

Methods for Structure Identifiability

Seminar on causality and causal inference

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Review

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Markov property and faithfulness

The joint distribution P_X is said to be Markov with respect to the DAG \mathcal{G} if

 $\mathbf{A}, \mathbf{B} \text{ d-sep. } by \mathbf{C} \quad \Rightarrow \quad \mathbf{A} \underline{\parallel} \mathbf{B} | \mathbf{C}$

for all disjoint set **A**, **B**, **C**.

The joint distribution P_X is said to be faithful to the DAG \mathcal{G} if

$$\mathbf{A}, \mathbf{B} \text{ d-sep. } by \mathbf{C} \quad \Leftarrow \quad \mathbf{A} \perp \!\!\!\perp \!\!\!\mathbf{B} | \mathbf{C}$$

for all disjoint set **A**, **B**, **C**.

Under the Markov condition and faithfulness, the Markov equivalence class of G is identifiable from P_X .



Independence-Based methods



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- · Estimate the skeleton, that is, the undirected edges
- Orient as many edges as possible



Estimation of skeleton

Lemma [4]

The following two statements holds.

- (i) Two nodes X, Y in a DAG (X, E) are adjacent if and only if they cannot be d-separated by any subsets S ⊆ X \{X, Y}.
- (ii) If two nodes X, Y in a DAG (X, E) are not adjacent, then they are d-separated by either PA_X or PA_Y.

Lemma (i): IC algorithm, SGS algorithm Lemma (ii): PC algorithm



For each pair of nodes (X, Y), these methods search through all possible subsets $\mathbf{A} \subseteq \mathbf{X} \setminus \{X, Y\}$ of variables neither containing X nor Y and check whether X and Y are d-separated given **A**. After all those tests, X and Y are adjacent if and only if no set **A** was found that d-separates X and Y.



The PC algorithm starts with a fully connected undirected graph and step-by-step increases the size of the conditioning set **A**, starting with #**A** = 0. At iteration *k*, it considers sets **A** of size #**A** = *k*, using the following neat trick: to test whether *X* and *Y* can be d-separated, one only has to go through sets **A** that are subsets either of the neighbors of *X* or of the neighbors of *Y*.



a

PC algorithm(Example) [1]

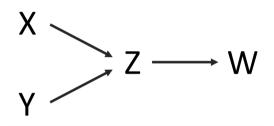


Figure: Original true causal graph.





PC algorithm: Estimation of skeleton







Figure: After step 1.

Figure: After step 2.

Figure: After step 3.

- 1. Form a complete undirected graph.
- 2. Eliminate edges between variables that are unconditionally independent.
- 3. For each pair of variables (*A*, *B*) having an edge between them, and for each variable *C* with an edge connected to either of them, eliminate the edge between *A* and *B* if *A*_⊥*B*|*C*.



PC algorithm: Estimation of skeleton

For each pair of variables (A, B) having an edge between them, and for each pair of variables C, D with edges both connected to A or both connected to B, eliminate the edge between A and B if A⊥⊥B|{C, D}.

Continue checking independencies conditional on subsets of variables of increasing size until there are no more adjacent pairs (A, B), such that there is a subset of variables such that all of the variables in the subset are adjacent to A or all adjacent to B.



PC algorithm: Orientation of edges



Figure: After step 5.



Figure: After step 6.

- 5. For each triple of variables (A, B, C) such that A and B are adjacent, B and C are adjacent, and A and C are not adjacent, orient the edges A − B − C as A → B ← C, if B was not in the set conditioning on which A and C became independent.
- 6. For each triple of variables such that $A \rightarrow B C$, and A and C are not adjacent, orient the edge B C as $B \rightarrow C$. This is called orientation propagation.



- There are other orientation propagation rules that are not illustrated here, such as Meek's orientation rules [2].
- In some examples, none of orientation rules will apply to a given undirected edge, and that edge will remain undirected in the output.



Conditional independence tests

- Statistical significance test
- · Kernel-based test
- Gaussian distributed variables: vanishing partial correlation
- Non-Gaussian distributed variables: nonlinear extension of partial correlation



Nonlinear extension of partial correlation [4]

- 1. (Nonlinearly) regress X on Z and test whether the residuals are independent of Y
- 2. (Nonlinearly) regress Y on Z and test whether the residuals are independent of X
- 3. If one of those two independences hold, conclude that $X \perp Y | Z$



Score-Based methods



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Best scoring graph

Given data $\mathcal{D} = (\mathbf{X}^1, \dots, \mathbf{X}^n)$ from a vector **X** of variables, that is, a sample containing *n* i.i.d. observations, the idea is to assign a score $S(\mathcal{D}, \mathcal{G})$ to each graph \mathcal{G} and search over the space of DAGs to find the graph with the highest score:

 $\hat{\mathcal{G}} := \operatorname*{argmax}_{\mathcal{G} \; \mathsf{DAG} \; \mathsf{over} \; \mathbf{X}} \mathcal{S}(\mathcal{D}, \mathcal{G})$

There are several possibilities to define such a scoring function *S*. Often a parametric model is assumed (e.g., linear Gaussian equations or multinomial distributions), which introduces a set of parameters $\theta \in \Theta$ [4].



For each graph we may consider the maximum likelihood estimator $\hat{\theta}$ for θ and then define a score function by the *BIC*

$$\mathcal{S}(\mathcal{D},\mathcal{G}) := \log p(\mathcal{D}|\hat{ heta},\mathcal{G}) - rac{\# extsf{parameters}}{2} \log n$$

where $\log p(\mathcal{D}|\hat{\theta}, \mathcal{G})$ is the log likelihood and *n* is the sample size [4].



