Estimation of (causal?) structure

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Causal interpretations are tied to the notion of *conditioning by intervention*

$$P(X = x \mid Y \leftarrow y) = P\{X = x \mid do(Y = y)\} = p(x \mid y), \quad (1)$$

which in general is quite different from conventional conditioning or conditioning by observation which is

$$P(X = x | Y = y) = P\{X = x | is(Y = y)\} = p(x | y) = p(x, y)/p(y).$$

A causal interpretation of a Bayesian network involves giving (1) a special form.

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We say that a BN is causal w.r.t. atomic interventions at $B\subseteq V$ if it holds for any $A\subseteq B$ that

$$p(x || x_A^*) = \prod_{v \in V \setminus A} p(x_v | x_{pa(v)}) \Big|_{x_A = x_A^*}$$

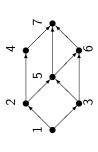
$$= \frac{\prod_{v \in V} p(x_v | x_{pa(v)})}{\prod_{v \in A} p(x_v | x_{pa(v)})} \Big|_{x_A = x_A^*}.$$

For $A = \emptyset$ we obtain standard factorisation.

Note that conditional distributions $p(x_v \mid x_{pa(v)})$ are stable under interventions which do not involve x_v . Such assumption must be justified in any given context.

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An example



$$p(x||x_5^*) = p(x_1)p(x_2|x_1)p(x_3|x_1)p(x_4|x_2) \times p(x_6|x_3,x_5^*)p(x_7|x_4,x_5^*,x_6)$$

$$p(x | x_5^*) \propto p(x_1)p(x_2 | x_1)p(x_3 | x_1)p(x_4 | x_2) \times p(x_5^* | x_2, x_3)p(x_6 | x_3, x_5^*)p(x_7 | x_4, x_5^*, x_6)$$

DAG ${\mathcal D}$ can also represent structural equation system:

$$X_{\nu} \leftarrow g_{\nu}(x_{\mathsf{pa}(\nu)}, U_{\nu}), \nu \in V, \tag{2}$$

where g_{ν} are fixed functions and U_{ν} are independent random disturbances.

Intervention in structural equation system can be made by replacement, i.e. so that $X_v \leftarrow x_v^*$ is replacing the corresponding line in 'program' (2).

Corresponds to g_{ν} and U_{ν} being unaffected by the intervention if intervention is not made on node ν . Hence the equation is structural.

Intervention by replacement in structural equation system implies \mathcal{D} causal for distribution of $X_{v}, v \in V$.

Occasionally used for justification of CBN.

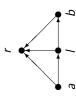
Ambiguity in choice of g_{ν} and U_{ν} makes this problematic.

May take stability of conditional distributions as a primitive rather

than structural equations.

Structural equations more expressive when choice of g_{ν} and U_{ν} can be externally justified.

Assessment of effects of actions



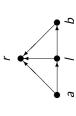
a - treatment with AZT; \prime - intermediate response (possible lung disease); b - treatment with antibiotics; r - survival after a fixed

period. Predict survival if $X_a \leftarrow 1$ and $X_b \leftarrow 1$, assuming stable conditional distributions.

Causal inference
Structural equation systems
Computation of effects
Estimation of DAG structure

Assessment of effects of actions

G-computation



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V set of variables, assume DAG $\mathcal D$ unknown and P given. Assume joint distribution P faithful to $\mathcal D$:

 $X_A \perp \!\!\!\perp X_B \mid X_S \iff A \perp_{\mathcal{D}} B \mid S$

Most distributions are faithful

Find ${\mathcal D}$ which matches conditional independence relations of ${\mathcal P}$.

 ${\cal D}$ and ${\cal D}'$ are Markov equivalent if the separation relations $\perp_{{\cal D}}$ and $\perp_{{\cal D}'}$ are identical.

 ${\cal D}$ can only be determined up to Markov equivalence.

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Markov equivalence

- ${\cal D}$ and ${\cal D}'$ are equivalent if and only if:
- 1. $\mathcal D$ and $\mathcal D'$ have same *skeleton* (ignoring directions)
 - $2.~\mathcal{D}$ and \mathcal{D}' have same unmarried parents

but

Step 1: Identify skeleton, using that, for a faithful distribution

$$u \nsim v \iff \exists S \subseteq V \setminus \{u,v\} : X_u \perp\!\!\!\perp X_v \mid X_S.$$

continue for increasing cardinality of S. PC-algorithm exploits that only S with $S\subseteq$ ne(u) or $S\subseteq$ ne(v) needs checking, where ne refers to current Begin with complete graph and check first for $S=\emptyset$ and remove edges when independence holds. Then skeleton graph.

Step 2: Identify directions to be consistent with independence relations found in Step 1.

Exact properties of PC-algorithm

If P is faithful to DAG \mathcal{D} , PC-algorithm finds \mathcal{D}' equivalent to \mathcal{D} . It uses N independence checks where N is at most

$$N \le 2 \binom{|V|}{2} \sum_{j=0}^d \binom{|V|-1}{j} \le \frac{|V|^{d+1}}{(d-1)!},$$

where d is the maximal degree of any vertex in \mathcal{D} . So worst case complexity is exponential, but algorithm fast for sparse graphs.

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Empirical independence checks

For finite samples, independence checks can be performed as

- significance tests for independence;
- asymptotic model selection criteria such as BIC, AIC, etc.

$$IC_{\kappa}(\mathcal{D}) = \log \hat{L}(\mathcal{D}) - \kappa \dim(\mathcal{D})$$

with $\kappa=1$ for AIC , or $\kappa=\frac{1}{2}\log N$ for BIC .

