Causal Discovery in Linear Non-Gaussian Models

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(joint work with Y. Samuel Wang)

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Goal: Estimate underlying causal relationships. What is possible?



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- Unique causal graph under special assumptions such as:
 - Non-linear functional relationships with additive noise
 - LiNGAM: Linear functional relationships with non-Gaussian errors (Shimizu, Hoyer, Hyvärinen, Kerminen, ...)

Causal Graphs



Directed Graph $G = (V, E_{\rightarrow})$:

- Nodes correspond to observed variables.
- Edges represent direct causal effects.

Terminology:

- If $v \to u$, then v is a parent of the child u.
- If $v \rightarrow \cdots \rightarrow u$, the v is an ancestor of the descendant u.
- Ayclic digraph = directed acyclic graph = DAG

LiNGAM (Linear Non-Gaussian Acyclic Model)

- Consider *p*-variate observation $Y = (Y_v)_{v \in V}$, so |V| = p.
- ▶ For convenience, assume *Y* centered.
- Linear system given by a DAG:

$$Y_{\mathbf{v}} = \sum_{u \in \mathrm{pa}(\mathbf{v})} \beta_{\mathbf{v}u} Y_{u} + \varepsilon_{\mathbf{v}}, \quad \mathbf{v} \in V,$$

where the error terms ε_v are independent and non-Gaussian.



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Theorem

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Practical implementations estimate W = A⁻¹ by maximizing "non-Gaussianity" of WY.

ICA-LiNGAM (Shimizu et al., 2006)

► LiNGAM:

$$Y = B Y + \varepsilon \iff Y = (I - B)^{-1} \varepsilon$$

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 - 1. Find an unmixing/separating matrix W, which has to equal I B up to permutation and scaling of rows.
 - 2. Permute rows of W to have no zero diagonal elements (resolves "up to permutation" as B corresponds to DAG).
 - 3. Scale diagonal elements to unity (resolves "up to scaling").

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• Practice: feasible method but issues (e.g., \hat{W} has all entries nonzero)

Direct-LiNGAM (Shimizu et al., 2011)

Main Idea:

- ▶ Regression residuals are linear combination of the independent errors.
- Source node is characterized by independence from residuals.

Theorem (Darmois-Skitovitch)

Let $\varepsilon_1, \ldots, \varepsilon_p$ be independent non-degenerate random variables. If $\sum_j a_j \varepsilon_j \perp \!\!\!\perp \sum_j b_j \varepsilon_j$, then

$$a_j b_j
eq 0 \implies arepsilon_j \sim Gaussian.$$

Direct-LiNGAM (Shimizu et al., 2011)

Example



$$\begin{split} Y_1 &= \varepsilon_1, \\ Y_2 &= \beta_{21} \, Y_1 + \varepsilon_2, \\ Y_3 &= \beta_{32} \, Y_2 + \varepsilon_3. \end{split}$$

Residuals adjusting for Y_1 satisfy:

$$\begin{aligned} Y_{2.1} &:= Y_2 - \mathbb{E}(Y_2 \mid Y_1) = Y_2 - \beta_{21}Y_1 &= \varepsilon_2, \\ Y_{3.1} &:= Y_3 - \mathbb{E}(Y_3 \mid Y_1) = Y_3 - \beta_{32}\beta_{21}Y_1 = \beta_{32}Y_{2.1} + \varepsilon_3. \end{aligned}$$

Observe that $Y_1 \perp (Y_{2.1}, Y_{3.1})$ and

Let $\Theta^{(z)} = (r_1, r_2, \dots, r_z)$ be the set of ordered nodes after step z.

Algorithm 1 Select an ordering
1:
$$\Theta^{(0)} = \emptyset$$
; $Y^{(0)} = Y$
2: for $z = 0, ..., p - 1$ do
3: Identify a source $r \notin \Theta^{(z)}$ using $Y^{(z)}$
4: for $v \notin \Theta^{(z)} \cup \{r\}$ do
5: $Y_v^{(z+1)} = Y_v^{(z)} - \hat{\beta}_{vr}Y_r^{(z)}$
6: end for
7: Update $\Theta^{(z+1)} = \text{Append}(\Theta^{(z)}, r)$.
8: end for
9: return $\Theta^{(p)}$ as an ordering
10: Prune ancestors which are not parents

$$\Theta^{(0)}=\emptyset$$

(a) "True" Graph of $Y^{(z)}$

(b) Estimated Graph

2

3

3

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$$\Theta^{(3)} = (1, 2, 3, 4)$$

(a) "True" Graph of $Y^{(z)}$





Two Problems

1. High-dimensional DAGs

- Allow for #variables = p > n = # observations.
- Assuming sparsity.
- Existing methods of Shimizu et al. (2006, 2011) and Hyvärinen and Smith (2013) not applicable.

