Direct Learning with Guarantees of the Difference DAG Between Structural Equation Models

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Abstract

Discovering cause-effect relationships between variables from observational data is a fundamental challenge in many scientific disciplines. However, in many situations it is desirable to directly estimate the change in causal relationships across two different conditions, e.g., estimating the change in genetic expression across healthy and diseased subjects can help isolate genetic factors behind the disease. This paper focuses on the problem of directly estimating the structural difference between two structural equation models (SEMs), having the same topological ordering, given two sets of samples drawn from the individual SEMs. We present an principled algorithm that can recover the difference SEM in \(O(d^2 \log p)\) samples, where \(d\) is related to the number of edges in the difference SEM of \(p\) nodes. We also study the fundamental limits and show that any method requires at least \(\Omega(d' \log(p/d'))\) samples to learn difference SEMs with at most \(d'\) parents per node. Finally, we validate our theoretical results with synthetic experiments and show that our method outperforms the state-of-the-art. Moreover, we show the usefulness of our method by using data from the medical domain.

1 Introduction and Related Work

Discovering causal relationships from observational studies is of tremendous importance in many scientific disciplines. In Pearl's framework of causality [11], such cause-effect relationships are modeled using directed acyclic graphs (DAGs). One of the central problems in causal inference is then to recover a DAG of cause-effect relationships over variables of interest, given observations of the variables. It is well known that the number of samples needed to recover a DAG over \(p\) variables and maximum number of neighbors \(d\) grows as \(\Theta(\text{poly}(d) \log p)\) [5][7]. Therefore, the presence of hub nodes makes it especially challenging to recover the DAG from a few samples. In many situations however, the changes in causal structures across two different settings is of primary interest. For instance, the changes in structure of the gene regulatory network between cancerous and healthy individuals might help shed light on the genetic causes behind the particular cancer. In this case, estimating the individual networks over healthy and cancerous subjects is not sample-optimal since many background genes do not change across the subjects or even across distant species [15]. While the individual networks might be dense, the difference between them might be sparse.

In this paper, we focus on the problem of learning the structural differences between two linear structural equation models (SEMs) (or Bayesian networks) given samples drawn from each of the model. We assume that the (unknown) topological ordering between the two SEMs remains consistent, i.e., there are no edge reversals. This is a reasonable assumption in many settings and have also been considered by prior work [17]. For instance, edges representing genetic interactions may appear or disappear or change weights, but generally do not change directions [2]. Furthermore, in the multi-task learning literature it is often assumed that the noise variances across different tasks are the same (c.f. [8]). Our primary goal in this paper is to develop an algorithm that directly learns the

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difference DAG by using a number of samples that depends only on the sparsity of the difference DAG. This is a much more challenging problem than structure learning of Bayesian networks since in the latter case when the causal ordering is known, structure learning boils down to regressing each variable against all other variables that come before it in the topological order and picking out the non-zero coefficients. However, the fact that the individual DAGs are dense, rules out performing regressions in the individual model and then comparing invariances of the coefficients across the two models.

The problem of learning the difference between undirected graphs (or Markov random fields) has received much more attention than the directed case. For instance [19] develop algorithms for estimating the difference between Markov random fields and Ising models with finite sample guarantees. Another closely related problem is estimating invariances between causal structure across multiple environments [12]. However, this is desirable when the common structure is expected to be sparse across environments, as opposed to our setting where the difference is expected to be sparse.

The problem of estimating the difference between DAGs has been previously considered by [17], who developed a PC-style algorithm [14], which they call DCI, for learning the difference between the two DAGs by testing for invariances between regression coefficients and noise variances between the two models. However, sample complexity guarantees are hard to obtain for their method due to the use of many approximate asymptotic distributions of test statistics. Since the primary motivation behind directly estimating the difference between two DAGs is sample-efficiency, a lack of finite sample guarantees is a significant shortcoming. In contrast, our algorithm works by repeatedly eliminating vertices and re-estimating the difference of precision matrix over the remaining vertices. Thereby, we are able to leverage existing algorithms for computing the difference of precision matrix to obtain finite sample guarantees for our method. Furthermore, the DCI algorithm estimates regression coefficients (and noise variances) in the individual DAGs, while our method never estimates weights or noise variances of individual SEMs. Consider the example given in Figure 1 where the difference DAG contains only one edge \(X_4 \rightarrow X_2\). In order to prune the edges \(X_1 \rightarrow X_4\) and \(X_3 \rightarrow X_4\) which are present in the difference undirected graph but not in the difference DAG, DCI would compute regression coefficients \(\theta^1_{4|S}\) and \(\theta^2_{4|S}\) for all \(S \subseteq \{1, 2, 3\}\), where \(\theta^1_{j|S}\) (resp. \(\theta^2_{j|S}\)) denotes regression coefficients obtained by regressing \(X_j\) against \(X_S\) in the first (resp. second) SEM. For linear SEMs, estimating regression coefficients is equivalent to estimating the precision matrix (Lemma 1 in [6]). Furthermore, Danaher et al. [3] have shown that directly estimating the difference between precision matrices is more sample efficient than estimating individual precision matrices and computing the difference.

**Our contributions.** The above results therefore call for methods that estimate the difference DAG directly without computing individual SEM parameters. Towards that end, we make the following four contributions in this paper:

1. We are the first to obtain high-dimensional finite sample guarantees for the problem of directly estimating the structural changes between two linear SEMs. When the noise variances of the variables across the DAGs are the same our algorithm recovers the difference DAG in \(O(d^2 \log p)\) samples where \(d\) is the maximum number of edges in the difference of the moralized sub-graphs of the two SEMs, here the maximum is computed over subsets of variables. In the general (unequal noise variance) case, our method returns a partially directed DAG with the correct skeleton and orientation of the directed edges.
We present a series of results leading up to our main algorithm for direct estimation of the difference DAG in terms of the entries of the difference of precision matrix.

We will often index the two SEMs by \( \kappa \) with no children, of the difference DAG, where \( \kappa \) is an autoregression matrix and \( D = \text{Diag}(\{ \sigma_i^2 \}) \) is a diagonal matrix of noise variances. The SEM \((B, D)\) defines the following generative model over \( X \):

\[
X_i = B_{i\kappa} X + \varepsilon_i, \quad (\forall i \in [p]),
\]

\( B_{i\kappa} = 0, \ E[\varepsilon] = 0 \) and \( \text{Var}[\varepsilon] = \sigma_i^2 < \infty \). We will denote the \( i \)-th row (resp. \( i \)-th column) of a matrix \( A \) by \( A_i \) (resp. \( A_i \)). Note that our notation of a linear SEM disregards the distribution the noise variables and only considers their second moment as our algorithm only utilizes the second moment of variables. An autoregression matrix \( B \) encodes a DAG \( G = ([p], \text{supp}(B)) \) over \([p]\), where \( \text{supp}(\cdot) \) denotes the support set of a matrix (or a vector), i.e., \( \text{supp}(B) = \{(i, j) \in [p] \times [p] \mid B_{i,j} \neq 0\} \). Note that the edge \((i, j)\) indexes the directed edge \( i \leftarrow j \).

Given two SEMs, \((B^{(1)}, D^{(1)})\) and \((B^{(2)}, D^{(2)})\), our goal in this paper is to recover the structural difference between the two DAGs, i.e., \( \text{supp}(\Delta_B) \triangleq \text{supp}(B^{(1)} - B^{(2)}) \). We assume that each of the individual autoregression matrices \((B^{(1)} \text{ and } B^{(2)})\) to be potentially dense but their difference to be sparse. Specifically, we assume that each row and column of \( \Delta_B \triangleq B^{(1)} - B^{(2)} \) to have at most \( d \) (\( \ll p \)) non-zero entries. We further assume that there are no edge reversals between \( B^{(1)} \) and \( B^{(2)} \), thereby resulting in \( \text{supp}(\Delta_B) \) being a DAG, which, as stated in the introduction, is a reasonable assumption in several practical problems [19, 2]. Formally, we are interested in the following problem:

**Problem 1.** Given two sets of observations \( X^{(1)} \in \mathbb{R}^{n_1 \times p} \) and \( X^{(2)} \in \mathbb{R}^{n_2 \times p} \), drawn from the unknown SEMs \((B^{(1)}, D^{(1)})\) and \((B^{(2)}, D^{(2)})\) respectively, estimate \( \text{supp}(\Delta_B) \).

We will often index the two SEMs by \( \kappa \in \{1, 2\} \). We will denote the set of parents of the \( i \)-th node in the SEM indexed by \( \kappa \) by \( \pi^{(\kappa)}(i) \), while the set of children are denoted by \( \phi^{(\kappa)}(i) \). We will denote the difference between the precision matrices of the two SEMs by: \( \Delta_B \), and the precision matrix over any subset of variables \( S \subseteq [p] \) by \( \Delta_B^S \). Similarly, \( \Omega^{\kappa,i,j} \) denotes the precision matrix over the subset \( S \) in the SEM indexed by \( \kappa \). We will denote the set of topological ordering induced by a DAG \( G = ([p], E) \) by \( T(G) = \{(\tau_1, \ldots, \tau_p) \in \Pi([p]) \mid (\tau_i, \tau_j) \in E \text{ if } i < j\} \), where \( \Pi([p]) \) is the set of permutations of \([p]\). The notation \( i \preceq_T j \) denotes that the vertex \( i \) comes before \( j \) (or \( i = j \)) in the topological order \( T \). Finally, we will always index precision matrices by vertex labels, i.e., \( \Omega_{i,j} \) denotes the precision matrix entry corresponding to the \( i \)-th and \( j \)-th node of the graph.

**3 Results**

We present a series of results leading up to our main algorithm for direct estimation of the difference between two DAGs. The following result characterizes the terminal (or sink) vertices, i.e., vertices with no children, of the difference DAG in terms of the entries of the difference of precision matrix.

