can obtain a MDI map of G relative to α by just removing arcs from H. However, G_α is the only MDI map of G relative to α.

Then, it follows from the proof of Theorem 5 that Method G2H's line 2 transforms G into G_α by a sequence of arc additions and covered arc reversals, and that after each operation in the sequence G is a DAG and $I(G_\alpha) \subseteq I(G)$. Thus, after each operation in the sequence $I(H) \subseteq I(G)$ because $I(H) \subseteq I(G_\alpha)$ since, as shown above, G_α is a subgraph of H. Moreover, Method G2H's line 3 transforms G from G_α to H by a sequence of arc additions. Of course, after each arc addition G is a DAG and $I(H) \subseteq I(G)$ because G_α is a subgraph of H.

□

7. The Corrected Methods A and B are Efficient

In this section, we show that Methods A and B are more efficient than any other solution to the same problem we can think of. Let n and a denote, respectively, the number of nodes and arcs in G. Moreover, let us assume hereinafter that a DAG is implemented as an adjacency matrix, whereas a node ordering is implemented as an array with an entry per node indicating the position of the node in the ordering. Since $I(G)$ is a graphoid, the first solution we can think of consists in applying the following characterization of G_α: For each node A, $Pa_{G_\alpha}(A)$ is the smallest subset $\mathbf{X} \subseteq Pre_\alpha(A)$ such that $A \perp_G Pre_\alpha(A) \setminus \mathbf{X} | \mathbf{X}$. This solution implies evaluating for each node A all the $O(2^n)$ subsets of $Pre_\alpha(A)$. Evaluating a subset implies checking a separation statement in G, which takes $O(a)$ time (Geiger et al., 1990, p. 530). Therefore, the overall runtime of this solution is $O(an2^n)$.

Since $I(G)$ satisfies the composition property in addition to the graphoid properties, a more efficient solution consists in running the incremental association Markov boundary (IAMB) algorithm (Peña et al., 2007, Thm. 8) for each node A to find $Pa_{G_\alpha}(A)$. The IAMB algorithm first sets $Pa_{G_\alpha}(A) = \emptyset$ and, then, proceeds with the following two steps. The first step consists in iterating through the following line until $Pa_{G_\alpha}(A)$ does not change: Take any node $B \in Pre_\alpha(A) \setminus Pa_{G_\alpha}(A)$ such that $A \not\perp_G B | Pa_{G_\alpha}(A)$ and add it to $Pa_{G_\alpha}(A)$. The second step consists in iterating through the following line until $Pa_{G_\alpha}(A)$ does not change: Take any node $B \in Pa_{G_\alpha}(A)$ that has not been considered before and such that $A \perp_G B | Pa_{G_\alpha}(A) \setminus \{B\}$, and remove it from $Pa_{G_\alpha}(A)$. The first step of the IAMB algorithm can add $O(n)$ nodes to $Pa_{G_\alpha}(A)$. Each addition implies evaluating $O(n)$ candidates for the addition, since $Pre_\alpha(A)$ has $O(n)$ nodes. Evaluating a candidate implies checking a separation statement in G, which takes $O(a)$ time (Geiger et al., 1990, p. 530). Then, the first step of the IAMB algorithm runs in $O(an^2)$ time. Similarly, the second step of the IAMB algorithm runs in $O(an)$ time. Therefore, the IAMB algorithm runs in $O(an^2)$ time. Since the IAMB algorithm has to be run once for each of the n nodes, the overall runtime of this solution is $O(an^3)$.

We now analyze the efficiency of Methods A and B. To be more exact, we analyze Methods A2 and B2 (recall Figure 3) rather than the original Methods A and B (recall Figure 1), because the former are more efficient than the latter. Methods A2 and B2 run in $O(n^3)$ time. First, note that Construct β runs in $O(n^3)$ time. The algorithm iterates n times through lines 3-10 and, in each of these iterations, it iterates $O(n)$ times through lines 5-8. Moreover, line 3 takes $O(n^2)$ time, line 6 takes $O(1)$ time, and line 9 takes $O(n)$ time. Now, note that Methods A2 and B2 iterate n times through lines 2-8 and, in each of these iterations, they iterate $O(n)$ times through lines 3-7. Moreover, line 4 takes $O(1)$ time, and line 5 takes $O(n)$ time because covering an arc implies updating the adjacency matrix accordingly. Consequently, Methods A and B are more efficient than any other solution to the same problem we can think of.

Finally, we analyze the complexity of Method G2H. Method G2H runs in $O(n^3)$ time: α can be constructed in $O(n^3)$ time by calling Construct $\beta(H, \gamma)$ where γ is any node ordering, running Method B2 takes $O(n^3)$ time, and adding to G the arcs that are in H but not in G can be done in $O(n^2)$ time. Recall that Method G2H is an alternative to the algorithm in the work of Chickering (2002). Unfortunately, no implementation details are provided in the work of Chickering and, thus, a comparison with the runtime of the algorithm there is not possible. However, we believe that our algorithm is more efficient.