2. Latent variables (Bow-free Acyclic Path Diagrams)

- Allow for certain types of unobserved confounding
- Existing methods involve difficult overcomplete ICA computations/require prior knowledge (Hoyer et al., 2008; Shimizu and Bollen, 2014) or may return inconclusive results (Entner and Hoyer, 2010; Tashiro et al., 2014)

Causal Discovery in High-Dimensional Settings https://arxiv.org/abs/1803.11273

Direct-LiNGAM Approach

- Problem in a high-dimensional setting:
 - Adjusting by all prior variables propagates error proportional to *p*.
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- Problem in a high-dimensional setting:
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 - Residuals are uninformative/zero if p > n.
- Solution: Only adjust by smallest set necessary.
- Need parameter/statistic to determine causal direction while adjusting for possible confounding.
- Selecting a source should be computationally inexpensive.

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Causal graph:

$$Y_1 \rightarrow Y_2$$

$$\frac{\mathbb{E}(Y_1Y_2)}{\mathbb{E}(Y_1^2)} = \frac{\mathbb{E}\left[\varepsilon_1(\beta_{21}\varepsilon_1 + \varepsilon_2)\right]}{\mathbb{E}(\varepsilon_1^2)} = \beta_{21}$$
$$\frac{\mathbb{E}(Y_1^2Y_2)}{\mathbb{E}(Y_1^3)} = \frac{\mathbb{E}\left[\varepsilon_1^2(\beta_{21}\varepsilon_1 + \varepsilon_2)\right]}{\mathbb{E}\left(\varepsilon_1^3\right)} = \beta_{21}$$

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 $\frac{\mathbb{E}(Y_1Y_2)}{\mathbb{E}(Y_1^2)} = \frac{\beta_{12}\mathbb{E}(\varepsilon_2^2)}{\beta_{12}^2\mathbb{E}(\varepsilon_2^2) + \mathbb{E}(\varepsilon_1^2)}$ $\frac{\mathbb{E}(Y_1^2Y_2)}{\mathbb{E}(Y_1^3)} = \frac{\beta_{12}^2\mathbb{E}(\varepsilon_2^3)}{\beta_{12}^3\mathbb{E}(\varepsilon_2^3) + \mathbb{E}(\varepsilon_1^3)}$

Now, $au_{1
ightarrow 2}
ot\equiv 0$.

 $(\neq 0$ generically, in particular, 3rd moments need to be non-Gaussian).

Moment Relation

For $u \neq v$, $C \subseteq V \setminus \{u, v\}$, and residual $Y_{v.C} = Y_v - \mathbb{E}(Y_v \mid Y_C)$:

$$\tau_{v.C \to u}^{(K)} := \mathbb{E}\left(Y_{v.C}^{K-1}Y_{u}\right) \mathbb{E}\left(Y_{v.C}^{2}\right) - \mathbb{E}\left(Y_{v.C}^{K}\right) \mathbb{E}\left(Y_{v.C}Y_{u}\right) \right|$$



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(i) If $u \notin pa(v)$, then

$$\min_{C} |\tau_{v.C \to u}^{(K)}| = 0.$$

Achieved for C = pa(v). If $|pa(v)| \le J$, testing $|C| \le J$ enough.

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(ii) If $u \in pa(v)$, then generically over sets $C \subseteq V \setminus (de(v) \cup \{v, u\})$

$$\min_{C} |\tau_{v.C \to u}^{(K)}| > 0$$

Using in Direct-LiNGAM recursion

- Given a set of already 'ordered nodes'.
- ► Find source v in subgraph of 'unordered nodes' by

$$\max_{u} \min_{C} |\tau_{v.C \to u}^{(K)}| = 0.$$

where $u \in$ 'unordered' and $|C| \leq J$ subset of 'ordered'.

- Add v to 'ordered nodes'.
- In practice take v with smallest 'max-min'.

Modified Direct-LiNGAM

Concentration inequalities for sample moments give:

Under 'strong parental faithfulness', for log-concave errors and DAG of in-degree J, modified Direct-LiNGAM is consistent if

$$rac{\log(p)J^{5/2}}{n^{1/(2K)}} \ o \ 0.$$

Parental faithfulness: Total effect between parent and child does not vanish when adjusting on non-descendants.

Computation:

- Testing restricted subsets becomes computationally demanding:

$$|\{C: C \subseteq V_1, |C| = J\}| = O(|V_1|^J)$$

- Pruning:

Record when moment relations indicate that node is ancestor but not parent of $v \in$ 'unordered'.

Illustration



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Causal Discovery with Unobserved Confounding

Capturing Unobserved Confounding



Figure: Children of a common unobserved parent

Capturing Unobserved Confounding



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Capturing Unobserved Confounding



Figure: Children of a common unobserved parent

- Mixed graph $G = (V, E_{\rightarrow}, E_{\leftrightarrow}).$
- Non-Gaussian Linear Model:

$$Y_{\mathbf{v}} = \sum_{u \in \mathrm{pa}(\mathbf{v})} \beta_{\mathbf{v}u} Y_u + \varepsilon_{\mathbf{v}}, \quad \mathbf{v} \in \mathbf{V},$$

with $\mathbb{E}(\varepsilon_v \varepsilon_u) = \omega_{vu} \neq 0$ only if u = v or $u \leftrightarrow v \in E_{\leftrightarrow}$ (siblings).