**Proposition 1.** Given two SEMs \((B^{(1)}, D^{(1)})\) and \((B^{(2)}, D^{(2)})\) and with precision matrices \( \Omega^{(1)} \) and \( \Omega^{(2)} \) respectively. If for any node \( i \) the edges incident on its children, and the corresponding noise variances remain invariant across the two SEMs, i.e., \( \forall j \in [p] : B_{i,j}^{(1)} = B_{i,j}^{(2)}, D_{i,j}^{(1)} = D_{i,j}^{(2)} \) and \( D_{i,i}^{(1)} = D_{i,i}^{(2)} \), then \( (\Delta_B)_{i,i} = 0 \). Furthermore, \( i \) is a terminal vertex in the difference DAG \( G = ([p], \Delta) \) with \( \Delta = \text{supp}(B^{(1)} - B^{(2)}) \).
The next result characterizes the edge weights and noise variances of the SEM obtained by removing a vertex \( i \), and plays a crucial role in developing our algorithm.

**Lemma 1.** Let \( (B, D) \) be a SEM with \( D = \text{Diag}(\{\sigma_j^2\}) \) and DAG \( G \). Then the SEM obtained by removing a subset of vertices \( U \subset [p] \), i.e., the SEM over \( X_{[p] \setminus U} \), is given by \((\tilde{B}, \tilde{D})\) with \( \tilde{D} = \text{Diag}(\{\tilde{\sigma}_j^2\}_{j \in [p] \setminus U}) \) and

\[
\tilde{\sigma}_j^2 = \sigma_j^2 \{ \sigma_k^2 - B_{j,U} (\Omega_j^A)_{U,U}^{-1} B_{j,U}^\top \}^{-1}, \quad \tilde{B}_{j,k} = \frac{\sigma_j^2}{\tilde{\sigma}_j^2} \left\{ B_{j,k} - B_{j,U} (\Omega_j^A)_{U,U}^{-1} (\Omega_j^A)_{U,k} \right\}
\]

\( \forall j \in [p] \setminus U \) and \( k \in A_j \), where \( A_j \) denotes the ancestors of node \( j \). Also, \( U_j = A_j \cap U \), and \( \Omega_j^A \) is the precision matrix over \( X_{A_j} \). Finally, for \( k \notin A_j \), \( \tilde{B}_{j,k} = 0 \).

As a corollary of the above lemma, we have the following result when \( U = \{ i \} \) and \( i \) is a terminal vertex, i.e., \( \phi(\tau)(i) = \emptyset \).

**Corollary 1.** Given a SEM \((B, D)\) with \( D = \text{Diag}(\{\sigma_j^2\})\), if \( i \) is a terminal vertex, then the SEM obtained by removing vertex \( i \) is given by \((B_{−1,−1}, D_{−1,−1})\).

With the above results in place, we are now ready to state our algorithm for learning the difference DAG. At a high level, the algorithm works as follows. Given the difference of precision matrix, we first remove the invariant vertices, i.e., vertices for which the corresponding rows and columns in the difference of precision matrix is all zeros. These vertices have no neighbors in the difference DAG and their noise variances remains the same across the two DAGs. Next, we estimate the topological ordering over the remaining vertices in the difference DAG. When the noise variances are the same, the algorithm returns a topological order over all the variables. Whereas when some of the noise variances differ between the two SEMs, then the topological order is computed over a subset of variables. After estimating the topological order, we orient the edges present in the difference of precision matrix according to the ordering to compute a super-graph of the difference DAG. We then perform a final pruning step to remove the “extra” edges to obtain the correct difference DAG. We show how all these steps can be performed by manipulating only the difference of precision matrix. Furthermore, estimating the topological order affords us with significant computational and statistical advantage as we will elaborate later.

First, we prove the correctness of Algorithm 1 in the population setting, i.e., when \( \Sigma^{(\kappa)} \) is the true covariance matrix of the SEM \((B^{(\kappa)}, D^{(\kappa)})\) for \( \kappa \in \{1, 2\} \). In this case \( \Delta_\Omega \) can be computed efficiently by solving the linear system: \( \Sigma^{(1)} (\Delta_\Omega) \Sigma^{(2)} = \Sigma^{(2)} - \Sigma^{(1)} \). Since \( \Sigma^{(\kappa)} \) is positive definite, the above system has a unique solution. To prove the correctness of our algorithm in the population setting we need the following assumption.

**Assumption 1.** Let \((B^{(1)}, D^{(1)})\) and \((B^{(2)}, D^{(2)})\) be two SEMs with the difference DAG given by \( \Delta_\Omega = ([p], \Delta) \), where \( \Delta = \text{supp}(B^{(1)} - B^{(2)}) \), and difference of precision matrix given by \( \Delta_\Omega \).

Let \( U = \{ i \in [p] \mid (\Delta_\Omega)_{i,i} = 0 \} \) and let \( V = [p] \setminus U \). Then the two SEMs satisfy the following assumptions:

(i) For \( i \in U \), the edges and noise variances are invariant.

(ii) Let \( S = \{ \tau_1, \ldots, \tau_k \} \subseteq [p] \) \( \tau \in T(\Delta_\Omega), 0 \leq k \leq |V| \). For each \((i, j) \in \Delta, \forall S \subseteq [p] \) such that \((i, j) \notin \Delta \), we have that \( \text{corr}^{(1)}(X_i, X_j | X_{S'}) \neq \text{corr}^{(2)}(X_i, X_j | X_{S'}) \), where \( S' = S \setminus \{i, j\} \).

In the above, \( \text{corr}^{(\kappa)}(\cdot) \) (resp. \( \text{corr}^{(\kappa)}(\cdot) \)) denotes partial correlation in the first (resp. second) SEM. Condition (i) in the above assumption essentially requires that none of the (undirected) edges incident on a vertex change in the moral graph of the two DAGs then the (directed) edges incident on the node remains invariant across the two DAGs. Condition (ii) above is essentially a restricted version of the faithfulness assumption which requires that if an edge \((i, j)\) changes across the two DAGs then \( X_i \perp \perp X_j \mid X_{S'} \).

The following theorem certifies the correctness of our algorithm in the population case, where \( \text{skel}(S) \) of a set of edges \( S \) denotes the undirected skeleton where the directed edges are converted to undirected edges, i.e., for all \((i, j) \in S, (j, i) \in \text{skel}(S) \).

**Theorem 1.** Let \( \Delta_\Omega = ([p], \Delta^*) \) be the true difference DAG, where \( \Delta^* = \text{supp}(B^{(1)} - B^{(2)}) \). Given the true covariance matrices \( \Sigma^{(1)} \) and \( \Sigma^{(2)} \), Algorithm 1 returns \( \Delta \) such that \( \text{skel}(\Delta) = \text{skel}(\Delta^*) \) and all the directed edges in \( \Delta \) are correctly oriented. Moreover, if \( D^{(1)} = D^{(2)} \) then \( \Delta = \Delta^* \).
Algorithm 1 Main algorithm

Input: $\Sigma^{(1)}$ and $\Sigma^{(2)}$
Output: $\Delta$

1: Estimate $\Delta_\Omega$
2: $V \leftarrow [p]$  \hfill \triangleright Set of invariant vertices
3: $U \leftarrow \{i \mid (\Delta_\Omega)_{i,\ast} = 0\}$ \hfill \triangleright Set of invariant vertices
4: $\Delta_\Omega \leftarrow (\Delta_\Omega)_{\cup U, \cup U}$
5: $\Sigma^{(1)} \leftarrow \Sigma_{\cup U, \cup U}^{(1)}$; $\Sigma^{(2)} \leftarrow \Sigma_{\cup U, \cup U}^{(2)}$
6: $V \leftarrow V_U$
7: $O, R \leftarrow \text{COMPUTEORDER}(\Delta_\Omega, \Sigma^{(1)}, \Sigma^{(2)}, V)$
8: $\Delta \leftarrow \text{ORIENTEDGES}(\Delta_\Omega, O, R)$
9: $\Delta \leftarrow \text{PRUNE}(\Delta, \Delta_\Omega, \Sigma^{(1)}, \Sigma^{(2)}, O, R)$
10: return $\Delta$

1: function $\text{ORIENTEDGES}(\Delta_\Omega, O, R)$
2: $\Delta \leftarrow \emptyset$
3: for $S \in O$ do
4: for $i \in S$ do
5: $N_i \leftarrow \{j \neq i \mid (\Delta_\Omega)_{i,j} \neq 0\}$
6: for $j \in N_i$ do
7: if $(j, i) \notin \Delta$ and $j \notin S$ then add $(i, j)$ in $\Delta$
8: $\Delta \leftarrow \Delta \cup \text{supp}((\Delta_R)_{O,R})$
9: return $\Delta$

1: function $\text{COMPUTEORDER}(\Delta_\Omega, \Sigma^{(1)}, \Sigma^{(2)}, V)$
2: $O \leftarrow \emptyset$ \hfill \triangleright Topological order
3: while $|V| > 1$ do
4: $S \leftarrow \{i \mid (\Delta_\Omega)_{i,\ast} = 0\}$
5: if $S = \emptyset$ then
6: return $O, V$
7: Add $S$ to end of $O$
8: Remove the vertices in $S$ from $V$
9: Re-estimate $\Delta_\Omega$ over $V$
10: Add $V$ to end of $O$
11: return $O, \emptyset$

Proof Sketch of Theorem 1. Let $V' = [p] \setminus U$, where $U$ is the set of invariant vertices defined in line 3 of the main algorithm. Let $T(\Delta_G)$ be the set of topological orderings induced by the true difference DAG. The correctness of Algorithm 1 follows from the following claims (proved in detail in Appendix A).

