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Causal Structure Learning

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Abstract

Graphical models can represent a multivariate distribution in a convenient and accessible form as a graph. Causal models can be viewed as a special class of graphical models that represent not only the distribution of the observed system but also the distributions under external interventions. They hence enable predictions under hypothetical interventions, which is important for decision making. The challenging task of learning causal models from data always relies on some underlying assumptions. We discuss several recently proposed structure learning algorithms and their assumptions, and we compare their empirical performance under various scenarios.

1. INTRODUCTION

A graphical model is a family of multivariate distributions associated with a graph, where the nodes in the graph represent random variables and the edges encode allowed conditional dependence relationships between the corresponding random variables (Lauritzen 1996). A causal graphical model is a special type of graphical model in which edges are interpreted as direct causal effects. This interpretation facilitates predictions under arbitrary (unseen) interventions, and hence the estimation of causal effects (e.g., Wright 1934, Spirtes et al. 2000, Pearl 2009). This ability to make predictions under arbitrary interventions sets causal models apart from standard models. We refer to Didelez (2018) for an introductory overview of causal concepts and graphical models.[1]

Structure learning is a model selection problem in which one estimates or learns a graph that best describes the dependence structure in a given data set (Drton & Maathuis 2017). Causal structure learning is the special case in which one tries to learn the causal graph or certain aspects of it, and this is what we focus on in this article. We describe various algorithms that have been developed for this purpose under different assumptions. We then compare the algorithms in a simulation study to investigate their performances in settings where the assumptions of a particular method are met, but also in settings where they are violated.

The outline of the article is as follows. Section 2 discusses the basic causal model and its various assumptions. Section 3 describes different target graphical objects, such as directed acyclic graphs (DAGs) or equivalence classes thereof, and describes algorithms that can learn them under certain assumptions. Section 4 describes the simulation setup, the evaluation scheme, and the results. We close with a brief discussion in Section 5.

2. THE MODEL

We formulate the model as a structural causal model (Pearl 2009). In particular, we consider a linear structural equation model (e.g., Wright 1921) for a p-dimensional random variable $X = (X_1, \ldots, X_p)^t$ under noise contributions $\varepsilon = (\varepsilon_1, \ldots, \varepsilon_p)^t$:

$$X_j \leftarrow \sum_{k=1}^{p} \beta_{j,k} X_k + \varepsilon_j \qquad \text{for} \quad j = 1, \ldots, p, \tag{1.}$$

or in vector notation,

$$X \leftarrow BX + \varepsilon, \tag{2.}$$

where B is a $p \times p$ matrix with entries $B_{j,k} = \beta_{j,k}$. Thus, the distribution of X is determined by the choice of B and the distribution of ε.

This model is called structural since it is interpreted as the generating mechanism of X (emphasized by the assignment operator $\leftarrow$), where each structural equation is assumed to be invariant to possible changes in the other structural equations. This is also referred to as autonomy [Haavelmo 1944, Frisch 1995 (1938)]. This assumption is key for causality since it allows the derivation of the distribution of X under external interventions. For example, a gene knockout experiment can be modeled by replacing the structural equation of the relevant gene while keeping the other structural equations unchanged. If the gene knockout experiment has significant off-target effects (e.g., Cho et al. 2014), then this approach is problematic with respect to the autonomy assumption. A possible remedy consists of modeling the experiment as a simultaneous intervention on all genes that are directly affected by the experiment.

[1] Causal inference is also possible without graphs, using, for example, the Neyman-Rubin potential outcome model (e.g., Rubin 2005). Single world intervention graphs (Richardson & Robins 2013) provide a unified framework for potential outcome and graphical approaches to causality.

2.1. Interventions

In this article, we consider the following two types of interventions:

1. A do-intervention (also called surgical intervention): This intervention is modeled by replacing the structural equation

$$X_j \leftarrow \sum_{k=1}^{p} \beta_{j,k} X_k + \varepsilon_j \quad \text{by} \quad X_j \leftarrow Z_j,$$

   where Z_j is the (either deterministic or random) value that variable X_j is forced to take in this intervention.
2. An additive intervention (also called shift intervention): This intervention consists of adding additional noise, modeled by replacing the structural equation

$$X_j \leftarrow \sum_{k=1}^{p} \beta_{j,k} X_k + \varepsilon_j \quad \text{by} \quad X_j \leftarrow \sum_{k=1}^{p} \beta_{j,k} X_k + \varepsilon_j + Z_j,$$

   where Z_j is the additional noise (again either deterministic or random) that is added to variable X_j. Shift interventions are standard in the econometric literature on instrumental variables with binary treatments where the additive shift of an exogenous instrument changes the probability of a binary treatment variable (Angrist et al. 1996). Shift interventions are also natural in biological settings where an inhibitor or enhancer can amplify or decrease the presence of, for example, mRNA in a cell. If the concentrations are amplified by a fixed factor, then this corresponds to an additive shift in the log-concentrations.

2.2. Graphical Representation

We can represent the model defined in Equation 1 as a directed graph (DG) G, where each variable X_k is represented by a node k, $k = 1, \ldots, p$, and there is an edge from node k to node j ($k \neq j$) if and only if $\beta_{j,k} \neq 0$. Thus, the parents $\mathrm{pa}(j, G)$ of node j in G correspond to the random variables that appear on the right-hand side of the jth structural equation. In other words, $X_{\mathrm{pa}(j,G)} := \{X_i : i \in \mathrm{pa}(j, G)\}$ are the variables that are involved in the generating mechanism of X_j and are also called the direct causes of X_j (with respect to $X_1, \ldots, X_p$). In this sense, edges in G represent direct causal effects, and G is also called a causal graph. The nonzero $\beta_{j,k}$s can be depicted as edge weights of G, yielding a weighted graph. This weighted graph and the distribution of ε fully determine the distribution of X.

The graph G is called acyclic if it does not contain a cycle.[2] A directed acyclic graph is also called a DAG. A DG is acyclic if and only if there is an ordering of the variables, called a causal order, such that the matrix B in Equation 2 is triangular. In terms of the causal mechanism, acyclicity means that there are no feedback loops. We refer to Section 2.5 for more details on cycles.

2.3. Factorization and Truncated Factorization

If $\varepsilon_1, \ldots, \varepsilon_p$ are jointly independent and G is a DAG, then the probability density function $f(\cdot)$ of X factorizes according to G:

$$f(x) = f(x_1, \ldots, x_p) = \prod_{i=1}^{p} f(x_i | x_{\mathrm{pa}(i,G)}). \qquad 3.$$

[2] A cycle (sometimes also called directed cycle) is formed by a directed path from i to j together with the edge $j \to i$.

Moreover, f is then called Markov with respect to G. This means that for pairwise disjoint subsets A, B, and S of V ($S = \emptyset$ is allowed), the following holds: If A and B are separated by S in G according to a graphical criterion called d-separation (Pearl 2009), then X_A and X_B are conditionally independent given X_S in f.

One can model an intervention on X_j by replacing the conditional density $f(x_j|x_{\mathrm{pa}(j)})$ by its conditional density under the intervention, keeping the other terms unchanged. For example, a do-intervention on X_j yields the following factorization:

$$f(x|\mathrm{do}(x_j)) = g(x_j) \prod_{i=1, i\neq j}^{p} f(x_i|x_{\mathrm{pa}(i)}),$$

where $g(\cdot)$ is the density of Z_j (allowed to be a point mass). When intervening on several variables simultaneously, one simply conducts such replacements for all intervention variables. The resulting factorization is known as the *g*-formula (Robins 1986), the manipulated density (Spirtes et al. 2000), or the truncated factorization formula (Pearl 2009).

2.4. Counterfactuals

We note that the structural causal model is often discussed in the context of counterfactual outcomes. In particular, if one assumes that ε is identical under different interventions, the model defines a joint distribution on all possible counterfactual outcomes. The problematic aspect is clearly that the realizations of the noise under different interventions can never be observed simultaneously, and any statement about the joint distribution of the noise under different interventions is thus in principle unfalsifiable and untestable (Dawid 2000). Without assuming anything on the joint noise distributions under different interventions, a causal model can equivalently be formulated via structural equations, a graphical model, or potential outcomes (Richardson & Robins 2013, Imbens 2014). For the causal structure learning methods discussed in this article, no assumption on the joint noise distribution is necessary, and we chose to use the structural equation framework for ease of exposition.

