# 732A96 Advanced Machine Learning Graphical Models and Hidden Markov Models

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Lecture 4: Structure Learning

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- Structure Learning for BNs
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## Literature

- Main source
  - Koski, T. J. T. and Noble, J. M. A Review of Bayesian Networks and Structure Learning. *Mathematica Applicanda* 40, 51-103, 2012.

• We can get a DAG H such that  $p(X) = \prod_i p(X_i|pa_H(X_i))$  and, thus, that we can use for probabilistic reasoning as follows:

Let  $Y_{1:n}$  be any ordering of the random variables  $X_{1:n}$ For each  $Y_i$  do Set  $pa_H(Y_i)$  to be any minimal subset of  $Y_{1:i-1}$  such that  $Y_i \perp_p Y_{1:i-1} \smallsetminus pa_H(Y_i)|pa_H(Y_i)$ 

- Exercise. Prove the previous statement.
- Note that H has the minimum number of edges among the DAGs that are consistent with the ordering considered.
- However, H may not have the minimum number of edges among all the DAGs, i.e. the ordering considered may not be optimal.

$A \perp_{p} B$	H with ordering A, B, C	H with ordering $C, A, B$
A B	A B	$A \xrightarrow{C} B$

• We can get one such optimal DAG H without searching over the n! orderings assuming **faithfulness**, i.e.  $U_{\perp_p}V|Z$  if and only if  $U_{\perp_G}V|Z$  for some DAG G.

#### Parents and children (PC) algorithm

Let H be the complete undirected graph

I := 0

Repeat while  $l \le n-2$ 

For each ordered pair of nodes  $X_i$  and  $X_j$  in H such that  $X_i \in ad_H(X_j)$  and  $|ad_H(X_i) \setminus X_j| \ge I$ If there is some  $S \subseteq ad_H(X_i) \setminus X_i$  such that |S| = I and  $X_i \perp_D X_j |S|$ , then

 $S_{ij} := S_{ji} := S$ 

Remove the edge  $X_i - X_j$  from HI := I + 1

Apply the rule R1 to H while possible

Apply the rules R2-R3 to H while possible

R1: 
$$X_i \longrightarrow X_j \longrightarrow X_k \implies X_i \longrightarrow X_j \longleftarrow X_k$$
  
  $\land B \notin S_{ik}$ 

R2: 
$$X_i \longrightarrow X_j \longrightarrow X_k \implies X_i \longrightarrow X_j \longrightarrow X_k$$

R3: 
$$X_i \xrightarrow{X_j} X_k \Rightarrow X_i \xrightarrow{X_j} X_k$$



- In practice, we do not have access to p but to a finite sample from it. Then, replace  $X_i \perp_p X_j | S$  in the PC algorithm with an independece test, preferably with one that is consistent so that the algorithm is asymptotically correct.
- ▶ Let  $d_{1:N}$  be a complete sample. Then,  $X_i \perp_p X_j | S$  implies that

$$N_{x_i,x_j,s} \approx N p(x_i|s)p(x_j|s)$$

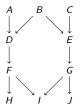
where  $N_{x_i,x_j,s}$  is the number of instances in  $d_{1:N}$  where  $x_i$ ,  $x_j$  and s.

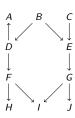
We can measure the deviance from the expected situation above by

deviance = 
$$\sum_{a,b,s} \frac{\left[N_{x_i,x_j,s} - N p(x_i|s)p(x_j|s)\right]^2}{N p(x_i|s)p(x_j|s)}$$

- ▶ If the deviance is too large, then reject the hypothesis that  $X_i \perp_p X_j | S$ .
- Asymptotically, the deviance follows a  $\chi^2$  distribution with the appropriate number of degrees of freedom. Then, we can control the probability of falsely rejecting the hypothesis, a.k.a. p-value.

Exercise. Run the PC algorithm assuming that p is faithful to the following DAGs.





- Two DAGs represent the same independencies (i.e. they are equivalent) if and only if they have the same adjacencies and unshielded colliders, i.e. subgraphs X<sub>i</sub> → X<sub>k</sub> ← X<sub>j</sub> where X<sub>i</sub> and X<sub>j</sub> are not adjacent.
- The output of the PC algorithm is not a DAG in general, but an essential graph (EG):
  - ▶ H has an edge  $X_i o X_j$  if and only if  $X_i o X_j$  is in **every** DAG that is equivalent to G.
  - ▶ In other words, H has an edge  $X_i X_j$  if and only if  $X_i \to X_j$  is in some DAG that is equivalent to G and  $X_i \leftarrow X_j$  is in some other DAG that is equivalent to G.
- ▶ A naive way to convert *H* into a DAG that is equivalent to *G* is as follows:

