

# BUILD with Precision: Bottom-Up Inference of Linear DAGs

Gonzalo Mateos

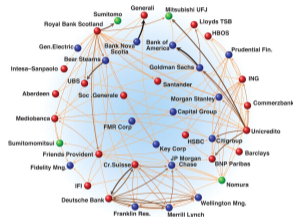
Dept. of Electrical and Computer Engineering and Goergen Institute for Data Science and AI  
University of Rochester  
gmateosb@ece.rochester.edu

**Collaborators:** Hamed Ajorlou, Samuel Rey, Geert Leus, and Antonio G. Marques  
**Acknowledgment:** NSF Award ECCS-2231036, Spanish AEI PID2022-136887NB-I00

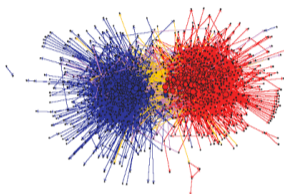
June 10, 2026

- ▶ Graphs are natural models for relational data that can help to learn in various timely applications

Economic Networks



Social and Information Networks



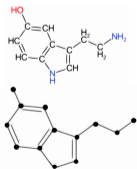
Internet



3D Meshes



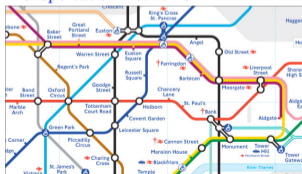
Molecules



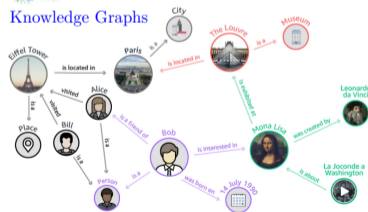
Brain Connectomes



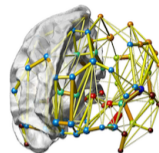
Transportation Networks



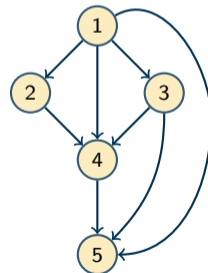
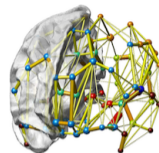
Knowledge Graphs



- ▶ **Undirected topology inference** from nodal observations [Kolaczyk'09]
  - ▶ Partial correlations and conditional dependence [Dempster'74]
  - ▶ Sparsity [Friedman et al'07] and consistency [Meinshausen-Buhlmann'06]
- ▶ Key in neuroscience and bioinformatics
  - ⇒ Functional network from fMRI signals [Sporns'10]
  - ⇒ Gene-regulatory networks from microarray data [Mazumder-Hastie'12]



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- ▶ **This work:** learn the structure of **directed acyclic graphs (DAGs)**
- ▶ DAGs have become prominent models in various ML applications
  - ⇒ Conditional independences among variables in Bayesian networks
  - ⇒ DAG edges may have **causal interpretations**
  - ⇒ Bio [Sachs et al'05], genetics [Zhang et al'13], finance [Sanford-Moosa'12]
- ▶ **Challenges:** directionality, acyclicity (combinatorial constraint), identifiability



Background: Linear SEMs and DAG learning

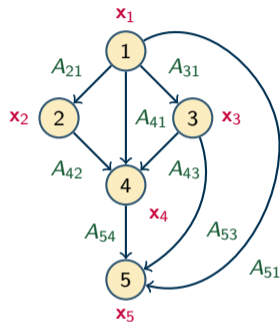
Idea: Precision matrix structure and the BUILD algorithm

Experimental performance evaluation

Concluding remarks

H. Ajorlou *et al*, "BUILD with precision: Bottom-up inference of linear DAGs," *ICASSP*, 2026; see also arXiv:2512.16111 [cs.LG]