2.5. Assumptions

We consider various assumptions for the model defined by Equation 2.

- Causal sufficiency: Causal sufficiency refers to the absence of hidden (or latent) variables (Spirtes et al. 2000). There are two common options for the modeling of hidden variables:[3] They can be modeled explicitly as nodes in the structural equations or they can manifest themselves as a dependence between the noise terms $(\varepsilon_1, \ldots, \varepsilon_p)$, where the noise terms are assumed to be independent in the absence of latent confounding.
- Causal faithfulness: We saw in Section 2.3 that the distribution of X generated from Equation 2 is Markov with respect to the causal DAG, meaning that if A and B are d-separated by S in the causal DAG, then X_A and X_B are conditionally independent given X_S. The reverse implication is called causal faithfulness. Together, the causal Markov and causal faithfulness assumptions imply that d-separation relationships in the causal DAG have a one-to-one correspondence with conditional independencies in the distribution.

[3] In this article we look at the behavior of various methods under the presence and absence of latent confounding. Throughout, we do not allow hidden selection variables, that is, unmeasured variables that determine if a unit is included in the data sample. More details on selection variables can be found in, for example, Spirtes et al. (1999).

- Acyclicity: Cycles can be used to model instantaneous feedback mechanisms. In the presence of cycles, the structural equations (Equation 1) are typically interpreted (implicitly) as a dynamical system. There are various assumptions that can be made about the strength of cycles in the graph, including the following.[4]
    1. Existence of a unique equilibrium solution of Equation 2: Is there a unique solution X for each realization ε such that $X = BX + \varepsilon$ or, equivalently, $(I - B)X = \varepsilon$, where I is the p-dimensional identity matrix? Existence of a unique equilibrium requires that $I - B$ is invertible. In this case the equilibrium is
    $$X = (I - B)^{-1}\varepsilon.$$
    2. Convergence to a stable equilibrium: Iterating Equation 2 from any starting value $X^{(0)}$ for X (and for a fixed and constant realization of the noise ε), we can form an iteration $X^{(k)} = BX^{(k-1)} + \varepsilon$ for $k \in \mathbb{N}$. The question is then whether the iterations converge to the equilibrium, that is, whether $\lim_{k\to\infty} X^{(k)} = (I - B)^{-1}\varepsilon$. This convergence requires that the spectral radius of B is smaller than 1.
    3. Existence of a stable equilibrium under do-interventions: This requires that the cycle product (the maximal product of the coefficients along all loops in the graph) is smaller than 1 (see, e.g., Rothenhäusler et al. 2015).

  DAGs fulfill all three assumptions above trivially as their spectral radius and cycle product both vanish identically.
- Gaussianity of the noise distribution: We consider both Gaussian distributions and t-distributions with various degrees of freedom.
- One or several experimental settings: We consider both homogeneous data, where all observations are from the same experimental setting, and heterogeneous data, where the observations come from different experimental settings. In particular, we consider settings with unknown shift-interventions and known do-interventions.
- Linearity: While the assumptions and the models have been discussed in the context of linear models, the ideas can be extended to nonlinear models and to discrete random variables to various degrees.

3. METHODS

Since different structure learning methods output different types of graphical objects, we first discuss the various target graphical objects in Section 3.1. To conduct a comparison based on such different graphical targets, we focus on certain ancestral relationships that can be read off from all objects (see Section 3.2). The different algorithms and their assumptions are discussed in Section 3.3, and their assumptions are summarized in **Table 1**.

3.1. Target Graphical Objects

The structure learning methods that we compare use different types of data ranging from purely observational data to data with clearly labeled interventions and from data that do not allow hidden variables and cycles to data that allow both of these. As a result, the different methods learn the

[4]We exclude self-loops (an edge from a node to itself), as models would be unidentifiable if self-loops were allowed (see, e.g., Rothenhäusler et al. 2015).

Table 1 The assumptions (see Section 2.5) and output format for different structure learning methods

	(rank)PC	(rank)FCI	(rank)GES	(rank)GIES	MMHC	LINGAM	backShift
Causal sufficiency	Yes	No	Yes	Yes	Yes	Yes	No
Causal faithfulness	Yes	Yes	Yes	Yes	Yes	No	No
Acyclicity	Yes	Yes	Yes	Yes	Yes	Yes	No
Non-Gaussian errors	No	No	No	No	No	Yes	No
Unknown shift interventions	No	No	No	No	No	No	Yes
Known do-interventions	No	No	No	Yes	No	No	No
Output	CPDAG	PAG	CPDAG	PDAG	DAG	DAG	DG

(For example, PC requires acyclicity, causal faithfulness and causal sufficiency, and LINGAM requires non-Gaussian errors.) Note that linearity is not explicitly listed, but all versions of the algorithms based on rank-correlations allow certain types of nonlinearities. Abbreviations: CPDAG, completed partially directed acyclic graph; DAG, directed acyclic graph; DG, directed graph; FCI, fast causal inference; GES, greedy equivalence search; GIES, greedy interventional equivalence search; LINGAM, linear non-Gaussian acyclic models; MMHC, max-min hill climbing; PAG, partial ancestral graph; PC, Peter-Clark; PDAG, partially directed acyclic graph.

underlying causal graph at different levels of granularity. At the finest level of granularity, a method learns the underlying DG from Equation 1. If the method assumes acyclicity (no feedback), then the target object is a DAG.

Under the model of Equation 2 with acyclicity, independent and multivariate Gaussian errors and independent and identically distributed (i.i.d.) observational data, the underlying causal DAG is generally not identifiable. Instead, one can identify the Markov equivalence class of DAGs, that is, the set of DAGs that encode the same set of d-separation relationships (Pearl 2009). A Markov equivalence can be conveniently summarized by another graphical object called a completed partially directed acyclic graph (CPDAG) (Andersson et al. 1997, Chickering 2002a). A CPDAG can be interpreted as follows: $i \to j$ is in the CPDAG if $i \to j$ in every DAG in the Markov equivalence class, and $i \circ\!\!-\!\!\circ j$ in the CPDAG if there is a DAG with $i \to j$ and a DAG with $i \leftarrow j$ in the Markov equivalence class. Thus, edges of the type $\circ\!\!-\!\!\circ$ represent uncertainty in the edge orientation.

DAGs are not closed under marginalization. In the presence of latent variables, some algorithms therefore aim to learn a different object called a maximal ancestral graph (MAG) (Richardson & Spirtes 2002). In general, MAGs contain three types of edges, $i \multimap j$, $i \to j$, and $i \leftrightarrow j$, but in our settings without selection variables (see footnote 3), $i \multimap j$ does not occur. A MAG encodes conditional independencies via m-separation (Richardson & Spirtes 2002). Every DAG with latent variables can be uniquely mapped to a MAG that encodes the same conditional independencies and the same ancestral relationships among the observed variables. Ancestral relationships can be read off from the edge marks of the edges: A tail mark $i \multimap\!\!* j$ means that i is an ancestor of j in the underlying DAG, and an arrowhead $i \leftarrow\!\!* j$ means that i is not an ancestor of j in the underlying DAG, where $*$ represents any of the possible edge marks (again assuming no selection variables).

Several MAGs can encode the same set of conditional independence relationships. Such MAGs form a Markov equivalence class, which can be represented by a partial ancestral graph (PAG) (Richardson & Spirtes 2002, Ali et al. 2009). A PAG can contain the edges $i \to j$, $i \multimap j$, $i \multimap\!\!\circ j$, $i \leftrightarrow j$, $i \circ\!\!\to j$, and $i \circ\!\!-\!\!\circ j$, but the edges $i \multimap j$ and $i \multimap\!\!\circ j$ do not occur in our setting without selection variables. The interpretation of the edge marks is as follows. A tail mark means that this tail mark is present in all MAGs in the Markov equivalence class, and an arrowhead means that this arrowhead is present in all MAGs in the Markov equivalence class. A circle mark represents uncertainty about the edge mark, in the sense that there is a MAG in the Markov equivalence class where this edge mark is a tail, as well as a MAG where this edge mark is an arrowhead.