#### Repeat while possible

Replace any edge  $X_i - X_j$  in H with  $X_i \to X_j$  if this does not create a directed cycle or a new unshielded collider

If H is not a DAG, then backtrack

 Alternatively, we can choose the DAG G with maximum posterior probability (a.k.a Bayesian score):

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

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

Moreover

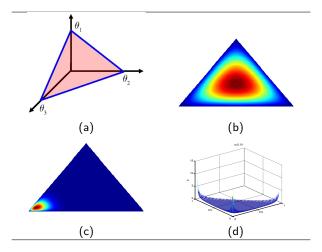
$$p(d_{1:N}|G) = \int p(d_{1:N}|\theta_G, G)p(\theta_G|G)d\theta_G$$

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.

• Assuming that  $p(\theta_G|G) = \prod_i \prod_j p(\theta_{X_i|pa_G(X_i)=j}|G)$  and  $p(\theta_{X_i|pa_G(X_i)=j}|G) \sim Dirichlet(\alpha_{ij1}, \dots, \alpha_{ijk_i})$ , 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  $pa_G(X_i) = j$ , and  $N_{ij} = \sum_k N_{ijk}$ .



(a) The Dirichlet distribution over a 3-valued random variable is defined over the simplex represented by the triangular surface. Points in this surface satisfy  $0 \le \theta_i \le 1$  and  $\sum_i \theta_i = 1$ . (b) Dirichlet(2,2,2). (c) Dirichlet(20,2,2). (d) Dirichlet(0.1,0.1,0.1). Source: Murphy (2012).

 The Bayesian score is score equivalent (i.e. it gives the same score to equivalent DAGs) if and only if

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

where  $\alpha$  is the user-defined imaginary sample size (the higher the more regularization) and p'(ijk) is a prior probability distribution. For instance,  $p'(ijk) = 1/[k_i \prod_{X_i \in pa_G(X_i)} k_i]$  results in the so-called BDeu score.

• Under the Dirichlet parameter prior assumption and when  $N \to \infty$ , we have that

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

where dim(G) is the dimension or number of free parameters of G, i.e.  $\sum_i (k_i - 1) \prod_{X_i \in pa_G(X_i)} k_i$ .

This approximation is called Bayesian information criterion (BIC), and it shows that the Bayesian score favours models that trade off fit of data and model complexity.

- 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. Then, a heuristic search must be performed instead.

### Hill-climbing (HC)

Let G be the empty DAG

Repeat until no change occurs

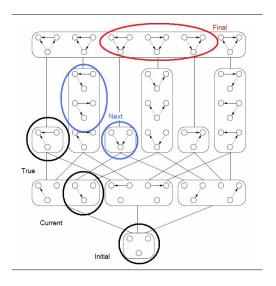
Add, remove or reverse any edge in  ${\it G}$  that improves the Bayesian score the most

▶ The log Bayesian score is **decomposable** if log p(G) is so. That is

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

 Then, adding, removing or reversing a edge in G implies recomputing only one or two factors.

Unfortunately, HC is not asymptotically correct.



• We can get an UG H such that  $p(X) = \prod_i \varphi(C_i)/Z$  and, thus, that we can use for probabilistic reasoning as follows:

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For each X_i do Set ad_H(X_i) to be any minimal subset of X \times X_i such that X_i \perp_p X \times ad_H(X_i)|ad_H(X_i)
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Luckily, we can get H without searching over the  $2^{n-1}$  possible adjacent sets for each node if we assume **faithfulness**, i.e.  $U \perp_{p} V | Z$  if and only if  $U \perp_{G} V | Z$  for some UG G.

Incremental associative Markov boundary algorithm (IAMB)

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For each X_i do ad_H(X_i) := \emptyset

Repeat until no change occurs if there exists X_j \notin ad_H(X_i) \cup X_i such that X_i \not\perp_p X_j | ad_H(X_i) then ad_H(X_i) := ad_H(X_i) \cup X_j

Repeat until no change occurs if there exists X_j \in ad_H(X_i) such that X_i \perp_p X_j | ad_H(X_i) \setminus X_j then ad_H(X_i) := ad_H(X_i) \setminus X_j
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- Exercise. Sketch how to perform structure learning for MNs. Consider issues such as score decomposability, existence of closed form expressions, and problems due to equivalent MNs.
- Exercise. Sketch how to perform structure learning for BNs and MNs from an incomplete sample. Consider issues such as score decomposability, existence of closed form expressions, and problems due to equivalent BNs and MNs.