## Causal Inference with Graphical Models

Jose M. Peña STIMA, IDA, LiU

### Lecture 1: Causal Models and Learning Algorithms

## Contents

- Causal Models
- IC Algorithm
- Projections
- IC\* Algorithm
- Restricted Causal Models
- RESIT Algorithm
- Score Based Algorithms

### Literature

#### Main sources

- Pearl, J. Causality: Models, Reasoning, and Inference (2nd ed.). Cambridge University Press, 2009. Chapters 1 and 2.
- Peters, J., Janzing, D. and Schölkopf, B. *Elements of Causal Inference*. MIT Press, 2017. Chapters 3, 4, 6 and 7.

#### Additional sources

- Verma, T. S. Graphical Aspects of Causal Models. Technical Report R-191, UCLA, 1993.
- Pearl, J. Causality: Models, Reasoning, and Inference (1st ed.). Cambridge University Press, 2000. Chapters 1 and 2.

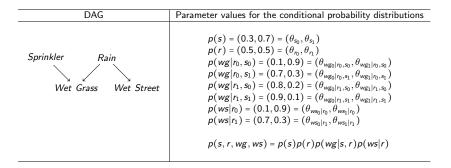
## **Causal Models**

- A causal structure over a set of variables V is a DAG over V.
- A causal model consists of a causal structure, a set of functions  $x_i = f_i(pa_i, u_i)$  for each  $X_i \in V$ , and a distribution  $p(u_i)$  for each  $U_i$ .
- The functions are also called structural equations, which is different from algebraic equations since the equality sign should be read as an assignment or determination, i.e. it is asymmetric.
- For now, the error, noise or disturbance terms U<sub>i</sub> are assumed to be independent one of another. They may be seen as representing unmodeled or unobserved causes.
- Note that  $f_i(pa_i, u_i)$  and  $p(u_i)$  together define a conditional distribution  $p(x_i|pa_i)$ . Then, a causal model defines a distribution over V:

$$p(v) = \prod_i p(x_i | pa_i).$$

A causal model can be obtained from knowledge of the physics behind the phenomenon being modeled, from interventional experiments such as randomized control trials, or from passive observations.

### **Causal Models**



# IC Algorithm

- A distribution p is stable or faithful or isomorphic wrt a DAG D when  $X \perp_p Y | Z$  iff  $X \perp_D Y | Z$ .
- In other words, the independences in p are structural and not formed by incidental parameter equalities. The unstable distributions have measure zero when the parameters are chosen at random.
- A pattern is a mixed graph that represents an equivalence class of DAGs:
  - It contains the edge  $A \rightarrow B$  if the edge is in every member of the class, and
  - the edge A B if  $A \rightarrow B$  is in some members and  $A \leftarrow B$  in some others.

Inductive causation (IC) algorithm

Input: A distribution p over V that is stable wrt some DAG DOutput: The pattern G corresponding to the equivalence class of D

Let G be a complete undirected graph For each pair of nodes A,  $B \in V$ If  $A \perp_p B | S_{AB}$  for some  $S_{AB} \subseteq V$ , then delete the edge A - B from G For each pair nodes A,  $B \in V$  st A - B is not in G If  $A \multimap C \multimap B$  is in G and  $C \notin S_{AB}$ , then add the orientations  $A \to C \leftarrow B$  to G Orient as many edges in G as possible without creating inmoralities or directed cycles

The algorithm's steps can be systematized and optimized.

# IC Algorithm

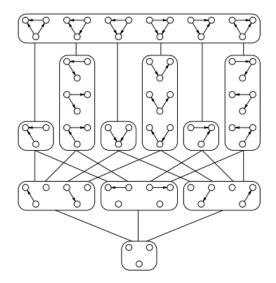


Figure 2: Hasse diagram of the space of Markov equivalence classes of Bayesian network structures over three variables.

## Projections

- A latent structure L is a causal structure over V ∪ U st V are observable and U are latent. The variables in U are not necessarily independent anymore.
- Note that L induces a distribution over V:

$$p(v) = \sum_{U} \prod_{i} p(x_i | pa_i).$$

It may be convenient to work with the projection of L onto V.