3.2. Ancestral and Parental Relationships

To compare methods that output the different graphical objects discussed above, we focus on the following two basic questions for any variable X_j, $j \in \{1, \ldots, p\}$ and the underlying causal DAG G:

1. What are the direct causes of X_j, or equivalently, what is $\mathrm{pa}_G(j)$? The parents are important since they completely determine the distribution of X_j. Hence, the conditional distribution $X_j | X_{\mathrm{pa}(j)}$ is constant, even under arbitrary interventions on subsets of $X_{\{1,\ldots,p\}\setminus\{j\}}$. The set of parents is unique in this respect and allows making accurate predictions about X_j even under arbitrary interventions on all other variables. Moreover, the (possible) parents of X_j can be used to estimate (bounds on) the total causal effect of X_j on any of the other variables (Maathuis et al. 2009, 2010; Stekhoven et al. 2012; Nandy et al. 2017b).
2. What are the causes of X_j, or equivalently, what is the set of ancestors $\mathrm{an}_G(j)$ (the set of nodes from which there is a directed path to j in G)? The ancestors are important since any intervention on ancestors of X_j has an effect on the distribution of X_j, as long as no other do-type interventions happen along the path. Thus, if we want to manipulate the distribution of X_j, we can consider interventions on subsets of $X_{\mathrm{an}_G(j)}$.

3.3. Considered Methods

We include at least one algorithm from each of the following five main classes of causal structure learning algorithms: constraint-based methods, score-based methods, hybrid methods, methods based on structural equation models with additional restrictions, and methods exploiting invariance properties. Limiting ourselves to algorithms with an implementation in `R` (R Core Team 2017), we obtain the following selection of methods, with assumptions summarized in **Table 1**:

- Constraint-based methods: Peter-Clark (PC) (Spirtes et al. 2000), rankPC (Harris & Drton 2013), fast causal inference (FCI) (Spirtes et al. 2000), and rankFCI[5]
- Score-based methods: greedy equivalence search (GES) (Chickering 2002b), rankGES (Nandy et al. 2017a), greedy interventional equivalence search (GIES) (Hauser & Bühlmann 2012), and rankGIES[6]
- Hybrid methods: max-min hill climbing (MMHC) (Tsamardinos et al. 2006)
- Structural equation models with additional restrictions: linear non-Gaussian acyclic models (LINGAM) (Shimizu et al. 2006)
- Exploiting invariance properties: backShift (Rothenhäusler et al. 2015)

We do not include methods for time series data, mixed data, or Bayesian methods. Other excluded methods that make use of interventional data include those of Cooper & Yoo (1999), Tian & Pearl (2001), and Eaton & Murphy (2007); the last does not require knowledge of the precise location of interventions, in a similar spirit to the method of Rothenhäusler et al. (2015). Hyttinen et al. (2012) also make use of intervention data to learn feedback models, assuming do-interventions, whereas Peters et al. (2016) permit building a graph nodewise by estimating the parental set of each node separately.

3.3.1. (rank)PC and (rank)FCI. The PC algorithm (Spirtes et al. 2000) is named after its inventors, Peter Spirtes and Clark Glymour. It is a constraint-based algorithm that assumes acyclicity,

[5] rankFCI is obtained by using rank correlations in FCI, analogously to rankPC.

[6] rankGIES is obtained by using rank correlations in GIES, analogously to rankGES.

causal faithfulness, and causal sufficiency. It conducts numerous conditional independence tests to learn about the structure of the underlying DAG. In particular, it learns the CPDAG of the underlying DAG in three steps: (*a*) determining the skeleton, (*b*) determining the v-structures, and (*c*) determining further edge orientations. The skeleton of the CPDAG is the undirected graph obtained by replacing all directed edges by undirected edges. The PC algorithm learns the skeleton by starting with a complete undirected graph. For $k = 0, 1, 2, \ldots$ and adjacent nodes i and j in the current skeleton, it then tests conditional independence of X_i and X_j given X_S for all $S \subseteq \text{adj}(i) \setminus \{j\}$ with $|S| = k$, and for all $S \subseteq \text{adj}(j) \setminus \{i\}$ with $|S| = k$. The algorithm removes an edge if a conditional independence is found (that is, the null hypothesis of independence was not rejected at some level α), and stores the corresponding separating set S. Step (*a*) stops if the size of the conditioning set k equals the degree of the graph.

In step (*b*), all edges are replaced by $\circ\!\!-\!\!\circ$, and the algorithm considers all unshielded triples, that is, all triples $i \circ\!\!-\!\!\circ j \circ\!\!-\!\!\circ k$ where i and k are not adjacent. Based on the separating set that led to the removal of $i - k$, the algorithm determines whether the triple should be oriented as a v-structure $i \to j \leftarrow k$ or not. Finally, in step (*c*), some additional orientation rules are applied to orient as many of the remaining undirected edges as possible.

The PC algorithm was shown to be consistent in certain sparse high-dimensional settings (Kalisch & Bühlmann 2007). There are various modifications of the algorithm. We use the order-independent version of Colombo & Maathuis (2014). The PC algorithm does not impose any distributional assumptions, but conditional independence tests are easiest in the binary and multivariate Gaussian settings. Harris & Drton (2013) proposed a version of the PC algorithm for certain Gaussian copula distributions. We include this algorithm in our comparison and refer to it as rankPC. There is also a version of the PC algorithm that allows cycles (Richardson & Spirtes 1999), but we did not find an `R` implementation of it.

The fast causal inference (FCI) algorithm (Spirtes et al. 1999, 2000) is a modification of the PC algorithm that drops the assumption of causal sufficiency by allowing arbitrarily many hidden variables. The output of the FCI algorithm can be interpreted as a PAG (Zhang 2008a). The first step of the FCI algorithm is the same as step *a* of the PC algorithm, but the FCI algorithm needs to conduct additional tests to learn the correct skeleton. There are also additional orientation rules, which were shown to be complete by Zhang (2008b). Because the additional tests can slow down the algorithm considerably, faster adaptations have been developed, such as really fast causal inference (RFCI) (Colombo et al. 2012) and FCI+ (Claassen et al. 2013). Colombo et al. (2012) proved high-dimensional consistency of FCI and RFCI. The idea of Harris & Drton (2013) can also be applied to FCI, leading to rankFCI.

3.3.2. (rank)GES and (rank)GIES. Greedy equivalence search (GES) (Chickering 2002b) is a score-based algorithm that assumes acyclicity, causal faithfulness, and causal sufficiency. Score-based algorithms use the fact that each DAG can be scored in relation to the data, typically using a penalized likelihood score. The algorithms then search for the DAG or CPDAG that yields the optimal score. Since the space of possible graphs is typically too large, greedy approaches are used. In particular, GES learns the CPDAG of the underlying causal DAG by conducting a greedy search on the space of possible CPDAGs. Its greedy search consists of a forward phase, in which it conducts single edge additions that yield the maximum improvement in score, and then a backward phase, in which it conducts single edge deletions. Despite the greedy search, Chickering (2002b) showed that the algorithm is consistent under some assumptions (for fixed p). Nandy et al. (2017a) showed high-dimensional consistency of GES.

Greedy interventional equivalence search (GIES) (Hauser & Bühlmann 2012) is an adaptation of GES to settings with data from different known do-interventions. Due to the additional

information from the interventions, its target graphical object is a so-called interventional Markov equivalence class, which is a subclass of the Markov equivalence class of the underlying DAG and can be seen as a partially directed acyclic graph (PDAG).

Nandy et al. (2017a) showed a close connection between score-based and constraint-based methods for multivariate Gaussian data. As a result, the copula methods that can be used for the PC and FCI algorithms can be transferred to the GES and GIES algorithms. We include these algorithms in our comparison and refer to them as rankGES and rankGIES.