Bayesian scoring functions

We define priors $p_{pr}(\mathcal{G})$ and $p_{pr}(\theta)$ over DAGs and parameters, respectively, and consider the log posterior as a score function (note that $p(\mathcal{D})$ is constant over all DAGs):

$$oldsymbol{S}(\mathcal{D},\mathcal{G}) := \log p(\mathcal{G}|\mathcal{D}) \propto \log p_{
m pr}(\mathcal{G}) + \log p(\mathcal{D}|\mathcal{G}),$$

where $p(\mathcal{D}|\mathcal{G})$ is the marginal likelihood

$$p(\mathcal{D}|\mathcal{G}) = \int_{\theta \in \Theta} p(\mathcal{D}|\mathcal{G}, \theta) p_{pr}(\theta, \mathcal{G}) d\theta.$$

Here the resulting estimator $\hat{\mathcal{G}}$ is usually called a maximum a posteriori (MAP) estimator [4].



At each step there is a candidate graph and a set of neighboring graphs. For all these neighbors, one computes the score and considers the best-scoring graph as the new candidate. If none of the neighbors obtains a better score, the search procedure terminates (not knowing whether one obtained only a local optimum).

A neighborhood relation: Starting from a graph G, we may define all graphs as neighbors from G that can be obtained by removing, adding, or reversing one edge [4].



Exact methods

Here, "exact" means that they aim at finding (one of) the best scoring graphs for a given finite data set.

Due to the Markov factorization, we have for $\mathcal{D} = (\mathbf{X}^1, \cdots, \mathbf{X}^n)$ that

$$\log p(\mathcal{D}|\hat{\theta}, \mathcal{G}) = \sum_{j=1}^{d} \sum_{i=1}^{n} \log p(X_j^i | X_{\mathsf{PA}_j^G}^i, \hat{\theta}),$$

which is a sum of d 'local' scores.

Other techniques:

- ILP framework: represent graphical structures as vectors
- Restrict the number of parents [4]



Additive Noise Models



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Score-based method combined with greedy search

Nonlinear Gaussian case:

For a given graph structure $\mathcal{G},$ we regress each variable on its parents and obtain the score

$$\log p(\mathcal{D}|\mathcal{G}) = \sum_{j=1}^{d} - \log \widehat{var}[R_j],$$

here, $var[R_j]$ is the empirical variance of the residuals R_j obtained from the regression of variable X_j on its parents [4].



If the noise cannot be assumed to have a Gaussian distribution [3]

For each DAG G_i we follow the three-step procedure:

- 1. For each node *k* estimate the residuals $\hat{\epsilon}_k$ by nonparametrically regressing X_k on $\{X_l\}_l \in pa_{\mathcal{G}_l(k)}$. If $pa_{\mathcal{G}_l(k)} = \emptyset$, set $\hat{\epsilon}_k = x_k$.
- 2. For each node *k* estimate the residual densities $\hat{p}_{\epsilon k}$ from the estimated residuals $\hat{\epsilon}_k$.
- 3. Compute the penalized likelihood score

$$S_i^n = rac{1}{n}\sum_{j=1}^n\sum_{k=1}^d \log \hat{p}_{\epsilon k}(\hat{\epsilon}_k^j) - \#(edges)_i \cdot a_n,$$

where a_n controls the strength of the penalty.



Independence tests

Algorithm 1 Regression with subsequent independence test (RESIT)

1: Input: I.i.d. samples of a *p*-dimensional distribution on (X_1, \ldots, X_p)

2:
$$S := \{1, \dots, p\}, \pi := []$$

- 3: PHASE 1: Determine causal order.
- 4: repeat
- 5: for $k \in S$ do
- 6: Regress X_k on $\{X_i\}_{i \in S \setminus \{k\}}$.
- 7: Measure dependence between residuals and $\{X_i\}_{i \in S \setminus \{k\}}$.
- 8: **end for**
- 9: Let k^* be the k with the weakest dependence.

10:
$$S := S \setminus \{k^*\}$$

11:
$$pa(k^*) := S$$

- 12: $\pi := [k^*, \pi]$ (π will be the causal order, its last component being a sink)
- 13: **until** #S = 1

Figure: PHASE 1



14: PHASE 2: Remove superfluous edges. 15: for $k \in \{2, ..., p\}$ do 16:for $\ell \in pa(\pi(k))$ do 17:Regress $X_{\pi(k)}$ on $\{X_i\}_{i \in \operatorname{pa}(\pi(k)) \setminus \{\ell\}}$. if residuals are independent of $\{X_i\}_{i \in \{\pi(1),\dots,\pi(k-1)\}}$ then 18: $\operatorname{pa}(\pi(k)) := \operatorname{pa}(\pi(k)) \setminus \{\ell\}$ 19:end if $20 \cdot$ end for 21:22: end for 23: **Output:** $(pa(1), \ldots, pa(p))$

Figure: PHASE 2 [5]

Note: This method is based on the fact that for each node X_i the corresponding noise variable N_i is independent of all non-descendants of X_i .



Intervention



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Intervention

- Known intervention targets
- Unknown intervention targets



Unknown intervention targets

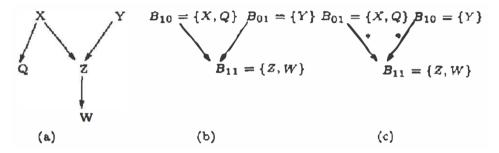


Figure: (a) A causal diagram; (b) The order graph without knowing the intervention target; (c) The marked order graph.[6]



References



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References

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