#### Projection algorithm

Input: A latent structure *L* over  $V \cup U$ Output: The projection *G* of *L* over *V* 

Let G be the empty graph over V For each pair of nodes  $A, B \in V$ If L has a directed path from A to B st every internal node is in U, then add the edge  $A \rightarrow B$  to G If L has a divergent path between A and B st every internal node is in U, then add the edge  $A \leftrightarrow B$  to G

- The separation criterion for DAGs can be extended to projections: Simply, redefine the term collider as follows.
  - A node B in a path  $\rho$  is a collider when  $A \rightarrow B \leftarrow C$  or  $A \rightarrow B \leftrightarrow C$  or  $A \leftrightarrow B \leftrightarrow C$  is a subpath of  $\rho$ .
- Interestingly, L and G represent the same independence model over V.

# IC\* Algorithm

#### IC<sup>\*</sup> algorithm

Input: A distribution p over V that is stable wrt the projection of some latent structure LOutput: A marked pattern G of the projection of L over V

- 0. Let G be a complete undirected graph
- 1. For each pair of nodes  $A, B \in V$

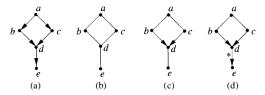
If  $A \perp_p B | S_{AB}$  for some  $S_{AB} \subseteq V$ , then delete the edge A - B from G

2. For each pair nodes  $A, B \in V$  st A - B is not in G

If  $A \multimap C \multimap B$  is in G and  $C \notin S_{AB}$ , then add the arrowheads  $A \hookrightarrow C \hookleftarrow B$  to G

- 3. Add as many arrowheads and marks to G as possible according to the following rules:
  - 3.1. If G has a marked directed path from A to B and  $A \sim B$ , then add the arrowhead  $A \leftrightarrow B$  to G
  - 3.2. If  $A \hookrightarrow C \multimap B$  is in G and  $A \multimap B$  is not in G, then add the arrowhead  $C \to B$  to G and mark the edge with \*
- Every \*-marked directed edge in G corresponds to a directed path in L, i.e. genuine causation.
- Every unmarked directed edge in *G* corresponds to a directed or divergent path in *L*, i.e. potential causation.
- Every bidirected edge in G corresponds to a divergent path in L, i.e. spurious association.
- Undirected edges in *G* correspond to undetermined relationships.
- The algorithm's steps can be systematized and optimized.
- There exist more sophisticated algorithms that allow even selection bias.

# IC\* Algorithm



**Figure 2.3** Graphs constructed by the IC\* algorithm. (a) Underlying structure. (b) After step 1. (c) After step 2. (d) Output of IC\*.

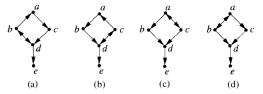


Figure 2.4 Latent structures equivalent to those of Figure 2.3(a).

### Restricted Causal Models

- Let  $X \sim F_X$ , where  $F_X$  is a continuous CDF. Then,  $Y = F_X(x) \sim U(0,1)$ .
- Proof:

$$F_Y(y) = p(Y \le y) = p(F_X(x) \le y) = p(X \le F_X^{-1}(y)) = F_X(F_X^{-1}(y)) = y.$$

- Useful for sampling random variables (a.k.a. inverse CDF method): Let  $Y \sim U(0,1)$  and let  $F_X$  be a continuous CDF. Then,  $X = F_X^{-1}(y) \sim F_X$ .
- Any joint probability distribution p(x, y) admits causal models in both directions, i.e.

$$X \rightarrow Y : x = f_X(u_X)$$
 and  $y = f_Y(x, u_Y)$  with  $X \perp U_Y$ .

 $Y \rightarrow X : y = f_Y(u_Y)$  and  $x = f_X(y, u_X)$  with  $Y \perp U_X$ .

- ▶ Proof: Let  $F_{Y|x}(y) = p(Y \le y|X = x)$  and let  $f_Y(x, u_Y) = F_{Y|x}^{-1}(u_Y)$  where  $U_Y \sim U(0,1)$  and  $X \perp U_Y$ .
- So, there is no chance of identifying the true causal model from observations alone unless further assumptions are made.

### Restricted Causal Models

• Assume that p(x, y) admits the causal model

 $y = \alpha x + u_Y$  with  $X \perp U_Y$ 

where the random variables are continuous. Then,

$$x = \beta y + u_X$$
 with  $Y \perp U_X$ 

iff X and  $U_Y$  are Gaussian.