3.3.3. Max-min hill climbing. MMHC (Tsamardinos et al. 2006) is a hybrid algorithm that assumes acyclicity, causal faithfulness, and causal sufficiency. Hybrid algorithms combine ideas from both constraint-based and score-based approaches. In particular, MMHC first learns the CPDAG skeleton using the constraint-based max-min parents and children algorithm and then performs a score-based hill-climbing DAG search to determine the edge orientations. Its output is a DAG. Nandy et al. (2017a) showed that the algorithm is not consistent for fixed p, due to the restricted score-based phase.

3.3.4. LINGAM. LINGAM (Shimizu et al. 2006) is an acronym derived from "linear non-Gaussian acyclic models" and has been designed for the model in Equation 2 with non-Gaussian noise. It assumes acyclicity and causal sufficiency. It is based on the fact that $X = A\varepsilon$ with $A = (I - B)^{-1}$. This can be viewed as a source separation problem, where identification of the matrix B is equivalent to identification of the mixture matrix A. It was shown by Comon (1994) that whenever at most one of the components of ε is Gaussian, the mixing matrix is identifiable up to scaling and permutation of columns, via independent component analysis (ICA). This observation lies at the basis of the LINGAM method. There are various modifications of LINGAM, for example, to allow for hidden variables (Hoyer et al. 2008) or cycles (Lacerda et al. 2008). There is also a different implementation called DirectLINGAM (Shimizu et al. 2011) that uses a pairwise causality measure instead of ICA. Since only ICA-based LINGAM assuming acyclicity and causal sufficiency is available in R, we include this version in our comparison.

3.3.5. backShift. backShift (Rothenhäusler et al. 2015) makes use of non-i.i.d. structure in the data and unknown shift interventions on variables. Assume that the data are divided into distinct blocks $\mathcal{E}$. Let $\Gamma_e \in \mathbb{R}^{p\times p}$ be the empirical Gram matrix of the p variables in block $e \in \mathcal{E}$ of the data. In the absence of shift interventions, the expected values of Γ_e would be identical for all $e \in \mathcal{E}$. Under unknown shift interventions, the Gram matrices can change from block to block. However, for the true matrix B of causal coefficients from Equation 2, it can be shown that the expected value of

$$(I - B)(\Gamma_e - \Gamma_{e'})(I - B)^t$$

is a diagonal matrix for all $e, e' \in \mathcal{E}$, even in the presence of latent confounding. backShift estimates $I - B$ (and hence B) by a joint diagonalization of all Gram differences $\Gamma_e - \Gamma_{e'}$ for all pairs $e, e' \in \mathcal{E}$. A necessary and sufficient condition for identifiability of the causal matrix B is as follows. Let $\eta_{e,k}$ be the variance of the noise interventions at variable $k \in \{1, \ldots, p\}$ in setting $e \in \mathcal{E}$. Full identifiability requires that we can find for each pair of variables (k, l) two settings $e, e' \in \mathcal{E}$ such that the product $\eta_{e,k}\eta_{e',l}$ is not equal to the product $\eta_{e,l}\eta_{e',k}$. A consequence of this necessary and sufficient condition for identifiability is $|\mathcal{E}| \geq 3$, that is, we need to observe at least three different blocks of data for identifiability.

4. EMPIRICAL EVALUATION

We conducted an extensive simulation study to evaluate and compare the methods, paying particular attention to sensitivity of the methods to model violations. We are also interested in realistic boundaries (in terms of the number of variables, the sample size, and other simulation parameters) beyond which we cannot expect a reasonable reconstruction of the underlying graph.

In Section 4.1, we describe the data-generating mechanism used in the simulation study. Section 4.2 discusses the framework for comparison of the considered methods, and Section 4.3 contains the results.

The code is available in the `R` package `CompareCausalNetworks` (Heinze-Deml & Meinshausen 2017), along with further documentation. All methods are called through the interface offered by the `CompareCausalNetworks` package, which depends on the packages `backShift` (Heinze-Deml 2017), `bnlearn` (Scutari 2010), and `pcalg` (Kalisch et al. 2012) for the code of the considered methods. In particular, backShift is in `backShift`, MMHC is in `bnlearn`, and all other considered methods are in `pcalg`.

4.1. Data Generation

We generate data sets that differ with respect to the following characteristics: the number of observations n; the number of variables p; the expected number of edges in B; the noise distribution; the correlation of the noise terms; the type, strength, and number of interventions; the signal-to-noise ratio; the presence and strength of a cycle in the graph; and possible model misspecifications in terms of nonlinearities. The function `simulateInterventions()` from the package `CompareCausalNetworks` implements the simulation scheme that we describe in more detail below.

We first generate the adjacency matrix B. Assume the variables with indices $\{1, \dots, p\}$ are causally ordered. For each pair of nodes i and j, where i precedes j in the causal ordering, we draw a sample from Bernoulli(p_s) to determine the presence of an edge from i to j. After having sampled the nonzero entries of B in this fashion, we sample their corresponding coefficients from Unif$(-1, 1)$. As described below, the edge weights are later rescaled to achieve a specified signal-to-noise ratio. We exclude the possibility of $B = \mathbf{0}$, that is, we resample until B contains at least one nonzero entry.

Second, we simulate the interventions. We let n_I denote the total number of (interventional and observational) settings that are generated. Let $I \in \{0, 1\}^{n_I \times p}$ be an indicator matrix, where an entry $I_{e,k} = 1$ indicates that variable k is intervened on in setting e and a zero entry indicates that no intervention takes place. For each variable k, we first set the kth column $I_{\cdot k} \equiv 0$ and then sample one setting e' uniformly at random and set $I_{e'k} = 1$. In other words, each variable is intervened on in exactly one setting. It is possible that there are settings where no interventions take place, corresponding to zero rows of the matrix I, which represents the observational setting. Similarly, there may be settings where interventions are performed on multiple variables at once. After defining the settings, we sample (uniformly at random with replacement) what setting each data point belongs to. So, for each setting, we generate approximately the same number of samples. In any generated data set, the interventions are all of the same type, that is, they are either all shift or all do-interventions (with equal probability). In both cases, an intervention on a variable X_j is modeled by sampling Z_j from a t-distribution as $Z_j \sim \sigma_Z \cdot t(df_\varepsilon)$ (see Section 2.1). If $\sigma_Z = 0$ is sampled, it is taken to encode that no interventions should be performed. In that case, all interventional settings correspond to purely observational data.

Third, the noise terms ε are generated by first sampling from a p-dimensional zero-mean Gaussian distribution with covariance matrix Σ, where $\Sigma_{i,i} = 1$ and $\Sigma_{i,j} = \rho_\varepsilon$. The magnitude of ρ_ε models the presence and the strength of hidden variables (see Section 2.5). For a positive value of ρ, the correlation structure corresponds to the presence of a hidden variable that affects each observed variable. To steer the signal-to-noise ratio, we set the variance of the noise terms of all nodes except for the source nodes to ω, where $0 < \omega \leq 1$. Stepping through the variables in causal order, for each variable X_j that has parents, we uniformly rescale the edge weights $\beta_{j,k}$ in the jth structural equation such that the variance of the sum $\sum_{k=1}^{p} \beta_{j,k} X_k + \varepsilon_j$ is approximately equal to one in the observational setting. In other words, the parameter ω steers what proportion of the variance stems from the noise ε_j. The signal-to-noise ratio can then be computed as $\mathrm{SNR} = (1 - \omega)/\omega$ (in the absence of hidden variables).

Fourth, if the causal graph contains a cycle, we sample two nodes i and j such that adding an edge between them creates a cycle in the causal graph. We then compute the coefficient for this edge such that the cycle product is 1. Subsequently, we sample the sign of the coefficient with equal probability and set the magnitude by scaling the coefficient by w_c, where $0 < w_c < 1$.

Fifth, we transform the noise variables to obtain a t-distribution with df_ε degrees of freedom. X is then generated as $X = (I - B)^{-1}\varepsilon$ in the observational case; under a shift intervention X can be generated as $X = (I - B)^{-1}(\varepsilon + Z)$, where the coordinates of Z are only nonzero for the variables that are intervened on. Under a do-intervention on X_j, $\beta_{j,k}$ for $k = 1, \ldots, p$ are set to 0 to yield B' and ε_j is set to Z_j to yield ε'_j. We then obtain X as $X = (I - B')^{-1}\varepsilon'$.