► Bayes factors in local Bayesian approach;

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Situation less clear if P is not known, but estimated:

Constraint-based: Independence checks may randomly give errors.

Algorithms more robust than PC exist.

Most checks are made with separation set ${\cal S}$ small, so power high.

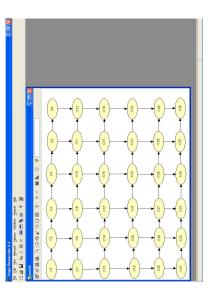
Asymptotically correct if e.g. marginal BIC or BF used in checks.

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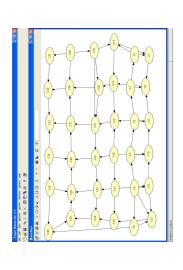
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Markov mesh model

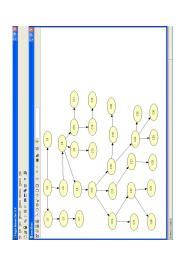






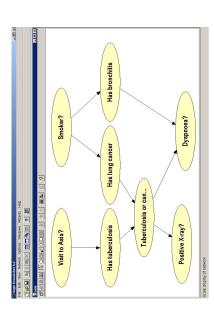
PC algorithm (HUGIN), 10000 simulated cases



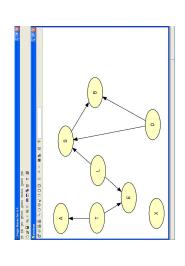


PC algorithm, 10000 cases, correct reconstruction

Chest clinic

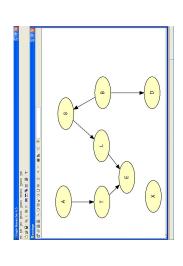






10000 simulated cases





100000 simulated cases

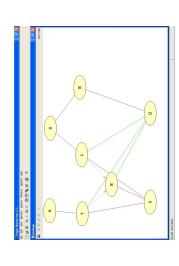
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This algorithm avoids early acceptance of conditional independences.

- ▶ if a dependence is established, believe it;
- ▶ if an independence is established, put it on hold for a while;
- condition (NPC): if a conditional dependence is established at proceed as in the PC algorithm, but insist on necessary path some point, there must be a connecting path explaining it.

Non-unique identification, involving ambiguous regions. User may resolve these.

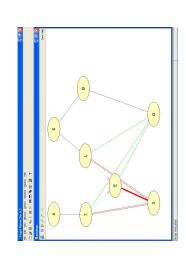




First stage

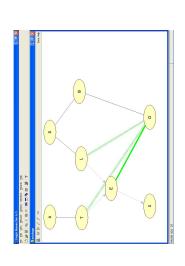
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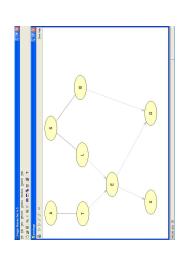
Resolving one ambiguity





Resolving another





Final model

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Structural equation systems
Computation of effects
Estimation of DAG structure
Constraint-based search
Constraint-based search

Searches directly in equivalence classes of DAGS.

Define score function $\sigma(P,\mathcal{D})$, measuring the adequacy of \mathcal{D} for P with the property that

$$\mathcal{D} \equiv \mathcal{D}' \Rightarrow \sigma(P, \mathcal{D}) = \sigma(P, \mathcal{D}').$$

Typically the score function will penalise ${\cal D}$ with unnecessary many links. BIC score satisfies condition. So does fully Bayesian score for certain classes of priors.

Equivalence class with maximal score is sought.

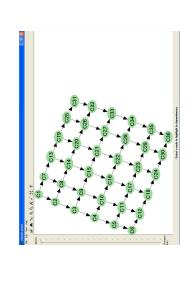
Greedy equivalence search

- 1. Initialize with empty DAG
- additional edge and go to class with highest score until no 2. Repeatedly search among equivalence classes with a single improvement.
- 3. Repeatedly search among equivalence classes with a single edge less and move to one with highest score - until no improvement.

For suitable score functions, this algorithm identifies correct equivalence class for P. Asymptotically correct if using BIC or fully Bayesian approach.

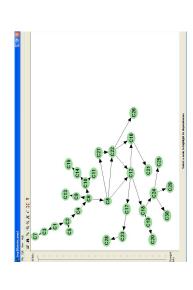
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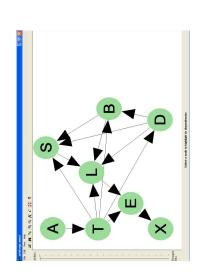
Crudest algorithm (WinMine), 10000 simulated cases

Bayesian GES on tree





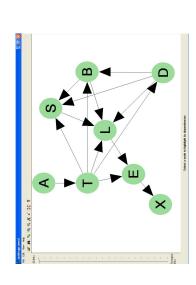
Bayesian GES on Chest Clinic



10000 cases



Bayesian GES on Chest Clinic



100000 cases

Structural equation systems
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Constraint-based search

More serious that one would rarely expect all causally relevant variables to be measured. Selection effects are also an issue.

More relevant to assume data obtained from P by marginalisation to subset V and conditioning with subset C so $W = V \cup U \cup C$, data represents P_V^C , where P is faithful to some DAG \mathcal{D} . Graphs that describe independence relations in such cases are Maximal Ancestral Graphs. Constraint-based methods for

Bayesian approach for MAGs seems out of hand.

identifying MAGs exist: FCI-algorithm.