In other words, identifiability for linear non-Gaussian models is possible.

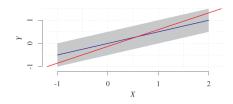


Figure 4.1: Joint density over *X* and *Y* for an identifiable example. The blue line is the function corresponding to the forward model *Y* :=  $0.5 \cdot X + N_Y$ , with uniformly distributed *X* and  $N_Y$ ; the gray area indicates the support of the density of (X, Y). Theorem 4.2 states that there cannot be any valid backward model since the distribution of  $(X, N_Y)$  is non-Gaussian. The red line characterized by (b, c) is the least square fit minimizing  $\mathbb{E}[X - bY - c]^2$ . This is not a valid backward model  $X = bY + c + N_X$  since the resulting noise  $N_X$  would not be independent of *Y* (the size of the support of  $N_X$  would differ for different values of *Y*).

## Restricted Causal Models

• Assume that p(x, y) admits the causal model

$$y = f_Y(x) + u_Y$$
 with  $X \perp U_Y$ 

where the random variables are continuous. Then, p(x, y) does not admit in general a model of the same form in the backward direction.

- In other words, identifiability for non-linear additive models is possible in general, i.e. for all but some "rare" or "non-generic" or "fine-tuned" cases.
- The precise characterization is rather technical. Exception: When X and  $U_Y$  are Gaussian, p(x, y) admits the backward model iff  $f_Y$  is linear.
- Assume that p(x, y) admits the causal model

$$y = g_Y(f_Y(x) + u_Y)$$
 with  $X \perp U_Y$ 

where the random variables are continuous. Then, p(x, y) does not admit **in general** a model of the same form in the backward direction.

In other words, identifiability for post-nonlinear models is possible in general.

### **RESIT** Algorithm

Regression with subsequent independence test (RESIT) algorithm

Input: A sample from p(x, y)Output: The non-linear additive model  $X \rightarrow Y$  or  $Y \rightarrow X$  or nothing

Perform a non-linear regression from Y on X to write  $y = \hat{f}_Y(x) + \hat{u}_Y$ Perform the hypothesis test  $H_0: X \perp \hat{U}_Y$ Repeat the two steps above exchanging the roles of X and Y If  $H_0$  is accepted in one direction and rejected in the other, then infer the former as the causal direction

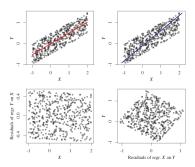


Figure 4.5: We are given a sample from the underlying distribution and perform a linear regression in the directions  $X \rightarrow Y$  (left) and  $Y \rightarrow X$  (right). The fitted functions are shown in the top row, the corresponding residuals are shown in the bottom row. Only the direction  $X \rightarrow Y$  yields independent residuals; see also Figure 4.1.

## **RESIT** Algorithm

#### Regression with subsequent independence test (RESIT) algorithm

Input: A sample from a distribution  $p(x_1, \ldots, x_n)$  that is generated by a non-linear additive model that is faithful to a DAG G

Output: The DAG G (in the large sample limit and using a consistent regression method and independence test)

 $S = \{1, ..., n\}$  $\pi = []$ // Phase 1: Determine a topological order by identifying a sink node, i.e. // a node whose residual is independent of the rest of the nodes Repeat For  $k \in S$  do Regress  $X_k$  on  $X_{S \setminus \{k\}}$ Measure the dependence between the residuals and  $X_{S \setminus \{k\}}$ Let  $k^*$  be the k with the weakest dependence  $S = S \setminus \{k^*\}$  $Pa_{\iota*} = S$  $\pi = [k^*, \pi]$ Until  $S = \emptyset$ // Phase 2: Remove superfluous edges without violating the sink condition, i.e. // the residual of a node is independent of its predecessors or non-descendants For  $k \in \{2, ..., n\}$  do For  $\ell \in Pa_{\pi(k)}$  do Regress  $X_{\pi(k)}$  on  $X_{Pa_{\pi(k)} \setminus \{\ell\}}$ If the residuals are independent of  $X_{\pi(1:k-1)}$ , then remove  $\ell$  from  $Pa_{\pi(k)}$ 

Note that the noise variables are jointly independent (cf. IC\* algorithm).