Sixth, if nonlinearity is to be introduced, we marginally transform all variables as $X_j \leftarrow \tanh(X_j)$.

Last, we randomly permute the order of the variables in X before running the algorithms. Methods that are order-dependent therefore cannot exploit any potential advantage stemming from a data matrix with columns ordered according to the causal ordering or a similar one.

4.1.1. Considered settings. We sample the simulation parameters uniformly at random from the following sets.

- Sample size $n \in \{500, 2000, 5000, 10000\}$
- Number of variables $p \in \{2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 20, 50, 100\}$
- Edge density parameter $p_s \in \{0.1, 0.2, 0.3, 0.4\}$
- Number of interventions $n_I \in \{3, 4, 5\}$
- Strength of the interventions $\sigma_Z \in \{0, 0.1, 0.5, 1, 2, 3, 5, 10\}$
- Degrees of freedom of the noise distribution $df_\varepsilon \in \{2, 3, 5, 10, 20, 100\}$
- Strength of hidden variables $\rho_\varepsilon \in \{0, 0.1, 0.2, 0.5, 0.8\}$
- Proportion of variance from noise $\omega \in \{0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9\}$
- Strength of cycle $w_c \in \{0.1, 0.25, 0.5, 0.75, 0.9\}$

In total, we consider 842 different configurations. For each sampled configuration, we generate 20 different causal graphs with one data set per graph. **Supplemental Appendix Section 6.2** summarizes the number of simulation settings for different values of the simulation parameters.

Supplemental Material

4.2. Evaluation Methodology

As the targets of inference differ between the considered methods, we evaluate a method's accuracy for recovering parental and ancestral relations (see also Section 3.2). For each of these, we look at a method's performance for predicting (*a*) the existence of a relation, (*b*) the absence of a relation, and (*c*) the potential existence of a relation. We formulate these different categories as so-called queries, which are further described in Section 4.2.1.

An additional challenge in comparing a diverse set of methods involves choosing the options and the proper amount of regularization that determines the sparsity of the estimated structure. We address this challenge in two ways. First, we run different configurations of each method's tuning parameters and options, as detailed in **Supplemental Appendix Section 6.1**. In the evaluation of the methods for a certain metric, we choose the method's configuration that yielded the best results under the considered metric in each simulation setting (averaged over the twenty data sets for each setting). This means that the results are optimistically biased, but we found that the ranking was largely insensitive to the tuning parameter choices. Second, we use a subsampling scheme (stability ranking) so that each method outputs a ranking of pairs of nodes for a given query. For instance, the first entry in this ranking for the existence of parental relations is the edge most likely to be present in the underlying DAG. Further details are given in Sections 4.2.2 and 4.2.3.

4.2.1. Considered queries. For both the parental and ancestral relations, we consider three queries. The existence of a relation is assessed by the queries `isParent` and `isAncestor`, the absence of a relation is assessed by the queries `isNoParent` and `isNoAncestor`, and the potential existence of a relation is assessed by the queries `isPossibleParent` and `isPossibleAncestor`.

All queries return a connectivity matrix, which we denote by A. The interpretations of the entries of A differ according to the considered query. For parental relations, we have the following:

1. `isParent`: This query cannot be easily answered by methods that return a PAG. For the other graphical objects, $A_{i,j} = 1$ if $i \to j$ in the estimated graph, and $A_{i,j} = 0$ otherwise.
2. `isPossibleParent`: Entry $A_{i,j} = 1$ if there is an edge of type $i \multimap j$ or $i \circ\!\!-\!\!\ast\, j$ in the estimated graph. Concretely, for methods estimating DGs or DAGs, $A_{i,j} = 1$ if $i \to j$ in the estimated graph; for PDAGs and CPDAGs, $A_{i,j} = 1$ if $i \to j$ or $i \circ\!\!-\!\!\circ j$ in the estimated graph; and for PAGs, $A_{i,j} = 1$ if $i \to j$, $i \multimap j$, $i - j$, $i \circ\!\!\to j$, $i \circ\!\!-\!\!\circ j$ or $i \circ\!\!- j$ in the estimated graph. Otherwise, $A_{i,j} = 0$.
3. `isNoParent`: This is the complement of the query `isPossibleParent`. If the latter returns the connectivity matrix A', then entry $A_{i,j} = 1$ if $A'_{i,j} = 0$ and $A_{i,j} = 0$ if $A'_{i,j} = 1$.

For ancestral relations, we have the following:

1. `isAncestor`: Entry $A_{i,j} = 1$ if there is a path from i to j with edges of type $\multimap$. For example, for DGs, DAGs, and CPDAGs this reduces to a directed path. Otherwise, $A_{i,j} = 0$.
2. `isPossibleAncestor`: Entry $A_{i,j} = 1$ if there is a path from i to j such that no edge on the path points toward i (possibly directed path), and $A_{i,j} = 0$ otherwise. In general, such a path can contain edges of the types $i \multimap j$ and $i \circ\!\!-\!\!\ast\, j$. For DAGs and DGs, this again reduces to a directed path, and for CPDAGs it is a path with edges $\circ\!\!-\!\!\circ$ and $\to$.
3. `isNoAncestor`: This is the complement of the query `isPossibleAncestor`. If the latter returns the connectivity matrix A', then entry $A_{i,j} = 1$ if $A'_{i,j} = 0$ and $A_{i,j} = 0$ if $A'_{i,j} = 1$.

4.2.2. Stability ranking. To obtain a ranking of pairs of nodes for a given query, we run the method under consideration on $n_{\text{sim}} = 100$ random subsamples of the data, where each subsample contains approximately $n/2$ data points. More specifically, we use the following stratified sampling scheme: In each round, we draw samples from $1/\sqrt{2} \cdot n_I$ settings, where n_I denotes the total number of (interventional and observational) settings. In each chosen setting s, we sample $1/\sqrt{2} \cdot n_s$ observations uniformly at random without replacement, where n_s denotes the number of observations in setting s. After a random permutation of the order of the variables, we run

the method on each subsample and evaluate the method's output with respect to the considered query.

For each subsample k and a particular query q, we obtain the corresponding connectivity matrix A. We can then rank all pairs of nodes i, j according to the frequency $\pi_{i,j} \in [0,1]$ of the occurrence of $A_{i,j} = 1$ across subsamples. Ties between pairs of variables can be broken with the results of the other queries—for instance, if the query is `isParent`, ties are broken with counts for `isPossibleParent`. This stability ranking scheme is implemented in the function `getRanking()` in the package `CompareCausalNetworks`. Further details about the tie-breaking scheme are given in the package documentation.

4.2.3. Metrics. For a chosen query and cutoff value of $t \in (0,1)$, we select all pairs (i, j) for which $\pi_{i,j} \geq t$. This leads to a true-positive rate $\mathrm{TPR}_t = |\{(i,j) : \pi_{i,j} \geq t\} \cap S|/|S|$, where $S := \{(i,j) : A_{i,j} = 1\}$ is the set of correct answers (for example, the set of true direct causal effects for the query `isParent`). The corresponding false-positive rate is $\mathrm{FPR}_t = |\{(i,j) : \pi_{i,j} \geq t\} \cap S^c|/|S^c|$, with $S^c := \{(i,j) : A_{i,j} = 0\}$. The four metrics we consider are as follows.