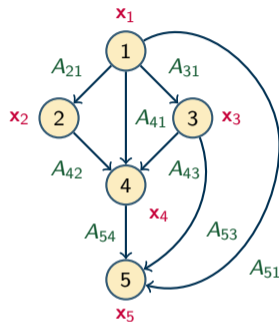
- ▶ DAG  $\mathcal{D}(\mathcal{V}, \mathcal{E}, \mathbf{A}) \in \mathbb{D}$ , vertices  $\mathcal{V} = \{1, \dots, N\}$ , edges  $\mathcal{E} \subseteq \mathcal{V} \times \mathcal{V}$ 
  - ⇒ Adjacency matrix  $\mathbf{A} = [\mathbf{a}_1, \dots, \mathbf{a}_N] \in \mathbb{R}^{N \times N}$  of edge weights
  - ⇒ Entry  $A_{ij} \neq 0$  indicates a directed link from node  $j$  to  $i$
- ▶ Random vector  $\mathbf{x} = [x_1, \dots, x_N] \in \mathbb{R}^N$ , joint Markov  $p(\mathbf{x})$  w.r.t.  $\mathcal{D}$ 
  - ⇒ DAG  $\mathcal{D}$  encodes conditional independencies among variables in  $\mathbf{x}$
  - ⇒ Each  $x_i$  depends only on its parents  $PA_i = \{j \in \mathcal{V} : A_{ij} \neq 0\}$



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- ▶ Linear structural equation model (SEM) to generate  $p(\mathbf{x})$

$$x_i = \sum_{j \in PA_i} A_{ij} x_j + z_i, \quad \forall i \in \mathcal{V}$$

$\Rightarrow$  Mutually independent, exogenous noises  $\mathbf{z} = [z_1, \dots, z_N]^T$

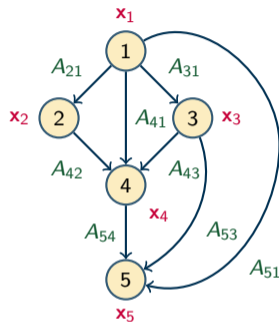


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- ▶ Q: Estimate  $\mathbf{A}$  (learn DAG  $\mathcal{D}$ ) using dataset  $\mathbf{X} \in \mathbb{R}^{N \times M}$  with  $M$  i.i.d. samples from  $p(\mathbf{x})$ ?



- ▶ **Learning** a DAG **solely** from observational data **X** is **NP-hard** [Chickering'96]
- ▶ **Combinatorial search:** GES [Chickering'02], PC algorithm [Spirtes et al'00]
  - ⇒ Scale poorly:  $|\mathbb{D}|$  grows **super-exponentially** in  $N$
- ▶ **Continuous optimization:** smooth acyclicity functions  $\mathcal{H}(\mathbf{A}) = 0 \iff \mathcal{D} \in \mathbb{D}$ 
  - ⇒ NOTEARS [Zheng et al'18], DAGMA [Bello et al'22], CoLiDE [Saboksayr et al'24]
  - ⇒ Scale well, but face **non-convex** optimization challenges
- ▶ **Order-based:** recover causal ordering, then estimate edges
  - ⇒ TOPO [Deng et al'23], information theoretic scheme [Daskalakis et al'25]
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**Our contribution:** a **deterministic**, **bottom-up** algorithm that leverages the **precision matrix** structure to recover DAGs **without** continuous optimization or combinatorial search

► **Linear Gaussian SEM:**  $\mathbf{x} = \mathbf{Ax} + \mathbf{z}$ , with  $\mathbf{z} \sim \mathcal{N}(\mathbf{0}, \sigma^2 \mathbf{I}_N)$

⇒ Signal covariance:  $\mathbf{\Sigma} = \mathbb{E}[\mathbf{xx}^\top] = \sigma^2 (\mathbf{I}_N - \mathbf{A})^{-1} (\mathbf{I}_N - \mathbf{A}^\top)^{-1}$

⇒ **Precision matrix:**  $\mathbf{\Theta} = \mathbf{\Sigma}^{-1} = \sigma^{-2} (\mathbf{I}_N - \mathbf{A} - \mathbf{A}^\top + \mathbf{A}^\top \mathbf{A})$

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**Lemma 1 (Precision matrix entries).** Let  $\text{CH}_j = \{i \in \mathcal{V} : A_{ij} \neq 0\}$  be the **children** of  $j$ . Then:

$$\sigma^2 \Theta_{ij} = \begin{cases} 1 + \sum_{k \in \text{CH}_i} A_{ki}^2, & i = j \\ -A_{ij} + \sum_{k \in \text{CH}_i \cap \text{CH}_j} A_{ki} A_{kj}, & i > j \end{cases}$$