Claim (i): Denote the SEMs obtained by removing the vertices in $U$ from the initial SEMs $(B^{(\kappa)}, D^{(\kappa)})$ by $(\tilde{B}^{(\kappa)}, \tilde{D}^{(\kappa)})$, for $\kappa \in \{1, 2\}$ respectively. Then we have that $\tilde{D}^{(1)} = \tilde{D}^{(2)} = \text{Diag}((\tilde{\sigma}_{j,i})_{j \in V'}); \text{supp}(\tilde{B}^{(1)} - \tilde{B}^{(2)}) = \text{supp}(B^{(1)} - B^{(2)}) = \Delta^*.$

Claim (ii): The function $\text{COMPUTEORDER}$ returns a list of sets $O = (S_1, \ldots, S_m)$ such that for every $i \in S_a$ and $j \in S_b$ with $a < b$, we have $i \prec \tau_j$ for some $\tau \in T(\Delta_G)$. The set of vertices in $R$ occurs before all the vertices in $O$ in the causal order $\tau$ for all $\tau \in T(\Delta_G)$.

Claim (iii): For $O = (S_1, \ldots, S_m)$ and any $i, j \in S_a$ for $a \in [m]$, the nodes $i$ and $j$ do not have an edge between them in $\Delta^*$.

Claim (iv): The function $\text{ORIENTEDGES}$ returns a $\Delta$ such that $\Delta \supseteq \Delta^*$.

Claim (v): The function $\text{PRUNE}$ returns a $\Delta$ such that $\text{skel}(\Delta) = \text{skel}(\Delta^*)$. Further, if $D^{(1)} = D^{(2)}$ then $\Delta = \Delta^*$.

Computational Complexity. Note that the $\text{ORIENTEDGES}$ step already removes quite a few edges from the difference DAG. Then in the $\text{PRUNE}$ step, for those edges in the difference of the precision matrix that are incident on variables present in $O$, we only test over subsets that are descendants of the nodes. Whereas, the method of [17] test for subsets over all $[p] \setminus U$ vertices for each edge in the difference of the precision matrix. Thus, our method is strictly more efficient than that of [17]. Further, the computational complexity of our algorithm lies between two extremes. When the noise variances are the same, we have $R = \emptyset$ and our algorithm runs most efficiently. While, if all the noise variances are different, i.e., $D_{i,i}^{(1)} \neq D_{i,i}^{(2)}$ for all $i$, then $O = \emptyset$ while $R = V$ and the computational complexity of our algorithm is the same as [17] in terms of the number of tests performed during pruning.
3.1 Finite-Sample Guarantees

In this section, we derive finite sample guarantees for our algorithm. The performance of our method depends on how accurately the difference between the precision matrices are estimated. The problem of directly estimating the difference between the precision matrices of two Gaussian SEMs (or more generally Markov Random Fields), given samples drawn from the two individual models, has received significant attention over the past few years [19, 1, 18, 9]. Among these, the KLEIP algorithm of [9] and the algorithm of [19] come with provable finite sample guarantees. We use the algorithm of [19] for estimating the difference of precision matrices. Given sample covariance matrices $\hat{\Sigma}^{(1)}$ and $\hat{\Sigma}^{(2)}$, [19] estimate the difference of precision matrix by solving the following optimization problem:

$$\hat{\Delta}_\Omega = \arg\min_{\Delta_\Omega} \| \Delta_\Omega \|_1 \text{ subject to } \left| \hat{\Sigma}^{(1)} \Delta_\Omega \hat{\Sigma}^{(1)} - \hat{\Sigma}^{(2)} \right|_{\text{max}} \leq \lambda_n,$$

where $\lambda_n$ is the regularization parameter and $\cdot |_{\text{max}}$ denotes maximum absolute value of the matrix. Denoting $\beta = \text{vec}(\Delta_\Omega)$ and by using the properties of Kronecker product, the above optimization problem can be written as follows:

$$\hat{\beta} = \arg\min_{\beta} \| \beta \|_1 \text{ subject to } \left| (\hat{\Sigma}^{(2)} \otimes \hat{\Sigma}^{(1)}) \beta - \text{vec}(\hat{\Sigma}^{(1)} - \hat{\Sigma}^{(2)}) \right|_{\text{max}} \leq \lambda_n. \quad (1)$$

However, to decouple the analysis of our algorithm from those of the algorithms for estimating the difference between precision matrices, we state our results with respect to a finite-sample oracle for estimation of the difference between precision matrices. Specifically, we make the following assumption:

**Assumption 2.** Given samples $X^{(1)} \in \mathbb{R}^{n_1 \times p}$ and $X^{(2)} \in \mathbb{R}^{n_2 \times p}$ drawn from two linear SEMs, there exists an estimator $\hat{\Delta}_\Omega$ for the difference between the precision matrices such that

$$\text{Pr}_{X_1,X_2} \left\{ \left| \hat{\Delta}_\Omega - \Delta_\Omega \right|_{\text{max}} \leq \varepsilon \right\} \geq 1 - \delta, \text{ if } \eta_1 \geq \eta_1(\varepsilon, \delta) \text{ and } \eta_2 \geq \eta_2(\varepsilon, \delta), \text{ for some } \varepsilon, \delta > 0$$

and functions $\eta_1, \eta_2$.

We will also need a finite sample version of the condition in Assumption 2 to obtain our finite sample guarantees.

**Assumption 3.** Let $(B^{(1)}, D^{(1)})$ and $(B^{(2)}, D^{(2)})$ be two SEMs with the difference DAG given by $\Delta_C = ([p], \Delta)$, where $\Delta = \text{supp}(B^{(1)} - B^{(2)})$, and difference of precision matrix given by $\Delta_\Omega$. Let $U = \{ i \in [p] \mid (\Delta_\Omega)_i,i = 0 \}$ and let $V = [p] \setminus U$. Then, the two SEMs satisfy the following assumptions:

(i) For $i \in U$, the edges and noise variances are invariant.

(ii) Let $S = \{ \{ \tau_1, \ldots, \tau_k \} \cup [p] \mid \tau \in T(\Delta_\Omega), 0 \leq k \leq |V| \}$. For each $(i, j) \in \Delta$ and for $S \subseteq S$:

$$i, j \in S, \text{ we have } \left| \text{corr}^{(1)}(X_i, X_j | X_S') - \text{corr}^{(2)}(X_i, X_j | X_S') \right| \geq \varepsilon, \text{ for } S' = S \setminus \{ i, j \} \text{ and for some } \varepsilon > 0.$$

**Remark 1.** The finite sample version of Algorithm 1 also takes as input a threshold $\varepsilon$, and thresholds the difference of precision matrices at $\varepsilon$.

The sample complexity of the finite sample algorithm depends on the number of non-zero entries (edges) in the difference of precision matrix. Throughout the course of our algorithm we compute difference of precision matrices over subsets $S \subseteq \mathcal{S}$, where $\mathcal{S}$ is defined in Assumption 3. In what follows, $d$ denotes the number of non-zero entries in the densest difference of precision matrix, i.e., $d = \max_{S \subseteq \mathcal{S}} \| \Delta_\Omega \|_0$. Our next theorems formally characterize the finite sample guarantees of our method given in Algorithm 1.

**Theorem 2.** Under Assumptions 2 and 3, let $\Delta_C = ([p], \Delta^*)$ be the true difference DAG, where $\Delta^* = \text{supp}(B^{(1)} - B^{(2)})$. Let $X^{(1)} \in \mathbb{R}^{n_1 \times p}$ be samples drawn from the two SEMs, and let $\hat{\Sigma}^{(\kappa)} = (1/n_\kappa) X^{(\kappa)\top} X^{(\kappa)}$ be the sample covariance matrices for $\kappa \in \{1, 2\}$. Given $\hat{\Sigma}^{(1)}, \hat{\Sigma}^{(2)}$ and $\varepsilon > 0$ as input, the finite sample version of Algorithm 1 returns $\Delta$ such that $\text{skel}(\Delta) = \text{skel}(\Delta^*)$ and all the directed edges in $\Delta$ are correctly oriented with probability at least $1 - \delta$ if $\eta_1 \geq \eta_1(\varepsilon, \delta)$ and $\eta_2 \geq \eta_2(\varepsilon, \delta)$ for some $\delta > 0$. Furthermore, if $D^{(1)} = D^{(2)}$ then $\Delta = \Delta^*$. 
Theorem 3 (Adapted from [19]). Let $\Sigma^{(1)}$ denote the true covariance matrices of the two SEMs respectively, for $\kappa \in \{1,2\}$. Also, let $X^{(\kappa)} \in \mathbb{R}^{n \times p}$ be samples drawn from the two SEMs, for $\kappa \in \{1,2\}$. Let $\Delta_{12}$ be the estimate of the difference of precision matrix obtained by solving (1). Define $K^\phi_{\text{max}} \overset{\text{def}}{=} \max_{i,j \neq (k,l)} |\Sigma^{(1)}_{i,j} \Sigma^{(2)}_{k,l}|$ and $K^d_{\text{min}} \overset{\text{def}}{=} \min_{i,j} \Sigma^{(1)}_{i,j} \Sigma^{(2)}_{i,j}$. Let $\lambda_{\min}(\cdot)$ denote the minimum eigenvalue of a matrix. If $K^\phi_{\text{max}} \leq \frac{\lambda_{\min}(\Sigma^{(1)}) \lambda_{\min}(\Sigma^{(2)})}{2\|\Delta_{12}\|_0}$, the regularization parameter, $\lambda_n$, and the number of samples, $n$, satisfy the following conditions:

$$n \geq \frac{C^2}{(K^d_{\text{min}})^2} \log \frac{2p}{\delta} \quad \text{and} \quad \lambda_n \geq C \sqrt{\frac{1}{n} \log \frac{2p}{\delta}},$$

where $C$ is a constant that depends linearly on $|\Delta_{12}|$. Let $\Delta^{(1)}$, $|\Sigma^{(1)}|_{\text{max}}$, and $\max(\Sigma^{(1)}_{i,i}, \Sigma^{(2)}_{i,i})$, then with probability at least $1 - \delta$ we have that $|\Delta_{12} - \Delta^{(1)}|_{\text{max}} \leq \varepsilon$.