1. AOC: The standard area under curve (AUC) measures the area below the graph $(\mathrm{FPR}_t, \mathrm{TPR}_t) \in [0,1]^2$ as t is varied between 0 and 1. Under random guessing, the area is 0.5 in expectation, and the optimal value is 1. Here, to make rates comparable, we look at the area over curve defined as AOC = 1−AUC, such that low values are preferable.
2. Equal-error rate (E-ER): This measures the false-negative rate $\mathrm{FNR}_t = 1 - \mathrm{TPR}_t$ at the cutoff t where it equals the false-positive rate FPR_t, that is, for the value $t \in (0,1)$ for which $1 - \mathrm{TPR}_t = \mathrm{FPR}_t$. The advantage over AOC is that it is a real error rate and is also identical whether we look at the missing edges or at the true edges. For random guessing, the expected value is 0.5 and does not depend on the sparsity of the graph.
3. No-false-positives error rate (NFP-ER). This measures the false negative rate $\mathrm{FNR}_t = 1 - \mathrm{TPR}_t$ for the minimal cutoff t at which $\mathrm{FPR}_t = 0$, that is, for the largest number of selections under the constraint that not a single false positive occurs. The expected value under random guessing depends on the sparsity of the graph.
4. No-false-negatives error rate (NFN-ER): This measures the false-positive rate $\mathrm{FPR}_t = 1 - \mathrm{TNR}_t$ for the maximally large cutoff t at which $\mathrm{FNR}_t = 0$, that is, for the smallest number of selections possible that not a single false negative occurs. The expected value under random guessing depends on the sparsity of the graph.

All four metrics are designed so that lower values are better.

4.3. Results

Below, we mostly present results for the `isAncestor` query and the metric E-ER. Results for other queries and metrics are similar in nature.

4.3.1. Multidimensional scaling. For each simulation setting and each method, we compute the E-ER for the `isAncestor` query. This yields a (number of simulation settings) × (number of methods) matrix with E-ER values. The Euclidean distance between two columns in this matrix is a distance between methods. Similarly, the Euclidean distance between two rows in the matrix is a distance between simulation settings.

Figure 1 shows a multidimensional scaling (MDS) plot based on distances between the methods, using least-squares scaling. We see that the rank-based methods rankFCI, rankPC, rankGES, and rankGIES are close to their counterparts FCI, PC, GES and GIES. It is

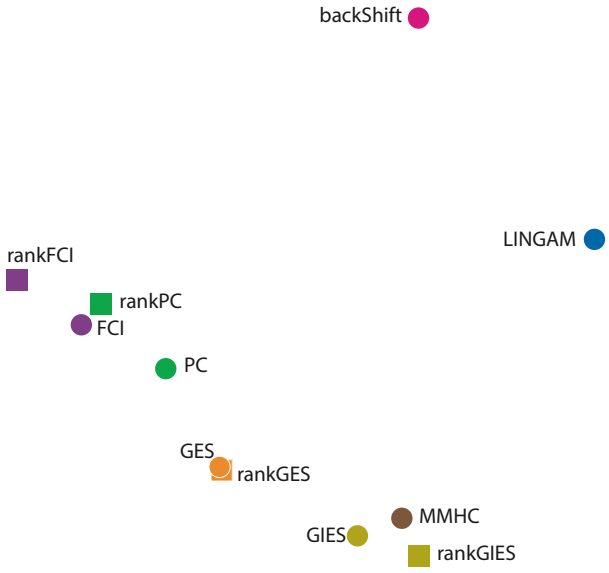

Figure 1

A multidimensional scaling (MDS) visualization of the methods considered in this review. The distance between two methods is taken to be the Euclidean distance between the equal-error rate of both methods across all settings for the `isAncestor` query. The MDS plot uses least-squares scaling.

somewhat unexpected that MMHC is closer to GIES and rankGIES than to PC and GES. The two methods that have the largest average distance to the other methods are LINGAM and backShift. This is perhaps expected, as these methods are of a very different nature than the other methods.

Figure 2 shows an MDS plot based on distances between the simulation settings, again using least-squares scaling. Thus, each point in the plot now corresponds to a simulation setting. The points are colored according to the best-performing method. We see that the regions where either LINGAM or backShift is optimal are relatively well separated, while the regions where GIES, MMHC, PC, GES, FCI, or their rank-based versions are optimal do not show a clear separation, as perhaps already expected from the previous result in **Figure 1**.

4.3.2. Pairwise comparisons. Next, we investigate whether there are methods that dominate the others. We compare the E-ER across all of the different settings in **Table 2**. It is apparent that no such dominance is visible among different pairs of methods. A block-structure is visible, however, with similar groups as in **Figure 1**. One block is formed by the constraint-based methods {PC, rankPC, FCI, rankFCI}: The E-ER of constraint-based methods is hardly ever substantially different. The second block is formed by the score-based approaches {GES, rankGIES}, and the third is given by the extensions and hybrid methods {GIES, rankGIES, MMHC}. This latter block is of interest, as MMHC makes fewer assumptions about the available data and does not need to know where interventions occurred. LINGAM and backShift do not fit nicely into any block in the empirical comparison and are more orthogonal to the other algorithms in that they perform substantially better *and* substantially worse in many settings, if compared with the other approaches.

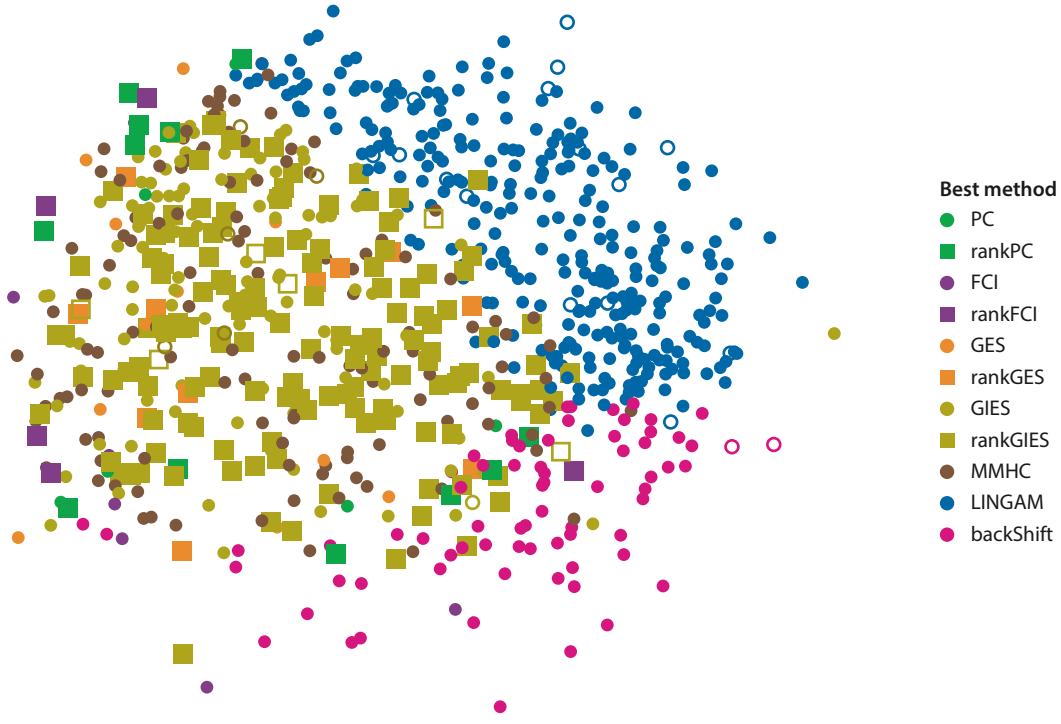

Figure 2

A multidimensional scaling (MDS) visualization of the simulation settings. The distance between two simulation settings is taken to be the correlation distance between the equal-error rate of both simulation settings across all methods for the `isAncestor` query. Each setting is shown as a sample point with color coding for the best-performing method. A filled symbol indicates that the performance metric was smaller than 0.3 and an unfilled symbol that it was larger. MDS uses least-squares scaling.

Table 2 A pairwise comparison of structure learning methods

	PC	rankPC	FCI	rankFCI	GES	rankGES	GIES	rankGIES	MMHC	LINGAM	backShift
PC	0	6	10	16	1	1	1	0	0	14	20
rankPC	0	0	9	10	1	2	0	0	0	11	17
FCI	1	9	0	5	1	1	1	0	0	11	17
rankFCI	0	1	0	0	1	1	0	0	0	10	16
GES	5	15	16	23	0	0	1	0	0	16	26
rankGES	6	15	16	24	0	0	1	0	1	16	25
GIES	18	29	26	35	10	11	0	0	2	25	35
rankGIES	26	36	34	44	17	17	4	0	1	27	38
MMHC	21	33	30	40	16	17	5	0	0	23	36
LINGAM	29	34	34	38	27	27	19	14	14	0	31
backShift	18	23	24	29	16	16	9	5	7	13	0

Each column shows the percentage of settings where methods were better by a margin of at least 0.1 in the equal-error rate compared with other methods in the given column. For example, LINGAM beats PC in 14% of the settings, while PC beats LINGAM by the given margin in 29% of the settings. There is no globally dominant algorithm, and a block-structure among related algorithms is visible. Abbreviations: FCI, fast causal inference; GES, greedy equivalence search; GIES, greedy interventional equivalence search; LINGAM, linear non-Gaussian acyclic models; MMHC, max-min hill climbing; PC, Peter-Clark.