► Support of  $\mathbf{\Theta}$  corresponds to the **moralized graph** of  $\mathcal{D}$  [Lauritzen'96]

⇒ Undirected graph, connecting all nodes in  $\text{PA}_i = \{j \in \mathcal{V} : A_{ij} \neq 0\}$ ,  $i \in \mathcal{V}$

- ▶ If node  $i$  is a **leaf** of  $\mathcal{D}$ , then  $\text{CH}_i = \emptyset$  and  $\mathbf{a}_i = \mathbf{0}_N$

**Corollary 1 (Leaf identification).** A node  $i \in \mathcal{V}$  is a leaf of  $\mathcal{D}$  if and only if  $\Theta_{ii} = \sigma^{-2}$

$\Rightarrow$  All **non-leaf** nodes must have  $\Theta_{jj} > \sigma^{-2}$

$\Rightarrow$  Resolution gap lower bounded by  $\Delta = \sigma^{-2} \min_{i,j \in \mathcal{V}} A_{ij}^2$

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- ▶ **Upshot:** Once a leaf  $i$  is identified, we can **recover its parents** and **edge weights**:

$$A_{ij} = \begin{cases} -\sigma^2 \Theta_{ij}, & j < i \\ 0, & j \geq i \end{cases}$$

$\Rightarrow$  Off-diagonal entries in the  $i$ -th row of  $\Theta$  are scaled copies of the  $i$ -th row of  $\mathbf{A}$  (i.e.,  $\text{PA}_i$ )

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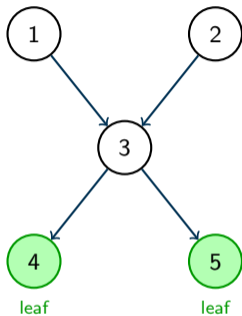
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- ▶ **Core idea:** iteratively **identify** leaf nodes  $\rightarrow$  **recover** their parents  $\rightarrow$  **prune** and repeat  
 $\Rightarrow$  **Bottom-up** reconstruction of the entire DAG given  $\Theta$



$\Theta$

	1	2	3	4	5
1	$> \sigma^{-2}$	★	$\neq 0$	0	0
2	★	$> \sigma^{-2}$	$\neq 0$	0	0
3	$\neq 0$	$\neq 0$	$> \sigma^{-2}$	$-\frac{A_{43}}{\sigma^2}$	$-\frac{A_{53}}{\sigma^2}$
4	0	0	$-\frac{A_{43}}{\sigma^2}$	$= \sigma^{-2}$	0
5	0	0	$-\frac{A_{53}}{\sigma^2}$	0	$= \sigma^{-2}$

- leaf:  $\Theta_{ij} = \sigma^{-2}$
- non-leaf:  $\Theta_{ij} > \sigma^{-2}$
- parent edges
- moralized

- ▶ Leaf rows of  $\Theta$  directly reveal parent identities and edge weights
  - ⇒ Off-diagonal entries  $\Theta_{ij}$  in leaf row  $i$ :  $A_{ij} = -\sigma^2 \Theta_{ij}$
  - ⇒ Moralized entries (★) arise from shared children, not direct edges

- ▶ After identifying leaf  $i$  and recovering its incident edges, **remove** its contribution

⇒ Partition  $\Theta$  with leaf  $i$  isolated

$$\Theta = \begin{bmatrix} [\Theta]_{ii} & [\Theta]_{i,\mathcal{R}} \\ [\Theta]_{\mathcal{R},i} & [\Theta]_{\mathcal{R},\mathcal{R}} \end{bmatrix}$$