For the proof of the above theorem, given in Appendix A, we adapt the proof of [19] to obtain finite sample results in the form required by Theorem 3. Specifically, we analyze the optimization problem given by (1), whereas [19] only estimate the upper diagonal of the difference of precision matrix $\Delta_{12}$ thereby improving the computational complexity of estimation at the cost of requiring more stringent conditions on the true covariance matrices. We also use concentration of covariance matrix results from [13] to obtain finite sample results in the form required by Theorem 3. From the above theorem we can conclude that the method of [19] requires an incoherence condition on the true covariance matrices — which is similar to known incoherence conditions for estimating precision matrices [13] — for direct estimation of the difference of precision matrices. Furthermore, the true difference of precision matrix essentially needs to have constant sparsity, i.e., the number of non-zero entries in the difference of precision matrix (\(\|\Delta_{12}\|_0\)) should be constant in the high-dimensional regime for the constant $C$ in the above theorem to not depend on $p$. Finally, we then have the following finite sample result on estimating the difference DAG using (1).

Corollary 2. Using (1) to estimate the difference of precision matrices, if $\min(n_1, n_2) = \Theta \left( \left( \frac{d^2}{\kappa^2} \right) \log \left( \frac{p}{\delta} \right) \right)$, $K^\phi_{\text{max}} \leq \frac{\lambda_{\min}(\Sigma^{(1)}) \lambda_{\min}(\Sigma^{(2)})}{2d}$, and $\lambda_n = \Omega \left( \sqrt{\frac{1}{n} \log \frac{2p}{\delta}} \right)$, where the constant $K^\phi_{\text{max}}$ is defined in Theorem 3 and the true difference DAG satisfies Assumption 3, then the following holds with probability at least $1 - \delta$. The finite sample version of Algorithm 1 returns $\Delta$ such that $\Delta = \Delta^*$ when $D^{(1)} = D^{(2)}$, otherwise $\text{skel}(\Delta) = \text{skel}(\Delta^*)$ and all the directed edges in $\Delta$ are correctly oriented.

The following proposition compares the sample complexity of our method against indirect methods that first learn the individual SEMs and then compute the difference. The detailed comparison can be found in Appendix B.

Proposition 2. If the incoherence condition $K^\phi_{\text{max}} \leq \frac{\lambda_{\min}(\Sigma^{(1)}) \lambda_{\min}(\Sigma^{(2)})}{2\|\Delta_{12}\|_0}$ is satisfied, then the sample complexity of our method is strictly better than indirect estimation methods [27], with the former only depending on $|\Delta_{12}|$ while the latter depending on $\|\Omega^{(\kappa)}\|_1^2$.

Lastly, in the absence of any sample complexity guarantees for DCI [17], it is difficult to make any theoretical comparison with it. However, given empirical results on the superiority of direct estimation methods for precision matrices [3], and that in the worst case when the noise variances are different, our method performs the same number of tests as [17] without computing individual regression coefficients, we believe our method to have strictly better sample complexity than [17].

### 3.2 Fundamental Limits

In this section, we obtain fundamental limits on the sample complexity of direct estimation of the difference DAG. Towards that end, we consider the minimax error of estimation which we define over the subsequent lines. Let $X^{(1)}$, $X^{(2)}$ be the two sets of $n$ samples generated from the product distribution $P^n = P^n_1 \times P^n_2$ where $P_\kappa$ corresponds to a Gaussian linear SEM for $\kappa \in \{1,2\}$. Let $P$ be the family of all such product distributions such that the DAGs $G^{(1)}$ and $G^{(2)}$ share the same causal order. We will denote the corresponding DAG for the distribution $P_\kappa$ by $G(P_\kappa)$ and we will denote the difference DAG by $\Delta_G(P)$. Let $\zeta$ be a decoder that takes as input the two sets of samples
Given a generative process described above, we generated 50 pairs of networks with $p = \{10, 50, 100\}$ variables with expected neighborhood size of $N_a = \{6, 35, 80\}$, respectively. That is, for each of those values of $p$, each network in the pair of DAGs is dense with expected number of $\{30, 875, 4000\}$ edges, respectively. We obtained that $\Delta = \Delta^*$ almost surely, after using our Algorithm \[1\] and the population covariance matrices as inputs.

Table 1: Following our generative process described above, we generated 50 pairs of networks with $p = \{10, 50, 100\}$ variables with expected neighborhood size of $N_a = \{6, 35, 80\}$, respectively. That is, for each of those values of $p$, each network in the pair of DAGs is dense with expected number of $\{30, 875, 4000\}$ edges, respectively. We obtained that $\Delta = \Delta^*$ almost surely, after using our Algorithm \[1\] and the population covariance matrices as inputs.

| $p$  | $N_a$ | Expected $|E|$ of each DAG | $\Pr\{\Delta = \Delta^*\}$ |
|------|-------|----------------------------|-----------------------------|
| 10   | 6     | 30                         | 1.0                         |
| 50   | 35    | 875                        | 1.0                         |
| 100  | 80    | 4000                       | 1.0                         |

$x$ and returns a difference DAG $\zeta(x)$. The minimax estimation error is then defined as:

$$p_{\text{err}} \overset{\text{def}}{=} \inf_{\zeta} \sup_{P \in \mathcal{P}} \Pr_{X \sim P^n} \{ \zeta(x) \neq \Delta_{G}(P) \},$$

where the infimum is taken over all decoders that take as input two sets of samples drawn from a distribution $P \in \mathcal{P}$ and return a difference graph. The following theorem lower bounds the minimax error.

**Theorem 4.** Given $n$ samples drawn from each of the two linear Gaussian SEMs with DAGs $G^{(1)}$ and $G^{(2)}$ such that the DAGs share the same causal order, and the difference DAG $\Delta_G$ is sparse with each node having at most $d'$ parents. If the number of samples $n \leq (d' / 2) \log(\sqrt{2d'} ) - (d' / p) \log 2$ then $p_{\text{err}} \geq 1/2$, where $p_{\text{err}}$ is defined in (2).

**Remark 2.** To the best of our knowledge, Theorem 4 is the first information-theoretic lower bound to the minimax error of difference-DAG estimation. Our result sheds lights on the necessary number of samples for learning the difference DAG under any method, and shows the logarithmic dependence on the number of variables.

Next, we compare the sample complexity of our method against indirect methods that first estimate the individual SEMs and then compute the difference.

## 4 Experiments

In this section, we describe empirical results from running our Algorithm [1] on synthetic data with the goal of verifying our theoretical contributions. For the population case, we test graphs of size up to $p = 100$ nodes, while for the finite-sample case, we test graphs of small size due to high computational cost of indirect methods. We also provide a real-world experiment in Appendix C.2, where the number of nodes is $p = 157$.

**Generative process.** For generating a random SEM pair, we first generate an Erdős-Rényi random DAG on $p$ nodes with average neighborhood size $N_a$. Then, we generate the second DAG by deleting an existing edge or adding a new edge, consistent with the topological ordering of the first DAG, with probability 0.05 each. Thus, each DAG has an average of $pN_a/2$ edges out of $p(p-1)/2$ possible edges. We set the edge weights to be uniformly at random in the set $[-1, -0.25] \cup [0.25, 1]$, while noise variances are set to follow a normal distribution $\mathcal{N}(0, 1)$.

**Population setting.** As dictated by Theorem 4, Algorithm [1] should return the exact structural difference of SEMs if given the population covariance matrix of each SEM. In Table 1, we show that on graphs of up to $p = 100$ nodes, in effect, Algorithm [1] returns the true difference DAG.

**Finite-sample setting.** For experiments with a finite number of samples, we also follow our generative process above. We generate 50 pairs of DAGs with $p = 10$ and $N_a = 6$, and make sure that the pair of SEMs have $\varepsilon \geq 0.1$ in Assumption 3. We then generate $[e^C \log p]$ number of samples from each SEM for $C \in [5, 13]$. In Figure 2, we compare against the algorithms: PC [14], GES [10], MMHC [16], and LiSTEN [7], all of which first learn each SEM separately and then output the difference of adjacency matrices as the difference DAG. Finally, we also compare against the DCI-C method [17], which, as in our setting, also estimates the difference of SEMs. We note how traditional
Figure 2: (Left) Average of F1 scores and (Right) proportion of exact recovery, computed across 50 repetitions.

Figure 3: (Left) Average of F1 scores, and (Right) Prob. of exact recovery, computed across 50 repetitions. In this case the number of samples was set to $C = 9$ (see finite-sample setting).

state-of-the-art methods (PC, GES, MMHC, LiSTEN) suffer learning the difference DAG as each DAG independently is dense. The closest to our results is the DCI-C method, although, as seen in Figure 2 (Left), our algorithm performs better in the small sample complexity regime.

Remark 3. We emphasize that the reason to set $p = 10$ in the above experiment is due to the exponential computational cost of the PC algorithm for learning each dense SEM separately.

Unequal noise variance. We now set out to understand the performance of our algorithm when we set different noise variances. As shown above, the DCI-C algorithm [17] is the most comparable method to ours, thus, here we compare against it. For this experiment, we sampled pairs of SEMs under the same finite-sample setting. However, instead of fixing the noise variance to be one for all nodes, we set the noise variance for each node to be one of $\{1 - \gamma, 1, \gamma\}$ with probability $1/3$, where $\gamma$ is a noise parameter. In Figure 3, we note that we still achieve close-to-perfect recovery in a stable manner, while the performance of DCI-C decreases as the change in noise variance increases.
Additional experiments. To conclude our empirical results, we present two additional experiments in the appendix. In Appendix C.1 we empirically corroborate the logarithmic dependence on the number of variables, while in Appendix C.2 we show an experiment on a real-world dataset with \( p = 157 \) variables from the medical domain, which demonstrates the applicability of our method.

5 Conclusion

In this paper we considered the problem of directly estimating the difference-DAG of two linear SEMs, that share the same causal order, from samples generated from the individual SEMs. We showed that if the number of samples from each SEM grows as \( O \left( d^2 \log p \right) \) where \( d \) is the number of edges in the (densest) difference of moral sub-graphs, and under an incoherence condition on the true covariance and precision matrices, our algorithm recovers either the correct DAG or partially directed DAG with the correct skeleton and correct orientation of directed edges depending on whether or not the noise variances are the same. We also showed that any algorithm requires \( \Omega \left( d' \log(p/d') \right) \) samples to estimate the difference DAG consistently where \( d' \) is the maximum number of parents of a node in the difference DAG.