8. Discussion

In this paper, we have studied the problem of combining several given DAGs into a consensus DAG that only represents independences all the given DAGs agree upon and that has as few parameters associated as possible. Although our definition of consensus DAG is reasonable, we would like to leave out the number of parameters associated and focus solely on the independencies represented by the consensus DAG. In other words, we would like to define the consensus DAG as the DAG that only represents independences all the given DAGs agree upon and as many of them as possible. We are currently investigating whether both definitions are equivalent. In this paper, we have proven that there may exist several non-equivalent consensus DAGs. In principle, any of them is equally good. If we were able to conclude that one represents more independencies than the rest, then we would prefer that one. In this paper, we have proven that finding a consensus DAG is NP-hard. This made us resort to heuristics to find an approximated consensus DAG. This does not mean that we discard the existence of fast super-polynomial algorithms for the general case, or polynomial algorithms for constrained cases such as when the given DAGs have bounded in-degree. This is a question that we are currently investigating. In this paper, we have considered the heuristic originally proposed by Matzkevich and Abramson (1992, 1993b). This heuristic takes as input a node ordering, and we have shown that finding the best node ordering for the heuristic is NP-hard. We are currently investigating the application of meta-heuristics in the space of node orderings to find a good node ordering for the heuristic. Our preliminary experiments indicate that this approach is highly beneficial, and that the best node ordering almost never coincides with any of the node orderings that are consistent with some of the given DAGs.

As said in Section 1, we aim at combining the BNs provided by multiple experts (or learning algorithms) into a single consensus BN that is more robust than the individual BNs. In this paper, we have proposed to combine the experts' BNs in two steps to avoid the problems discussed by Pennock and Wellman (1999). First, finding a consensus BN structure and, then, finding some consensus parameters for the consensus BN structure. This paper has focused only on the first step. We are currently working on the second step along the following lines. Let $(G^1, \theta^1), \ldots, (G^m, \theta^m)$ denote the BNs provided by the experts. The first element in each pair denotes the BN structure whereas the second denotes the BN parameters. Let $p^1, \ldots, p^m$ denote the probability distributions represented by the BNs provided by the experts. Then, we call $p^0 = f(p^1, \ldots, p^m)$ the consensus probability distribution, where f is any combination function, e.g. the weighted arithmetic or geometric mean. Let G_α denote a consensus BN structure obtained from $G^1, \ldots, G^m$ as described in this paper. We propose to obtain a consensus BN by parameterizing G_α such that $p_\alpha(A|Pa_{G_\alpha}(A)) = p^0(A|Pa_{G_\alpha}(A))$ for all $A \in \mathbf{V}$, where p_α is the probability distribution represented by the consensus BN. The motivation is that such a parameterization minimizes the Kullback-Leibler divergence between p_α and p^0 (Koller & Friedman, 2009, Thm. 8.7). Some hints about how to speed up the computation of this parameterization by performing inference in the experts' BNs can be found in the work of Pennock and Wellman (1999, Properties 3 and 4, and Section 5). Alternatively, one could first sample p^0 and, then, parameterize G_α such that $p_\alpha(A|Pa_{G_\alpha}(A)) = \hat{p}^0(A|Pa_{G_\alpha}(A))$ for all $A \in \mathbf{V}$, where $\hat{p}^0$ is the empirical probability distribution obtained from the sample. Again, the motivation is that such a parameterization minimizes the Kullback-Leibler divergence between p_α and $\hat{p}^0$ (Koller & Friedman, 2009, Thm. 17.1) and, of course, $\hat{p}^0 \approx p^0$ if the sample is sufficiently large. Note that we use p^0 to parameterize G_α but not to construct G_α which, as discussed in Section 1, allows us to avoid the problems discussed by Pennock and Wellman (1999).

Finally, note that the present work combines the DAGs $G^1, \ldots, G^m$ although there is no guarantee that each G^i is a MDI map of $I(p^i)$, i.e. G^i may have superfluous arcs. Therefore, one may want to check if G^i contains superfluous arcs and remove them before the combination takes place. In general, several MDI maps of $I(p^i)$ may exist, and they may differ in the number of parameters associated with them. It would be interesting to study how the number of parameters associated with the MDI map of $I(p^i)$ chosen affects the number of parameters associated with the consensus DAG obtained by the method proposed in this paper.