Table 3 Marginal rank correlations between equal-error rate performance (for the `isAncestor` query) and parameter settings (shown only if absolute value exceeds 0.1, multiplied by 100, and rounded to the nearest multiple of 5)

	PC	rankPC	FCI	rankFCI	GES	rankGES	GIES	rankGIES	MMHC	LINGAM	backShift
n		15		10							−15
p	45	45	25	25	40	35	35	40	45	40	75
df_ε										15	
ρ_ε	50	60	55	60	55	55	65	50	50	35	
ω	10	10	10	10	15	10	20	15	10		20
p_s	20	15	20	15	25	25	25	30	30	15	25
do-interv			−10	−10							
n_I											
σ_Z	−35	−25	−35	−30	−35	−35	−25	−35	−30		−30
cyclic			−15	−15						35	
w_c			−15	−15						35	
nonlinear										20	

A positive value for p indicates, for example, that the method becomes less successful with increasing p. Abbreviations: FCI, fast causal inference; GES, greedy equivalence search; GIES, greedy interventional equivalence search; LINGAM, linear non-Gaussian acyclic models; MMHC, max-min hill climbing; PC, Peter-Clark.

4.3.3. Which causal graphs can be estimated well?. Which graphs can be estimated by some or all methods? To start answering the question, we show in **Table 3** the rank correlation between the E-ER for the `isAncestor` query and parameter settings for all methods. We see that the number of variables p and the strength of the hidden variables ρ_ε show the highest correlations. In both cases the correlation is positive, indicating that increased p or ρ_ε leads to higher E-ERs. Other parameters that show substantial correlations are ω, p_s, and σ_Z. For ω and p_s, we again see positive correlations, indicating that large noise contributions and denser graphs are associated with higher E-ERs. The correlation with σ_Z is negative for all methods except for LINGAM. While it is expected that backShift would benefit from strong interventions, the benefit for, for example, PC and FCI is unexpected.

We note that the strong effect of ρ_ε can be explained by the fact that we created a correlation ρ_ε between all pairs of noise variables. It is not surprising that this has a larger impact than adding, for example, a single cycle to the graph (which only seems to substantially affect the performance of LINGAM).

Figure 3 shows the average E-ER for the `isAncestor` query for each method as a function of the simulation parameters ρ_ε, ω, p_s, and σ_Z as identified from **Table 3**, split according to the number of variables p in the graph (small, medium-sized and large graphs). **Figure 4** shows the scaling of runtime with the number of variables. Again, we see that the size of the graph p and the strength of the hidden variables ρ_ε have the strongest effect on performance, with the exception that backShift is not much affected by ρ_ε (but this method is also perhaps less competitive in the absence of latent confounding). The strength of the interventions, the sparsity of the graph, and the signal-to-noise ratio also affect the average performance, but perhaps to a lesser extent.

The following are some other observations:

1. The most surprising outcome is perhaps that the number of samples n has only a very weak influence on the success despite it being varied between a few hundred and twenty thousand.

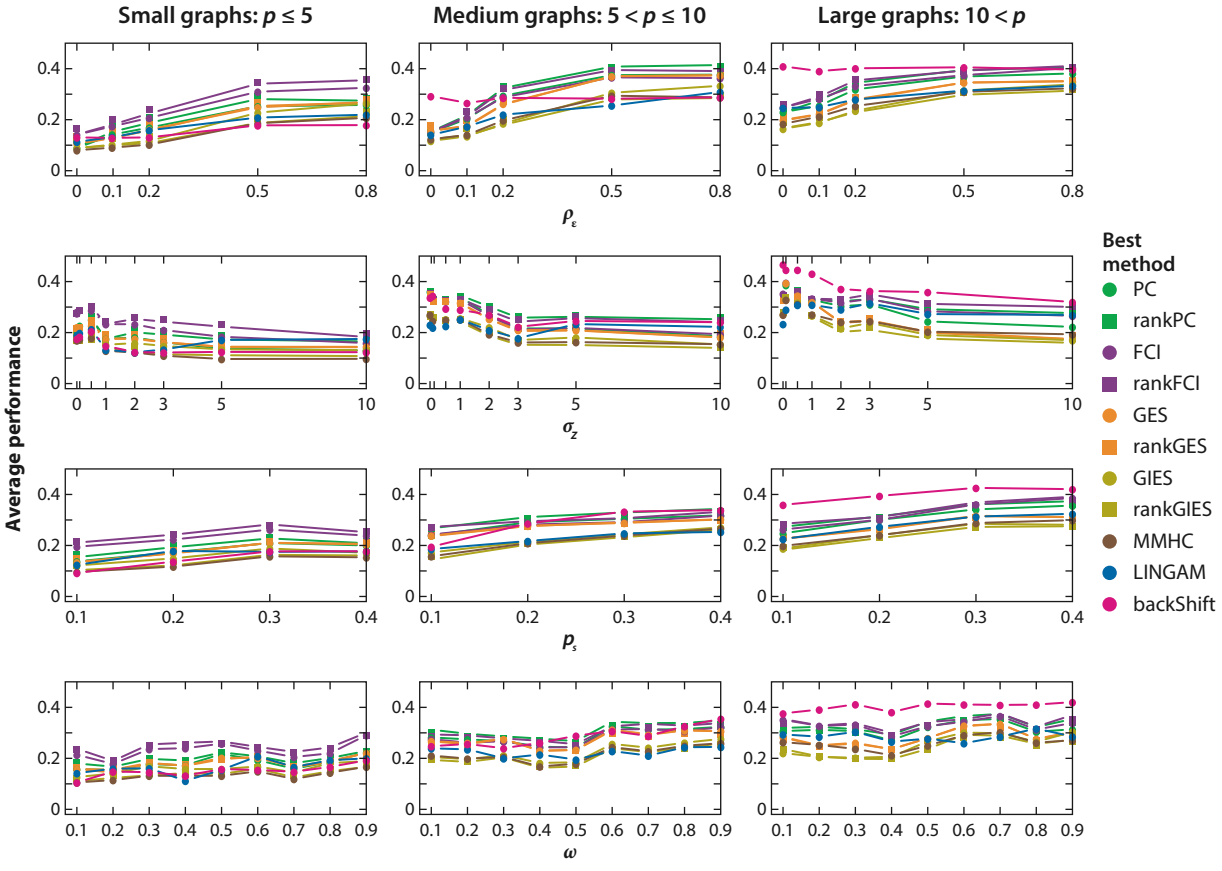

Figure 3

The average equal-error rate for the `isAncestor` query, for each method as a function of the four most important parameters (besides the number of variables p), ρ_ε, σ_Z, p_s, and ω.

2. Sparser graphs with fewer edges are consistently easier to estimate with all methods than dense graphs.
3. Less heavy tails in the error distribution have an adverse effect on the performance of LINGAM only, as it makes use of higher moments. LINGAM is also most affected when each variable undergoes a nonlinear transformation.
4. A cycle in the graph again has a detrimental effect on LINGAM (which is likely different in the version of LINGAM that allows for cycles; Lacerda et al. 2008).

4.3.4. Bounds on performance. The outcomes of the simulations show a large degree of variation. To further investigate the role of the number of variables p, we show in **Figure 5** the bounds of the performance as a function of p for the `isAncestor` query. Specifically, for each value of p, we consider the range of the four considered metrics when varying all other parameters for each method and show the lower and upper bounds in the figure.