### Score Based Algorithms

• Choose a DAG G with maximum posterior probability given some data  $d_{1:N}$  (a.k.a. Bayesian score), i.e.

$$p(G|d_{1:N}) = p(d_{1:N}|G)p(G)/P(d_{1:N}) \propto p(d_{1:N}|G)p(G)$$

where  $p(d_{1:N}|G)$  is the marginal likelihood of  $d_{1:N}$  given G, p(G) is a prior probability distribution over DAGs, and  $p(d_{1:N})$  is a normalization constant.

Moreover,

$$p(d_{1:N}|G) = \int p(d_{1:N}|\theta_G, G)p(\theta_G|G)d\theta_G$$

where  $p(d_{1:N}|\theta_G, G)$  is the likelihood function of  $d_{1:N}$  given G and  $\theta_G$ , and  $p(\theta_G|G)$  is a prior probability distribution over the parameter values of G.

For discrete variables  $X_i$  of cardinality  $k_i$ , and **assuming** that  $p(\theta_G|G) = \prod_i \prod_j p(\theta_{x_i|pa_i=j}|G)$  and  $p(\theta_{x_i|pa_i=j}|G) \sim Dirichlet(\alpha_{ij1}, \dots, \alpha_{ijk_i})$ , we have that

$$p(d_{1:N}|G) = \prod_{i} \prod_{j} \frac{\Gamma(\alpha_{ij})}{\Gamma(\alpha_{ij} + N_{ij})} \prod_{k} \frac{\Gamma(\alpha_{ijk} + N_{ijk})}{\Gamma(\alpha_{ijk})}$$

where  $\alpha_{ij} = \sum_k \alpha_{ijk}$ ,  $N_{ijk}$  is the number of instances in  $d_{1:N}$  where  $X_i = k$ and  $Pa_i = j$ , and  $N_{ij} = \sum_k N_{ijk}$ .

### Score Based Algorithms

- Two DAGs are called Markov equivalent if they represent the same set of separations.
- The marginal likelihood is the same for Markov equivalent DAGs iff

$$\alpha_{ijk} = \alpha p'(ijk)$$

where  $\alpha$  is the user-defined imaginary sample size and p'(ijk) is a prior probability distribution, e.g.  $p'(ijk) = 1/(k_i \prod_{X_{\ell} \in Pa_i} k_{\ell})$ .

• Under the Dirichlet parameter prior assumption and when  $N \rightarrow \infty$ , we get the Bayesian information criterion (BIC):

$$\log p(d_{1:N}|G) \approx \log p(d_{1:N}|\theta_G^{ML}, G) - \frac{\log N}{2} dim(G)$$

where  $\theta_G^{ML}$  are the maximum likelihood estimates of the parameters (i.e., proportions in  $d_{1:N}$ ), and dim(G) is the dimension or number of free parameters of G, i.e.  $\sum_i (k_i - 1) \prod_{X_{\ell} \in P_{a_i}} k_{\ell}$ .

Similar results exist for Gaussian random variables.

### Score Based Algorithms

- Number of DAGs with 1-12 nodes: 1, 3, 25, 543, 29281, 3781503, 1138779265, 783702329343, 1213442454842881, 4175098976430598143, 31603459396418917607425, 521939651343829405020504063
- Then, an exhaustive search is prohibitive and, thus, a heuristic search must be performed instead.

Hill-climbing Input: A sample  $d_{1:N}$  from a distribution p(v)Output: A DAG G over V

Let *G* be the empty DAG Repeat until no change occurs Add, remove or reverse any edge in *G* that improves the Bayesian score the most

• The log Bayesian score is **decomposable** if  $\log p(G)$  is so, i.e.

$$\log p(G|d_{1:N}) = \sum_{i} f(X_i, Pa_i, d_{1:N})$$

and, thus, adding, removing or reversing a edge in  ${\it G}$  implies recomputing only one or two factors.

- Unfortunately, hill-climbing is not asymptotically correct.
- Note that the noise variables are jointly independent (cf. IC\* algorithm).

# Summary

- Causal Models
- IC Algorithm
- Projections
- IC\* Algorithm
- Restricted Causal Models
- RESIT Algorithm
- Score Based Algorithms

Thank you