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A Detailed proofs

Proof of Lemma 7. From Proposition 3 of [7] we have that for a terminal vertex $j$: $\frac{1}{\sigma_j^2} = \Omega_{j,j}$. Thus for an arbitrary vertex $j$, the inverse of the noise variance of $j$ is given by the corresponding diagonal entry of the precision matrix obtained by removing all descendants of $j$. Further, the precision matrix over a subset of vertex $S \subseteq [p]$ is given by the Schur-complement $\Omega_{S,S} = \Omega_{S,S} - (\Omega_{S^c,S})^{-1}\Omega_{S^c,S}$, where $S^c$ denotes the complement of $S$. Note that $\mathcal{A}_j = \mathcal{A}_j \setminus U_j$, $\mathcal{A}_j^c = \mathcal{A}_j \cup U_j$, and $\mathcal{A}_j \cap U_j = \emptyset$. Therefore,

$\frac{1}{\sigma_j^2} = \Omega_{j,j} - (\Omega_{j,\mathcal{A}_j^c})(\Omega_{\mathcal{A}_j^c,\mathcal{A}_j})^{-1}(\Omega_{\mathcal{A}_j^c,j})$

$= \Omega_{j,j} - (\Omega_{j,\mathcal{A}_j^c},\Omega_{\mathcal{A}_j^c,j})\left[\frac{\Omega_{\mathcal{A}_j^c,\mathcal{A}_j^c}}{\Omega_{\mathcal{A}_j^c,j}}\right]^{-1}\left[\Omega_{\mathcal{A}_j^c,j}\right]$

$= \Omega_{j,j} - (\Omega_{j,\mathcal{A}_j^c},\Omega_{\mathcal{A}_j^c,j})\left[\frac{\Omega_{\mathcal{A}_j^c,\mathcal{A}_j^c} + P}{Q} + \frac{Q}{R}\right]\left[\Omega_{\mathcal{A}_j^c,j}\right]$,

where

$P \overset{\text{def}}{=} \Omega_{\mathcal{A}_j^c,\mathcal{A}_j^c}^{-1}\Omega_{\mathcal{A}_j^c,j}, R \overset{\text{def}}{=} 0$

$Q \overset{\text{def}}{=} -\Omega_{\mathcal{A}_j^c,\mathcal{A}_j^c}^{-1}\Omega_{\mathcal{A}_j^c,j}, R \overset{\text{def}}{=} \Omega_{\mathcal{A}_j^c,j}$

$= \Omega_{\mathcal{A}_j^c,\mathcal{A}_j^c}^{-1}\Omega_{\mathcal{A}_j^c,j}$

Now, writing

$\left[\frac{\sigma_{\mathcal{A}_j^c,\mathcal{A}_j^c} + P}{Q} + \frac{Q}{R}\right]\left[\Omega_{\mathcal{A}_j^c,j}\right]$, and some algebraic manipulations later we have that:

$\frac{1}{\sigma_j^2} = \frac{1}{\sigma_j^2} - (\Omega_{j,\mathcal{A}_j^c},\Omega_{\mathcal{A}_j^c,j},\Omega_{\mathcal{A}_j^c,j} - \Omega_{j,\mathcal{A}_j^c,j})R \times$

$(\Omega_{\mathcal{A}_j^c,\mathcal{A}_j^c}^{-1}\Omega_{\mathcal{A}_j^c,j},\Omega_{\mathcal{A}_j^c,j} - \Omega_{\mathcal{A}_j^c,j})$

$= \frac{1}{\sigma_j^2} - (\Omega_{j,\mathcal{A}_j^c},(\Omega_{\mathcal{A}_j^c,j}^{-1}\Omega_{\mathcal{A}_j^c,j})^{-1}(\Omega_{\mathcal{A}_j^c,j})$

$= \frac{1}{\sigma_j^2} - (\Omega_{\mathcal{A}_j^c,j}^{-1}\Omega_{\mathcal{A}_j^c,j})^{-1}(\Omega_{\mathcal{A}_j^c,j})$

where the last line follows from Proposition 4 of [7] since $j$ is a terminal vertex in the induced subgraph over $\mathcal{A}_j$. For characterizing the edge weights, observe once again that $j$ is a terminal vertex in the induced subgraph over $\mathcal{A}_j$, and therefore from from Proposition 4 of [7] we have that:

$\tilde{B}_{j,k} = -\frac{1}{\sigma_j^2}(\Omega_{j,k} - (\Omega_{j,\mathcal{A}_j^c})(\Omega_{\mathcal{A}_j^c,\mathcal{A}_j^c})^{-1}(\Omega_{\mathcal{A}_j^c,k}))$.

The final result follows from following the previously derived steps for the noise variance.

Proof of Theorem 7. Let $V' = [p] \setminus U$ and let $p' = |V'|$, where $U$ is the set of invariant vertices defined in line [3] of the main algorithm. Denote the two initial DAGs by $G^{(1)}$ and $G^{(2)}$. Let $T(\Delta_G)$ be the set of topological orderings induced by the true difference DAG. The correctness of Algorithm 1 follows from the following claims, which we prove subsequently.
• **Claim (i):** Denote the SEMs obtained by removing the vertices in $U$ from the initial SEMs $(B^{(1)}, D^{(1)})$ by $(\tilde{B}^{(1)}, \tilde{D}^{(1)})$, for $\kappa \in \{1, 2\}$ respectively. Then we have that $\tilde{D}^{(1)} = \tilde{D}^{(2)} = \text{Diag}(\{\tilde{\sigma}_j\}_j \in V')$, and $\text{supp}(\tilde{B}^{(1)} - \tilde{B}^{(2)}) = \text{supp}(B^{(1)} - B^{(2)}) = \Delta^*$. 

• **Claim (ii):** The function `COMPUTEORDER` returns a list of sets $O = (S_1, \ldots, S_m)$ such that for every $i \in S_a$ and $j \in S_b$ with $a < b$, we have $i \prec_j$ for some $\tau \in T(\Delta_G)$.

• **Claim (iii):** For $O = (S_1, \ldots, S_m)$ and any $i, j \in S_a$ for $a \in [m]$, the nodes $i$ and $j$ do not have an edge between them in $\Delta^*$.

• **Claim (iv):** The function `ORIENTEDGES` returns a $\Delta$ such that $\Delta \supseteq \Delta^*$.

**Proof of Claim (i).** Lemma [1] gives the characterization $(\tilde{B}^{(1)}, \tilde{D}^{(1)})$ for $\kappa \in \{1, 2\}$. By Assumption [1](i) we have that for each $j \in U$, $B^{(1)}_{i,j} = B^{(2)}_{i,j} \forall k$. Note that by definition of $U$, for any $u, v \in U$, we have that $\Omega^{(1)}_{u,v} = \Omega^{(2)}_{u,v}$. Next we will show that for any node $j \in V'$, $\Omega^{(1,A_j)} = \Omega^{(2,A_j)}$ for any $u, v \in U_j$ (recall that $U_j = U \cap A_j$ and $A_j$ is the set of ancestors of $j$ in the topological order in the initial SEMs). Since $\Omega^{(\kappa,A_j)}$ is the precision matrix for the SEM obtained by removing $A'_j$, we have that for any $u, v \in U_j$, $A'_j$ contains vertices that occur after $u$ and $v$ in the causal order. Therefore by Lemma [1]

$$\Omega^{(1,A_j)}_{u,v} = -B^{(1)}_{u,i}/\sigma_u - B^{(1)}_{v,i}/\sigma_v + \sum_{l \in \phi^{(1)}(u) \cap \phi^{(2)}(v) \cap A_j} B^{(1)}_{l,i}/\sigma_l$$

$$= -B^{(2)}_{u,i}/\sigma_u - B^{(2)}_{v,i}/\sigma_v + \sum_{l \in \phi^{(2)}(u) \cap \phi^{(2)}(v) \cap A_j} B^{(2)}_{l,i}/\sigma_l$$

Therefore, once again by Lemma [1] we have that $\Omega^{(1,A_j)} = \Omega^{(2,A_j)}$ and thus $\tilde{\sigma}^{(1)}_j = \tilde{\sigma}^{(2)}_j = \tilde{\sigma}_j$, and $\tilde{B}_{i,j}^{(1)} = \tilde{B}_{i,j}^{(2)}$, $\forall j, k \notin U$, where $\tilde{\sigma}_j$ and $\tilde{B}_{i,j}$ are given by Lemma [1]. Thus we have that $\text{supp}(\tilde{B}^{(1)} - \tilde{B}^{(2)}) = \text{supp}(B^{(1)} - B^{(2)}) = \Delta^*$.

From this point onwards all the arguments will be w.r.t. the two SEMs $(\tilde{B}^{(1)}, \tilde{D})$ and thus $\Delta_G$ will denote the difference of precision matrix over $(\tilde{B}^{(1)}, \tilde{D})$ and $(\tilde{B}^{(2)}, \tilde{D})$ having DAGs $\tilde{G}^{(1)}$ and $\tilde{G}^{(2)}$.

**Proof of Claim (ii).** From Assumption [1](i) and Proposition [1] we have that $i$ is a terminal vertex in $\Delta_G$ if and only if $(\Delta_G)_{i,i} = 0$. From Lemma [1] we have that removing a set of vertices does not change the topological ordering, i.e., $T(\tilde{G}^{(1)}) \subseteq T(G^{(1)})$, for $\kappa \in \{1, 2\}$. Therefore, the order in which the vertices are eliminated by the function `COMPUTEORDER` is consistent with the topological order of the difference DAG.

**Proof of Claim (iii).** For any two vertices $i, j$ such that $i, j \in S_a$ for $a \in [m]$, that means $i$ and $j$ were eliminated in the same iteration and $(\Delta_G)_{i,i} = (\Delta_G)_{j,j} = 0$. However, if $(i, j) \in \Delta^*$ then by Assumption [1](ii) $(\Delta_G)_{i,j} \neq 0$. Therefore, $(i, j) \notin \Delta^*$.