The upper bounds show the worst performance across all parameters while holding p constant. They can be compared with the expected value under random guessing, which is 0.5 for the E-ER and AOC metrics and 1 for NFP-ER and NFN-ER.

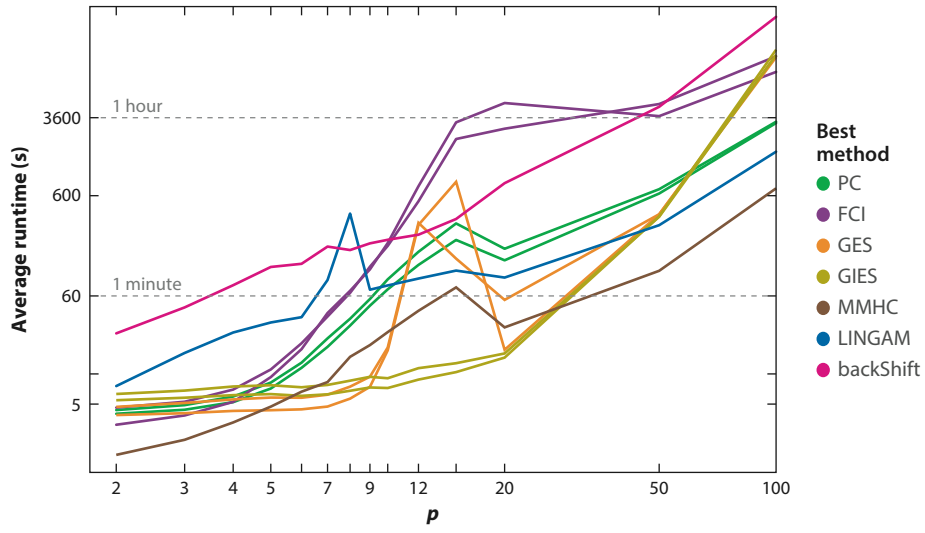

Figure 4

The average runtime in seconds of each method on a logarithmic scale as a function of the number of variables p on a logarithmic scale. The time includes the stability ranking. A single run is faster by a factor of 100 for all methods. (A single run of backShift already includes ten subsamples.)

The lower bound reveals in contrast the error rates in the best setting for a given p. The metric NFP-ER seems more difficult to keep at reasonable levels than NFN-ER, with the exception of LINGAM, which has very small values of NFP-ER in some settings up to $p \approx 20$. The NFN-ER is typically lower than NFP-ER, as there are typically more nonancestral pairs in the graphs (due to not connected components, for example) than ancestral pairs. This is confirmed by the third row of panels in **Figure 5**, which shows the error rates for the `isNoAncestor` query. Here, the roles of NFN-ER and NFP-ER are reversed owing to the relative abundance of nonancestral pairs.

5. DISCUSSION

We have tried to give a contemporaneous overview of structure learning for causal models that are available in R, and we have conducted an extensive empirical comparison. It is noteworthy that we found a clustering of methods into constraint-based approaches, score-based approaches, and other approaches that do not fall neatly into these categories. Methods from the same class behave empirically very similarly. We have also tried to quantify to what extent methods are negatively or positively affected by various parameters such as the size of the graph to learn, sparsity, and strength of hidden variables. The most important parameters in our setup are the size of the graph p and the strength of the hidden variables ρ_ε. An easily accessible interface to all methods is contributed as R package `CompareCausalNetworks`.

The results suggest that more efficient algorithms would be desirable from both a computational and a statistical point of view. As it stands, the success of the algorithms depends on both the assumptions made about the data-generating process (and how accurate these assumptions are) and the specific implementation details of each algorithm. It would be worthwhile for the relative importance of these two factors to be separated better by more modular estimation methods, and perhaps more work on worst-case bounds would also be beneficial. These latter bounds would allow quantifying to what extent the empirically poor statistical scalability is inherent to the problem or a consequence of choices made in the considered algorithms.

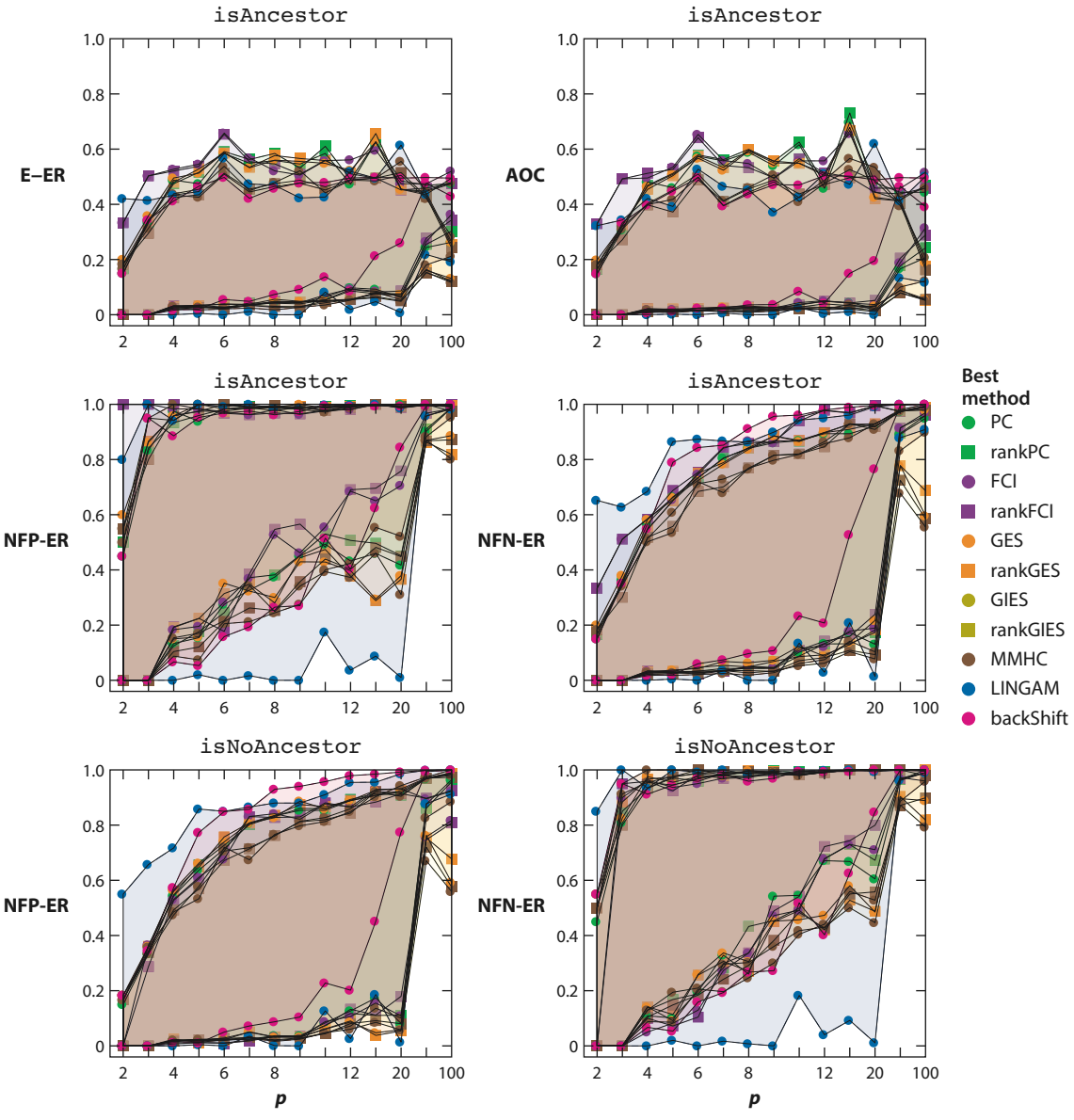

Figure 5

The range of equal-error rate (E-ER) for all methods as a function of the number of variables p for the `isAncestor` query (*top left panel*). The top right panel shows the same for the area over curve (AOC); the second row shows the no-false-positives error rate (NFP-ER) and no-false-negatives error rate (NFN-ER). The bottom row shows the corresponding plots to the second row but for the `isNoAncestor` query.

DISCLOSURE STATEMENT

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