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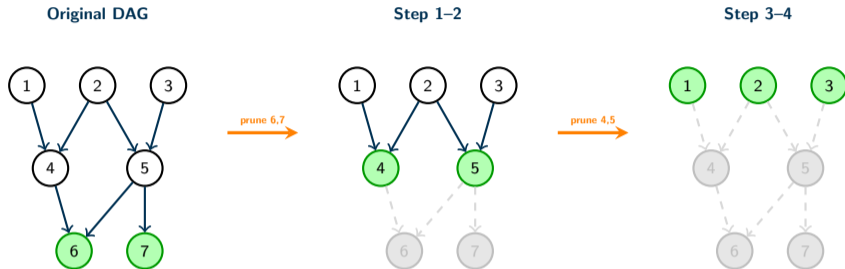
- ▶ **Updated precision matrix** for the reduced DAG

$$\Theta_{\mathcal{R}\mathcal{R}} = [\Theta]_{\mathcal{R},\mathcal{R}} - [\Theta]_{ii}^{-1}[\Theta]_{\mathcal{R},i}[\Theta]_{i,\mathcal{R}}$$

⇒ Since  $[\Theta]_{ii} = \sigma^{-2}$  for a leaf, this simplifies to a **rank-one update**

⇒ Resulting  $\Theta_{\mathcal{R}\mathcal{R}}$  describes conditional dependencies of the **pruned DAG**

- ▶ **Iterate**: find next leaf, recover parents, prune → **full DAG recovery**



► **Two phases:**

⇒ **Phase 1:** estimate  $\hat{\Theta}$  from data  $\mathbf{X}$     **Phase 2:** iterative bottom-up DAG recovery

► **Per step:** find leaf  $\mathcal{O}(N)$ , recover parents  $\mathcal{O}(d)$ , prune  $\mathcal{O}(d^2)$  ⇒ **Total:**  $\mathcal{O}(N^2)$  for Phase 2

► **Guarantee:** Given ensemble precision matrix  $\Theta$ , BUILD **exactly** recovers  $\mathbf{A}$

F. Kelner *et al*, "Learning some popular Gaussian graphical models without condition number bounds," *NeurIPS*, 2020

- ▶ **Graphs:** Erdős–Rényi DAGs,  $N = 200$  nodes, expected degree  $d = 4$ 
  - ⇒ Edge weights  $A_{ij}$  drawn uniformly from  $(-2, -0.5) \cup (0.5, 2)$
- ▶ **Data:**  $M = 1,000$  i.i.d. samples from linear SEM with **homoscedastic Gaussian** noise,  $\sigma^2 = 1$
- ▶ **Metrics:**
  - ⇒ **SHD** (Structural Hamming Distance): edge corrections to recover true graph
  - ⇒ **FDR** (False Discovery Rate): fraction of spurious edges
  - ⇒ **TPR** (True Positive Rate): fraction of correctly detected edges
  - ⇒ **NMSE**: normalized MSE of estimated edge weights
- ▶ **Baselines:** CoLiDE, DAGMA, Gao et al'22, Daskalakis et al'25
- ▶ **Reproducibility:** Code at <https://github.com/hamedajorlou/BUILD>

M. Gao *et al*, "Optimal estimation of Gaussian DAG models," *AISTATS*, 2022

C. Daskalakis *et al*, "Learning Gaussian DAG models without condition number bounds," *ICML*, 2025

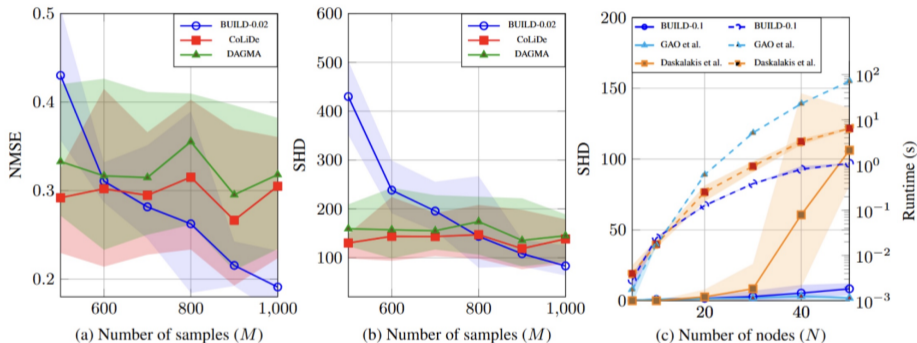
**Table:** Comparison for different refreshing rates. ER4 graphs,  $N = 200$ ,  $M = 1,000$ . Mean  $\pm$  std over 20 trials.