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Appendix A. Proofs of Lemmas 1-3

Lemma 1. *Method A(G, α) and Method A2(G, α) return the same DAG.*

Proof. It is evident that Methods A and A2 transform β into α and, thus, that they halt at some point. We now prove that they return the same DAG. We prove this result by induction on the number of times that Method A executes line 6 before halting. It is evident that the result holds if the number of executions is one, because Methods A and A2 share line 1. Assume as induction hypothesis that the result holds for up to $k-1$ executions. We now prove it for k executions. Let Y and Z denote the nodes involved in the first of the k executions. Since the induction hypothesis applies for the remaining $k-1$ executions, the run of Method A can be summarized as

```
If $Z \to Y$ is in $G$ then cover and reverse $Z \to Y$ in $G$
Interchange $Y$ and $Z$ in $\beta$
For $i = 1$ to $n$ do
  Percolate right-to-left in $\beta$ the leftmost node in $\beta$ that has not been percolated before
```

where n is the number of nodes in G. Now, assume that Y is percolated when $i = j$. Note that the first $j-1$ percolations only involve nodes to the left of Y in β. Thus, the run above is equivalent to

```
For $i = 1$ to $j - 1$ do
   Percolate right-to-left in $\beta$ the leftmost node in $\beta$ that has not been percolated before
If $Z \to Y$ is in $G$ then cover and reverse $Z \to Y$ in $G$
Interchange $Y$ and $Z$ in $\beta$
Percolate $Y$ right-to-left in $\beta$
Percolate $Z$ right-to-left in $\beta$
For $i = j + 2$ to $n$ do
   Percolate right-to-left in $\beta$ the leftmost node in $\beta$ that has not been percolated before.
```

Now, let $\mathbf{W}$ denote the nodes to the left of Z in β before the first of the k executions of line 6. Note that the fact that Y and Z are the nodes involved in the first execution implies that the nodes in $\mathbf{W}$ are also to the left of Z in α. Note also that, when Z is percolated in the latter run above, the nodes to the left of Z in β are exactly $\mathbf{W} \cup \{Y\}$. Since all the nodes in $\mathbf{W} \cup \{Y\}$ are also to the left of Z in α, the percolation of Z in the latter run above does not perform any arc covering and reversal or node interchange. Thus, the latter run above is equivalent to

```
For $i = 1$ to $j - 1$ do
   Percolate right-to-left in $\beta$ the leftmost node in $\beta$ that has not been percolated before
Percolate $Z$ right-to-left in $\beta$
Percolate $Y$ right-to-left in $\beta$
For $i = j + 2$ to $n$ do
   Percolate right-to-left in $\beta$ the leftmost node in $\beta$ that has not been percolated before
```

which is exactly the run of Method A2. Consequently, Methods A and A2 return the same DAG.

□

Lemma 2. *Method A2(G, α) and Method B(G, α) return the same DAG.*

Proof. We can prove the lemma in much the same way as Lemma 1. We simply need to replace Y by Z and vice versa in the proof of Lemma 1.

□

Lemma 3. *Method B(G, α) and Method B2(G, α) return the same DAG.*

Proof. It is evident that Methods B and B2 transform β into α and, thus, that they halt at some point. We now prove that they return the same DAG. We prove this result by induction on the number of times that Method B executes line 6 before halting. It is evident that the result holds if the number of executions is one, because Methods B and B2 share line 1. Assume as induction hypothesis that the result holds for up to $k-1$ executions. We now prove it for k executions. Let Y and Z denote the nodes involved in the first of the k executions. Since the induction hypothesis applies for the remaining $k-1$ executions, the run of Method B can be summarized as

```
If $Y \rightarrow Z$ is in $G$ then cover and reverse $Y \rightarrow Z$ in $G$
Interchange $Y$ and $Z$ in $\beta$
For $i = 1$ to $n$ do
  Percolate left-to-right in $\beta$ the rightmost node in $\alpha$ that has not been percolated before
```

where n is the number of nodes in G. Now, assume that Y is the j-th rightmost node in α. Note that, for all $1 \leq i < j$, the i-th rightmost node W_i in α is to the right of Y in β when W_i is percolated in the run above. To see it, assume to the contrary that W_i is to the left of Y in β. This implies that W_i is also to the left of Z in β, because Y and Z are neighbors in β. However, this is a contradiction because W_i would have been selected in line 2 instead of Y for the first execution of line 6. Thus, the first $j - 1$ percolations in the run above only involve nodes to the right of Z in β. Then, the run above is equivalent to

```
For $i = 1$ to $j - 1$ do
  Percolate left-to-right in $\beta$ the rightmost node in $\alpha$ that has not been percolated before
If $Y \rightarrow Z$ is in $G$ then cover and reverse $Y \rightarrow Z$ in $G$
Interchange $Y$ and $Z$ in $\beta$
For $i = j$ to $n$ do
  Percolate left-to-right in $\beta$ the rightmost node in $\alpha$ that has not been percolated before
```

which is exactly the run of Method B2.

□

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