**Proof of Claim (iv).** From Assumption [1](ii) we have that for any $(i, j) \in \Delta^*$, $(\Delta_G)_{i,j} \neq 0$. Also by Claim (ii) we have that the ordering $O$ is consistent with the topological ordering of the difference DAG $\Delta_G$. Therefore, we have that $\Delta \supseteq \Delta^*$.

**Proof of Claim (v).** Let $\Delta'$ denote the set of edges returned by `ORIENTEDGES`. For any $(i, j) \in \Delta' \setminus \Delta^*$ we have that $(\Delta_G)_{i,j} \neq 0$ and $i, j \notin S_a$ for some $S_a \in O$. Then we have that

$$(\Delta_G)_{i,j} = \sum_{l \in CC^{(1)}_{i,j}} 1/\tilde{\sigma}^{(1)}(\tilde{B}^{(1)}_{i,l} \tilde{B}^{(1)}_{l,j}) - \sum_{l \in CC^{(2)}_{i,j}} 1/\tilde{\sigma}^{(2)}(\tilde{B}^{(2)}_{i,l} \tilde{B}^{(2)}_{l,j})$$

where $CC^{(\kappa)}_{i,j} = \phi^{(\kappa)}(i) \cap \phi^{(\kappa)}(j)$ is the set of common children of $i$ and $j$ in the SEM indexed by $\kappa$. Therefore, if we remove the nodes $CC^{(1)}_{i,j} \cup CC^{(2)}_{i,j}$ from $V'$ and compute the difference of
precision matrix over \(S = V' \setminus CC_{i,j}^{(1)} \cup CC_{i,j}^{(2)}\), then by Lemma 1 \((\Delta_{ij}^S)_{i,j} = 0\). Since the nodes \(CC_{i,j}^{(1)} \cup CC_{i,j}^{(2)}\) are descendants of \(i\) and \(j\) in the difference DAG, the function PRUNE will correctly remove the edge \((i, j)\). Thus if \(\Delta\) is the set returned by PRUNE then \(\Delta = \Delta^*\).

**Proof of Theorem 2** Note that by Assumption 2 \(\|\hat{\Delta}_\Omega - \Delta_\Omega^S\|_{\max} \leq \varepsilon\) holds with probability at least \(1 - \delta\) simultaneously over all subsets \(S \subseteq [p]\). Therefore, in the finite sample version given an \(\varepsilon\)-accurate estimate of \(\Delta_\Omega\) and thresholding \(\Delta_\Omega\) at \(\varepsilon\), we have that each line involving \(\Delta_\Omega\) holds (by Assumption 3) with probability at least \(1 - \delta\) simultaneously. So the claim follows.

**Proof of Theorem 3** For the purpose of the proof, symbols superscripted by \(*\) will correspond to “true” objects (e.g. true covariance matrix), while symbols with a hat will denote the corresponding finite sample estimates. Let \(\hat{\Sigma} = \Sigma^{(1)} \otimes \Sigma^{(2)}, \Sigma^* = \Sigma^{(1)} \otimes \Sigma^{(2)}, \hat{b} = vec(\hat{\Sigma} - \hat{\Sigma}^2)\) and \(\beta^* = vec(\Delta_\Omega^S)\), where \(\Delta_\Omega^S\) is the true difference of precision matrices. Then,

\[
[S^*(\hat{\beta} - \beta^*)]_i = \sum_j \Sigma^*_{i,j}(\hat{\beta}_j - \beta^*_j) = \Sigma^*_{i,i}(\hat{\beta}_i - \beta^*_i) + \sum_{j \neq i} \Sigma^*_{i,j}(\hat{\beta}_j - \beta^*_j)
\]

\[
\Rightarrow \left| [S^*(\hat{\beta} - \beta^*)]_i - \Sigma^*_{i,i}(\hat{\beta}_i - \beta^*_i) \right| = \left| \sum_{j \neq i} \Sigma^*_{i,j}(\hat{\beta}_j - \beta^*_j) \right| (\forall i \in [p])
\]

\[
\Rightarrow K_{\min}^d |\hat{\beta}_i - \beta^*_i| \leq \frac{\sum_{j \neq i} |\Sigma^*_{i,j}|}{(a)} + \left| [S^*(\hat{\beta} - \beta^*)]_i \right| (\forall i \in [p])
\]

\[
\Rightarrow K_{\min}^d \left\| \hat{\beta} - \beta^* \right\|_1 \leq K_{\max}^o \left\| \hat{\beta} - \beta^* \right\|_1 + \left\| S^*(\hat{\beta} - \beta^*) \right\|_\infty , \tag{3}
\]

where (a) follows from reverse triangle inequality and (b) follows from taking max over \(i\). To upper bound \(\left\| \hat{\beta} - \beta^* \right\|_1\), we need to upper bound \(\left\| \hat{\beta} - \beta^* \right\|_1\) and \(\left\| S^*(\hat{\beta} - \beta^*) \right\|_\infty\). Next, we will upper bound \(\left\| \hat{\beta} - \beta^* \right\|_1\).

To upper bound \(\left\| \hat{\beta} - \beta^* \right\|_1\), assume that \(\beta^*\) is feasible (for which we will provide a proof at the end). Thus we have that \(\left\| \hat{\beta} \right\|_1 \leq \left\| \beta^* \right\|_1\). Let \(S\) be the support of \(\beta^*\), i.e., \(S \overset{def}{=} \{i \in [p] | \beta^*_i \neq 0\}\). Let \(S^c\) be the complement of the set \(S\). Then

\[
\left\| \hat{\beta}_S \right\|_1 + \left\| \hat{\beta}_{S^c} \right\|_1 \leq \left\| \beta^*_S \right\|_1
\]

\[
\Rightarrow \left\| \hat{\beta}_{S^c} \right\|_1 \leq \left\| \beta^*_S \right\|_1 - \left\| \hat{\beta}_S \right\|_1 \leq \left\| \beta^*_S - \hat{\beta}_S \right\|_1 \tag{4}
\]

From the above and the fact that \(\beta^*_{S^c} = 0\) we have

\[
\Rightarrow \left\| \beta^* - \hat{\beta} \right\|_1 \leq \left\| \beta^*_S - \hat{\beta}_S \right\|_1 + \left\| \beta^*_{S^c} - \hat{\beta}_{S^c} \right\|_1 \leq 2 \left\| \beta^*_S - \hat{\beta}_S \right\|_1 \tag{5}
\]

Next, let \(x = \hat{\beta} - \beta^*\) and \(\bar{x}_S = (\bar{x}_i)_{i \in [p]}\) such that

\[
\bar{x}_i = \begin{cases} x_i & i \in S \\ 0 & \text{otherwise} \end{cases}
\]
Next we have that
\[
\left| \hat{x}_S^T \Sigma^* x \right| = \left| \hat{x}_S^T \Sigma^* \bar{x}_S + \hat{x}_S^T \Sigma^* \bar{x}_{S^c} \right| \\
\geq \left| \hat{x}_S^T \Sigma^* \bar{x}_S \right| - \left| \hat{x}_S^T \Sigma^* \bar{x}_{S^c} \right| \\
\geq \lambda_{\text{max}}(\Sigma^*) \| x_S \|_2^2 - \sum_{i \in S} \sum_{j \in S^c} \Sigma_{i,j} x_i x_j \\
\geq \lambda_{\text{max}}(\Sigma^*) \| x_S \|_2^2 - K_{\text{max}} \sum_{i \in S} \sum_{j \in S^c} |x_i x_j| \\
\geq \lambda_{\text{max}}(\Sigma^*) \| x_S \|_2^2 - K_{\text{max}} \parallel x_S \parallel_1 \| x_{S^c} \parallel_1 \\
\quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \quad \ Quad
where $\Sigma^{(1)}$ and $\Sigma^{(2)}$ are the true covariance matrices corresponding to the true SEMs. From Lemma 1 of [13] and a union bound over $p^2$ entries of each $\hat{\Sigma}$ and $\hat{\Sigma}$, we have that with probability at least $1 - \delta$, for some $\delta \in (0, 1)$:

$$
\left\| \hat{\beta} - b^* \right\|_\infty \leq 2 \sqrt{\frac{c}{n} \log \frac{4p^2}{\delta}},
$$

(10)

where $c = 3200 \max_{\kappa \in \{1, 2\}} \max_{i \in [p]} (\Sigma^{(i)}_{i,i})^2$. Next, we will bound $\left\| \Sigma^* - \hat{\Sigma} \right\|_{\text{max}}$. For any $S \subseteq \Delta$, estimating the difference of precision matrix $\Sigma^{*}$ and $\hat{\Sigma}$, we have that with probability at least $1 - \delta$, for some $\delta \in (0, 1)$:

$$
\left\| \Sigma^* - \hat{\Sigma} \right\|_{\text{max}} \leq \max_{(a,b,c,d) \in [p]^4} \left| (\Sigma^{(a)}_{a,b})(\Sigma^{(c,d)}_{c,d}) - (\Sigma^{(a)}_{a,b})(\hat{\Sigma}^{(c,d)}_{c,d}) \right| = \max_{(a,b,c,d) \in [p]^4} \left| \Sigma^{(a)}_{a,b} - (\Sigma^{(a)}_{a,b} + \hat{\Sigma}^{(a)}_{a,b} + \Sigma^{(c,d)}_{c,d} - \hat{\Sigma}^{(c,d)}_{c,d}) \right| 
$$

$$
\leq \left\| \Sigma^{(a)}_{a,b} - \hat{\Sigma}^{(a)}_{a,b} \right\| + \left\| \Sigma^{(c,d)}_{c,d} - \hat{\Sigma}^{(c,d)}_{c,d} \right\| + \left\| \Sigma^{(a)}_{a,b} - \hat{\Sigma}^{(a)}_{a,b} \right\| 
$$