Baseline	SHD $\downarrow$	FDR $\downarrow$	TPR $\uparrow$	Time (s) $\downarrow$
BUILD-0.005	<b>17.40 <math>\pm</math> 3.64</b>	<b>0.004 <math>\pm</math> 0.003</b>	<b>0.983 <math>\pm</math> 0.004</b>	1203.20 $\pm$ 31.65
BUILD-0.01	45.20 $\pm$ 10.89	0.035 $\pm$ 0.012	0.981 $\pm$ 0.004	620.77 $\pm$ 15.81
BUILD-0.02	81.65 $\pm$ 28.53	0.072 $\pm$ 0.029	0.977 $\pm$ 0.004	323.72 $\pm$ 7.91
BUILD-0.04	122.90 $\pm$ 34.02	0.112 $\pm$ 0.030	0.971 $\pm$ 0.007	168.17 $\pm$ 3.80
CoLiDE	114.40 $\pm$ 43.11	0.031 $\pm$ 0.026	0.888 $\pm$ 0.031	109.01 $\pm$ 22.80
DAGMA	135.95 $\pm$ 36.19	0.035 $\pm$ 0.021	0.864 $\pm$ 0.027	<b>93.92 <math>\pm</math> 19.43</b>

- **BUILD-0.005** achieves **substantially lower SHD** and **higher TPR** than all baselines
  - ⇒ FDR **consistently decreases** with more frequent refreshing
  - ⇒ **Trade-off:** BUILD-0.04 matches CoLiDE accuracy at **comparable runtime**

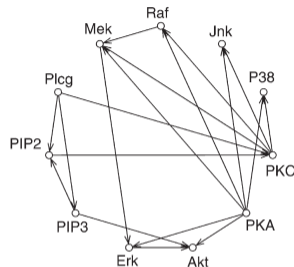
S. S. Saboksayr *et al*, "CoLiDE: Concomitant linear DAG estimation," *ICLR*, 2024

K. Bello *et al*, "DAGMA: Learning DAGs via M-matrices and a log-determinant acyclicity characterization," *NeurIPS*, 2022



- ▶ BUILD-0.02 **outperforms** CoLiDe and DAGMA once  $M \geq 800$  samples available
  - ⇒ Edge weight estimation (**NMSE**) also improves with more data
- ▶ Markedly **improved error-runtime tradeoffs** than order-based methods

- ▶ Tested **BUILD** on the Sachs dataset [Sachs et al'05]
  - ⇒ Cytometric measurements from human immune system
  - ⇒ Comprises  $N = 11$  proteins, 17 edges, and  $M = 853$  samples
  - ⇒ Associated DAG is obtained through experimental methods
  
- ▶ **BUILD** attains lowest SHD to date for this problem



**Table:** DAG recovery performance on the Sachs dataset

	GOLEM-EV	GOLEM-NV	DAGMA	SortNRegress	DAGuerreotype	GES	CoLiDE-EV	CoLiDE-NV
SHD	22	15	16	13	14	13	13	<b>12</b>
SID	49	58	52	47	50	56	47	<b>46</b>
SHD-C	19	<b>11</b>	15	13	12	<b>11</b>	13	14
FDR	0.83	0.66	<b>0.5</b>	0.61	0.57	<b>0.5</b>	0.54	0.53
TPR	0.11	0.11	0.05	0.29	0.17	0.23	0.29	<b>0.35</b>

K. Sachs et al, "Causal protein-signaling networks derived from multiparameter single-cell data," *Science*, 2005

- ▶ Proposed **BUILD**: a **deterministic**, **bottom-up** algorithm for DAG learning
  - ⇒ Exploits **precision matrix structure** of linear Gaussian SEMs (Lemma 1, Corollary 1)
  - ⇒ Iteratively identifies **leaf nodes**, recovers **parents and edge weights**, and **prunes**
  - ⇒ **Exact** recovery given the ensemble precision matrix in  $\mathcal{O}(N^2)$  time
  - ⇒ **Refreshing scheme** to mitigate finite-sample error propagation

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  - ⇒ **Refreshing scheme** to mitigate finite-sample error propagation
- ▶ **Ongoing and future work:**
  - ⇒ Formalizing **estimation error bounds** and **sample-complexity guarantees**
  - ⇒ Extension to **non-Gaussian** SEMs