- Continue to assume that E_{\rightarrow} is acyclic.
- ▶ In which settings might we be able to infer the underlying graph G?

Existing Work

Gaussian or conditional independence based methods:

- Constraint testing¹ and greedy methods² for maximal ancestral graphs
- ► Greedy search³ for bow-free acyclic path diagrams (BAPs)

Explicitly non-Gaussian:

- Overcomplete ICA⁴
- Bayesian specification⁵
- Conservative Direct-LiNGAM approach⁶
- ParceLiNGAM⁷ (still use independence of residuals from regression)

⁴Hoyer et al. (2008)

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<sup>7</sup>Tashiro et al. (2014)
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¹Richardson and Spirtes (2002),Colombo et al. (2012),Claassen et al. (2013)

²Triantafillou and Tsamardinos (2016)

³Nowzohour et al. (2017)

⁵Shimizu and Bollen (2014)

⁶Entner and Hoyer (2010)

Ancestral Graphs

- ParceLiNGAM applies Direct-LiNGAM (locating sources) and its "dual" (locating sinks) to all subsets of variables.
- Amounts to checks of

$$Y_{\nu.C} = Y_{\nu} - \mathbb{E}(Y_{\nu} \mid Y_C) \perp Y_C, \quad \nu \in V, \ C \subseteq V \setminus \{\nu\}.$$

- ParceLiNGAM is sound: returns a partial ordering that extends to a topological ordering of the mixed graph G.
- Example:



Theorem

ParceLiNGAM recovers a topological ordering of G iff G ancestral.

What's special about Ancestral Graphs?

A graph is ancestral if it does not contain semi-directed cycles of form

 $v \leftrightarrow w \rightarrow \cdots \rightarrow v$.

Theorem

(i) The graph G is ancestral if and only if

$$\mathbb{E}(Y_{v} \mid Y_{\mathrm{pa}(v)}) = \sum_{c \in \mathrm{pa}(v)} \beta_{vc} Y_{c} \quad \text{for all nodes } v.$$

(ii) The graph G is ancestral if and only if

$$\left[\varepsilon_{v} = Y_{v} - \sum_{u \in \mathrm{pa}(v)} \beta_{vu} Y_{u}\right] \perp \left[Y_{\mathrm{pa}(v)} = f(\varepsilon_{\mathrm{an}(v)})\right] \quad \text{for all nodes } v.$$

▶ Regression residual $Y_{\nu} - \mathbb{E}(Y_{\nu} | Y_{pa(\nu)}) = \varepsilon_{\nu}$ independent of $Y_{pa(\nu)}$.

Bow-Free Acyclic Graphs

Bow-free: At most one edge between any pair of nodes





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Complications exemplified (top right):

Bow-Free Acyclic Graphs

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Complications exemplified (top right):

Bow-free acyclic graphs can be recovered :

i) (β_{vu}) generically identifiable from Var(Y). In fact, each $\beta_{v,pa(v)}$ identifiable from Var $(Y_{an(v)})$ and $\mathbb{E}(Y_v \mid Y_{an(v)})$. ii) $\varepsilon_v \perp \varepsilon_{pa(v)}$.





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(b) Test again with adjusted observations and estimates of β_{vu} :



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(b) Test again with adjusted observations and estimates of β_{vu} :

- Discovery of $2 \rightarrow 3$ and β_{32} . Form $\overline{Y}_3 = Y_3 - \beta_{32}Y_2 = \varepsilon_3$, and find $\overline{Y}_3 \perp \overline{Y}_2 = \varepsilon_2$;
- Also, $1 \notin pa(3)$ as even after correct adjustment we have $\varepsilon_1 \not\perp \varepsilon_3$.

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(c) Repeat:

▶ Infer 2 → 4 and 3 → 4, so discover $pa(4) \subset \{2,3\}$ and $\{2,3\} \cap sib(4) = \emptyset$. Discover 1 $\notin pa(4)$.



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(d) Prune \rightarrow edges accounting for dependence induced by \leftrightarrow .



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- ▶ Also, $1 \notin pa(3)$ as even after correct adjustment we have $\varepsilon_1 \not\perp \varepsilon_3$.

(c) Repeat:

▶ Infer 2 → 4 and 3 → 4, so discover $pa(4) \subset \{2,3\}$ and $\{2,3\} \cap sib(4) = \emptyset$. Discover 1 $\notin pa(4)$.

(d) Prune \rightarrow edges accounting for dependence induced by \leftrightarrow .

Simulations: Maximal Ancestral Graphs



Figure: 1000 Random MAGs with p = 5. Solid lines are log-normal errors; dotted lines are Gaussian errors.

Simulations: BAPs



Figure: 1000 Random BAPs with p = 5. Solid lines are log-normal errors; dotted lines are Gaussian errors.

Data Example: Ecology Data from Grace et al. (2016)



(a) BAP representation of plot specific model from Grace et al. (2016).



(b) Discovered model matches 16 out of 28 edges. Probability of 16 or more edges by random guessing is .002.

To the organizers, a big:

THANK YOU!

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