From Lemma 1 of [13] we have that with probability at least $1 - 2\delta$ the following hold:

$$
\left\| \Sigma^{(a)}_{a,b} - \hat{\Sigma}^{(a)}_{a,b} \right\| \leq \sqrt{\frac{c_1}{n} \log \frac{4}{\delta}}
$$

$$
\left\| \Sigma^{(c,d)}_{c,d} - \hat{\Sigma}^{(c,d)}_{c,d} \right\| \leq \sqrt{\frac{c_2}{n} \log \frac{4}{\delta}},
$$

where $c_\kappa = 3200 \max_{i \in [p]} (\Sigma^{(i)}_{i,i})^2$. Since, $n \geq \log(4/s)$ and taking a union bound over $2p^2$ entries of the empirical covariance matrices we get that with probability $1 - \delta$, for some $\delta \in (0, 1)$:

$$
\left\| \hat{\Sigma} - \Sigma^* \right\|_{\text{max}} \leq c' \sqrt{\frac{c}{n} \log \frac{8p^2}{\delta}},
$$

where $c' = \sqrt{\log \left( |\Sigma^{(1)}|_{\text{max}} + |\Sigma^{(2)}|_{\text{max}} \right)}$. This implies the lower bound on $\lambda_n$ is given as follows:

$$
\lambda_n \geq 2 \sqrt{\frac{2c}{n} \log \frac{2p^2}{\delta} + c' \left\| \beta^* \right\|_1 \sqrt{\frac{3c}{n} \log \frac{2p^2}{\delta}} \geq C \sqrt{\frac{1}{n} \log \frac{2p^2}{\delta}},
$$

where the constant $C$ is given in the statement of the theorem. Setting the estimation error to be at most $\epsilon$ implies the following upper bound on $\lambda_n$:

$$
\lambda_n \leq \frac{K_{\min}^d \epsilon}{6}.
$$

Setting $n$ as given in the theorem ensures that the lower bound in less than the upper bound. Lastly, we show that the $\beta^*$ is feasible. We have the following:

$$
\left\| \hat{\Sigma} \beta^* - \hat{\beta} \right\|_\infty = \left\| \hat{\Sigma} - \Sigma^* \right\| \beta^* - (\hat{\beta} - \Sigma^* \beta^*) + \Sigma^* \beta^* - b^* \right\|_\infty
$$

$$
\leq \left\| \hat{\Sigma} - \Sigma^* \right\| \beta^*_1 + \left\| \hat{\beta} - \Sigma^* \beta^* \right\|_\infty \leq \lambda_n,
$$

where the second line follows from the fact that $\Sigma^* \beta^* - b^* = 0$ and the triangle inequality, and the last line follows from the assumption on $\lambda_n$. 

\textbf{Proof of Corollary 2} To prove the corollary, we just need to show that for any subset $S \subseteq [p]$ estimating the difference of precision matrix $\Delta_{ii}^*$ using (1), satisfies Assumption 2. For any subset $S \subseteq [p]$ denote the corresponding covariance matrices by $\Sigma^{(i,S)}$, for $i \in \{1, 2\}$. Let $K_{\max}^{o,S} = \max \{ \Sigma^{(1)}_{i,j} \Sigma^{(2)}_{k,l} \mid i, j, k, l \in S, (i, j) \neq (k, l) \}$ and $K_{\min}^{d,S} = \min \{ \Sigma^{(1)}_{i,j} \Sigma^{(2)}_{k,l} \mid i \in [S] \}$. Since, for any $S$ $\lambda_{\min}(\Sigma^{(i,S)}) \geq \lambda_{\min}(\Sigma^{(i)})$ for $i \in \{1, 2\}$, and $K_{\max}^{o,S} \leq K_{\max}^{o}$, we have:

$$
K_{\max}^{o,S} \leq K_{\max}^{o} \leq \frac{\lambda_{\min}(\Sigma^{(1)}) \lambda_{\min}(\Sigma^{(2)})}{2d} \leq \frac{\lambda_{\min}(\Sigma^{(1)}) \lambda_{\min}(\Sigma^{(2)})}{2 \left\| \Delta_{ii}^* \right\|_0},
$$

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where ($a$) follows from the Assumption in the corollary. Therefore, we have that estimating $\Delta_{\Omega}^{S}$ using (1) satisfies the incoherence condition (Theorem 3) for each $S$. Next, since the constant $C = O(d)$ for any set $S$, we have that the condition on the number of samples and regularization parameter (Theorem 3) are satisfied as well. Next from Lemma 1 [13] we have that with probability at least $1 - \delta$ we have that simultaneously for both $\kappa \in \{1, 2\}$:

$$\left| \Sigma^{(\kappa)} - \hat{\Sigma}^{(\kappa)} \right|_{\max} \leq \sqrt{\frac{c}{n} \log \frac{4p^2}{\delta}},$$

where $c = 3200 \max_{\kappa \in \{1, 2\}} \max_{i \in [p]} (\Sigma^{(\kappa)}_{i,i})^{2}$. Thus, we have that with probability at least $1 - \delta$ and simultaneously for all $S \subseteq [p]$ and $\kappa \in \{1, 2\}$

$$\left| \Sigma^{(\kappa, S)} - \hat{\Sigma}^{(\kappa, S)} \right|_{\max} \leq \sqrt{\frac{c}{n} \log \frac{4p^2}{\delta}}.$$

From the proof of Theorem 3 it is clear that using $\hat{\Sigma}^{(\kappa)}$ in (1) such that $\left| \Sigma^{(\kappa)} - \hat{\Sigma}^{(\kappa)} \right|_{\max} \leq \sqrt{\frac{c}{n} \log \frac{4p^2}{\delta}}$, we get an estimate $\hat{\Delta}_{\Omega}^{S}$, by solving (1), which satisfies $\left| \hat{\Delta}_{\Omega}^{S} - \Delta_{\Omega}^{S} \right|_{\max} \leq \varepsilon$. Combined with the fact that for each $S$ the condition required as per Theorem 3 for $n, \lambda_{n}$, and $K^{\kappa, S}_{\text{max}}$ are satisfied, we get that the finite sample algorithm that uses (1) to estimate the difference of precision (sub-)matrices satisfies Assumption 2. Thus, the final claim follows as per Theorem 2. \hfill $\square$

**Proof of Theorem 4.** Given two graphs $G = ([p], E)$ and $G' = ([p], E')$, let $G \oplus G' \overset{\text{def}}{=} ([p], (E \setminus E') \cup (E' \setminus E))$ denote the graph obtained by taking edges exclusive to the graphs $G$ and $G'$ and removing edges common to them. Let $\mathcal{G}$ be the set of DAGs over $[p]$ variables and for any DAG $G \in \mathcal{G}$ let $\mathcal{G}_{\Delta}(G)$ be the set of directed “difference” graphs having the same causal order as $G$. Let $\mathcal{G}_{\Delta} \overset{\text{def}}{=} \{ \mathcal{G}_{\Delta}(G) \mid G \in \mathcal{G} \}$. Given a DAG $G$, let $P_{\mathcal{G}}$ denote the distribution induced by the Gaussian linear SEM $(B(G), D)$ where the edge weight matrix $B(G)$ is given as follows:

$$B(G)_{i,j} = \begin{cases} \frac{1}{\sqrt{|\pi(i)|}} & j \in \pi(i), \\ 0 & \text{otherwise} \end{cases}$$

and $D = \sigma^{2} I_{p}$, where $I_{p}$ is the $p \times p$ identity matrix. Thus, given a DAG $G$ the distribution over the variables $\{X_{1}, \ldots, X_{p}\}$ is uniquely defined. Let $\mathcal{P}(\mathcal{G}, \mathcal{G}_{\Delta}) = \{ P_{\mathcal{G}(i)} \times P_{\mathcal{G}(i) \Delta} \mid G^{(i)} \in \mathcal{G}, \Delta_{(i)} \in \mathcal{G}_{\Delta}(G^{(i)}) \}$ be the set of distributions corresponding to the graph families $\mathcal{G}$ and $\mathcal{G}_{\Delta}$. Since $\mathcal{P}(\mathcal{G}, \mathcal{G}_{\Delta}) \subset \mathcal{P}$ and finite, the minimax error is lower bounded as follows:

$$p_{\text{err}} \geq \inf_{\zeta} \max_{P \in \mathcal{P}(\mathcal{G}, \mathcal{G}_{\Delta})} \Pr_{X \sim P_{\mathcal{G}}} \{ \zeta(X) \neq \Delta_{G}(P) \}.$$ 

Let $\mathcal{G} \subseteq \mathcal{G}$ and $\forall G \in \mathcal{G}$ $\mathcal{G}_{\Delta}(G) \subseteq \mathcal{G}_{\Delta}(G)$. Also, let $\mathcal{G}_{\Delta} = \{ \mathcal{G}_{\Delta}(G) \mid G \in \mathcal{G} \}$. Since $\mathcal{P}(\mathcal{G}, \mathcal{G}_{\Delta}) \subseteq \mathcal{P}(\mathcal{G}, \mathcal{G}_{\Delta})$, the minimax error is further lower bounded as follows:

$$p_{\text{err}} \geq \inf_{\zeta} \max_{P \in \mathcal{P}(\mathcal{G}, \mathcal{G}_{\Delta})} \Pr_{X \sim P_{\mathcal{G}}} \{ \zeta(X) \neq \Delta_{G}(P) \}.$$ 

We will construct the restricted ensembles $\mathcal{G}$ and $\mathcal{G}_{\Delta}$ as follows. Each $G = ([p], E) \in \mathcal{G}$ is a fully connected directed bipartite graph. That is, we partition the set $[p]$ in to $U$ and $V$ such that $|p| = |U \cup V|$, $U \cap V = \emptyset$, $|U| = \lfloor p/2 \rfloor$ and $|V| = \lceil p/2 \rceil$. The edge set $E = \{(u, v) \mid u \in U \text{ and } v \in V\}$. Note that $(v, u)$ denotes the directed edge $v \leftarrow u$. We will denote the graph $G$ by $(V, U, V \times U)$. For any $G = (V, U, V \times U) \in \mathcal{G}$, a DAG $G' = (V, U, E) \in \mathcal{G}_{\Delta}$ is generated as follows. For each node $v \in V$ we randomly pick a subset $U(v) \subseteq U$ such that $|U(v)| = d'$ and set the parents of $v$ to be $U(v)$. Therefore, the edge set $E' = \{(v, u) \mid v \in V, u \in U(v), U(v) \subset U, |U(v)| = d'\}$. Thus, the graph $G'$ is $d'$-sparse. Note that the graph $G \oplus G'$ is a fully connected bipartite DAG from which the edges in $G'$ have been deleted.

Note that for any $G \in \mathcal{G}$, $|\mathcal{G}_{\Delta}(G)| = (\frac{p}{d'})^{\frac{\lceil p \rceil}{2}}$.

We will be using the following results from [5].
Theorem 5 (Generalized Fano’s inequality Theorem 1 of [5]). Let $W, X,$ and $Y$ be random variables such that the conditional independence relationship between them are given by the following partially directed graph:

![Diagram](image)

Let $\hat{X}$ be any estimator of $X$. Then,

$$
\Pr \left\{ X \neq \hat{X} \right\} \geq 1 - \frac{I(Y; X|W) + \log 2}{H(X|W)},
$$

(11)

where in the second line the probability is over both $\hat{X} \sim P^n$ and $P$ drawn from the family $\mathcal{P}(\hat{G}, \hat{G}_\Delta)$. Next, we lower bound $\Pr_{\hat{X} \sim P^\circ \times P^n_{G \oplus \Delta_G}} \left\{ \zeta(\hat{X}) \neq \Delta_G(P) \right\}$ using Theorem 5. Towards that end we need to first upper bound the mutual information $I(\hat{X}; \Delta_G | G)$ and compute the conditional entropy $H(\Delta_G | G)$. Let $Q = \mathcal{N}(0, I)$ be the standard isotropic Gaussian distribution over $X$. We upper bound $I(\hat{X}; \Delta_G | G)$ by adapting Lemma 4 from [5] for our purpose which we state below.

Lemma 2 (Lemma 4 of [5]). Let $P_{G, \Delta_G} = P_G \times P_{G \oplus \Delta_G}$ denote the data distribution given a specific DAG $G$ and a specific difference DAG $D_G$. Then,

$$
I(\hat{X}; \Delta_G | G) \leq \frac{1}{|\mathcal{G}_\Delta(G)|} \sum_{\Delta_G \in \mathcal{G}_\Delta(G)} \text{KL} \left( P_{G, \Delta_G}^n \left| \left| Q' \right| \right. \right),
$$

where $Q' = \mathcal{N}(0, I)$ is the standard $2p$-dimensional isotropic Gaussian distribution.

From the above we have that

$$
I(\hat{X}; \Delta_G | G) \leq \frac{1}{|\mathcal{G}_\Delta(G)|} \sum_{\Delta_G \in \mathcal{G}_\Delta(G)} \text{KL} \left( P_{G, \Delta_G}^n \left| \left| Q' \right| \right. \right) = \frac{n}{|\mathcal{G}_\Delta(G)|} \sum_{\Delta_G \in \mathcal{G}_\Delta(G)} \text{KL} (P_G || Q) + \text{KL} (P_{G \oplus \Delta_G} || Q)
$$

Note that the distribution indexed by a DAG $G$ is $P_G = \mathcal{N}(0, \Sigma(G))$, with $\Sigma(G) = (I - B(G))^{-1} D (I - B(G))^{-T}$. $Q$ is the $p$-dimensional standard isotropic Gaussian distribution. From the KL-divergence characterization for multivariate Gaussian distribution we have that:

$$
\text{KL} (P_G || Q) = \frac{1}{2} \left\{ \text{tr}(\Sigma(G)) - p - \ln |\Sigma(G)| \right\}
$$

For any $u \in U$, $\text{Var} [X_u] = \sigma^2$, while for a $v \in V$, $\text{Var} [X_v] = (1/\sqrt{|V|}) \sum_{u \in U} X_u + \sigma^2 = 2\sigma^2$ since $X_u$’s are independent for all $u \in U$. Therefore, $\text{tr}(\Sigma(G)) = [n/2] \sigma^2 + 2 [n/2] \sigma^2 \leq (3/2)p\sigma^2$. 18
Next,

$$|\Sigma(G)| = \left| (I - B(G))^{-1}D(I - B(G))^{-T} \right| = \frac{1}{|(I - B(G))D^{-1}(I - B(G))^T|} = \frac{1}{|D^{-1}|} = |D| = (\sigma^2)^p$$

Setting $\sigma^2 = 2/3$, we have that $\mathbb{K}L \cdot (P_G \| Q) = 2/\{p - p + p\ln 3/2\} < (p/2)\ln 3/2$. Since each vertex in the DAG $\Delta_G$ has exactly $p - d'$ parents, $\mathbb{K}L \cdot (P_{G\cap \Delta'} \| Q) \leq (p/2) \log 2$. Therefore, $I(X; \Delta_G \mid G) \leq np \ln 3/2 < np/2$.

Finally, since $\Delta_G$ is picked uniformly at random from the set $\bar{G}_{\Delta}(G)$ and $G$ itself is also picked uniformly at random from $G_{\Delta}$, we have that $H(\Delta_G \mid G) = [p/2] \log \binom{\binom{p/2}{d'}}{\binom{p}{d'}} \leq (pd'/2) \log (np/2d')$. Therefore, from [13] and Theorem 5 we have that

$$p_{err} \geq 1 - \frac{np/2 + \log 2}{(pd'/2)\log(np/2d')}. $$

From the above we have that $p_{err} \geq 1/2$ if $n \leq \frac{d'}{2} \log \frac{p}{2d'} - \frac{2}{p} \log 2$. \hfill \Box

**B Comparison with indirect methods**

Ghosal and Honorio [7] have obtained optimal sample complexity guarantees for estimating linear SEMs with equal noise variance. Therefore, we compare our method against using their method to first estimate the individual DAGs and then compute their differences. Using the method of Ghosal and Honorio [7], the sample complexity of indirectly estimating the difference DAG depends on $(\max_{\kappa, i} \Sigma_{i,i}^{(1)} \| \Omega^{(2)} \|_1^2)^2$. In comparison, the sample complexity of our direct estimation method depends on $(\max_{\kappa, i} \Sigma_{i,i}^{(1)} \| \Omega^{(2)} \|_1^2)$. Note that our sample complexity also depends on $1/K_{\min}^d$, where $K_{\min}^d = \min \Sigma_{i,i}^{(1)} \Sigma_{i,i}^{(2)\top}$. Since $\Sigma_{i,i}^{(1)} \geq \sigma_i^2$, $K_{\min}^d$ can be ignored as a constant. While our method requires a mutual incoherence condition, their method for estimating the individual DAGs require the noise variances to be the same (or close to being the same). Therefore, if the incoherence condition is satisfied, our method has strictly lower sample complexity which depends only on the sparsity of the difference between the moral graphs of the two SEMs.

**C Additional Experiments**

**C.1 Logarithmic dependence on the number of variables**

In this section, we show the $\mathcal{O}(\log p)$ dependence of the sample complexity, as prescribed by Corollary 2 and Theorem 3. In Figure 4, we perform 30 repetitions to estimate the probability of exact recovery, where the SEM pairs are sampled according to Section 4. Then, for each pair, we obtain $\lceil C^p \log p \rceil$ samples for $C \in [3, 12]$ and $p \in \{5, 10, 15\}$.

**C.2 Real-world experiment**

In this section we tested our algorithm in the medical domain. The 1000 functional connectomes dataset contains resting-state fMRI of 1128 subjects collected on 41 sites around the world. The dataset is publicly available at [http://www.nitrc.org/projects/fcon_1000/](http://www.nitrc.org/projects/fcon_1000/). Resting-state fMRI is a procedure that captures brain function of a subject that is at wakeful rest (i.e., not focused on the outside world). Registration of the dataset to the same spatial reference template (Talairach space) and spatial smoothing was performed in SPM at [http://www.fil.ion.ucl.ac.uk/spm/](http://www.fil.ion.ucl.ac.uk/spm/).
Figure 4: Probability of exact recovery computed across 30 repetitions. The number of samples is set to \( \lfloor e^C \log p \rfloor \) for \( C \in [3, 12] \) and \( p \in \{5, 10, 15\} \). The x-axis is in log-scale. We can observe the logarithmic dependence on \( p \), as prescribed by Corollary 2 and Theorem 4.

We extracted voxels from the gray matter only, and grouped them into 157 regions (i.e., \( p = 157 \)) by using standard labels, given by the Talairach Daemon (http://www.talairach.org/). These regions span the entire brain: cerebellum, cerebrum and brainstem. In order to capture laterality effects, we have regions for the left and right side of the brain.

A relevant neuroscientific aim is to discover the changes in the default mode network (which is active during wakeful rest) in subjects who had the eyes open, versus subjects who had the eyes closed. This is known to make a significant difference in brain activity for activity-oriented tasks, but this is unclear in resting state. Our method recovered a difference DAG between brain regions that belong to the visual cortex (ventral and dorsal visual streams) in the back of the brain (see Figure 5). Thus, besides having strong theoretical guarantees, our method has the potential to also produce meaningful results in practice.

**Remark 4.** We emphasize that our goal here is to demonstrate the practicality of our method. It is beyond the scope of this work to make scientific discoveries in neuroscience.

Figure 5: Out of the 157 variables, only 12 variables participate in the difference DAG, i.e., the remaining 145 variables are disconnected. In this case, \( \epsilon \) was set to 0.1 for our finite-sample version of Algorithm 1 (see Remark 1). The red edges indicate important connections discovered. The visual cortex (nodes colored in green) includes: Brodmann areas 17, 19, 20. We note that Dentate is partially involved in the visuospatial function. Lateral Posterior Nucleus is also involved in vision, while Culmen is believed to mediate in visual reflexes.