Disentangling Mixtures of Unknown Causal Interventions

Introduction

Causal Bayesian Networks [1] have become a popular choice to model causal relationships in data. They are defined as DAGs whose nodes correspond to random variables and edges denote immediate causal relationships. They can simulate external intervention via the do() operator, which breaks the causal influence of parents and forcibly fixes variables to desired values. In real situations, interventions are not always perfect and often end up affecting unintended off-target variables [2]. Since these off-target effects could be stochastic, same intervention could lead to different off-target interventions on different individuals [3]. Thus the data collected becomes a mixture of unknown interventions, and disentangling it to uncover participating interventions can be of high value in many applications (e.g. gene-editing).

Problem Formulation

Definition: Given a CBN \mathcal{G} on $\mathbf{V} = \{V_1, \ldots, V_N\}$ having distribution $\mathbb{P}(V)$, a mixture of interventions is defined as,

 $\mathbb{P}_{mix}(oldsymbol{V}) = \sum_{i=1}^{m} \pi_i \mathbb{P}_{oldsymbol{t}_i}(oldsymbol{V})$ $\pi_i \in \mathbb{R}^+, \ \sum_{i=1}^m \pi_i = 1, \ \mathbb{P}_{t_i}(V) = \mathbb{P}(V|do(t_i)).$ Question: Given \mathcal{G} , $P(\mathbf{V})$, $\mathbb{P}_{mix}(V)$, identify the unknown intervention target set $\mathcal{T} = \{(\boldsymbol{t}_i, \pi_i) : i \in [m]\}$?

Assumptions

In general intervention target-set \mathcal{T} is not unique. To be able to identify this set from $\mathbb{P}_{mix}(V)$, we make additional assumptions: **1 Exclusion:** For every V_i , $\exists \bar{v}_i$ such that $\bar{v}_i \notin t_j$ for all $t_j \in \mathcal{T}$. **2** Positivity: $\mathbb{P}(\boldsymbol{v}) > 0$ for all settings \boldsymbol{v} of \boldsymbol{V} .

Main Result

Theorem: For $\mathbb{P}_{mix}(V)$ generated by \mathcal{T} satisfying *exclusion*: **1** There is a unique \mathcal{T} satisfying *exclusion* that generates it. Objective access to \mathcal{G} , $\mathbb{P}(\mathbf{V})$ and $\mathcal{P}_{mix}(\mathbf{V})$, \mathcal{T} can be identified in $n * (m * k_{max})^{O(1)}$ time. Moreover, the algorithm can be modified to work with finitely many samples from the distributions.

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Proof By Induction on |V|





Figure 1:Identifiability for |V| = 1

Induction Step

Inductive Hypothesis: Assume true for \mathcal{G} with N nodes and $\mathbb{P}_{mix}(V)$ satisfying exclusion.

Induction Step: Show for N + 1 nodes:

- Marginalize V_{N+1} in $\mathbb{P}(\mathbf{V})$, $\mathbb{P}_{mix}(\mathbf{V})$. • Recursively compute targets $s_i, i \in [q]$ for marginalized mixture.
- **3** Possible lifts of \boldsymbol{s}_i are $\boldsymbol{s}_i \cup \{v\}, v \in V_{N+1}$.
- **4** Traverse s_i in non-decreasing order. Evaluate Equation 2 on $v_{i,l} = s_i \cup s_{-i} \cup \{v^l\}$. Here, $s_{-i} = \{\bar{v}_i : V_i \notin S_i\}, v^l \in V_{N+1}$ **5** Equation 2 simplifies to:

$$\mathbb{P}_{mix}(\boldsymbol{v}_{i,l}) - \sum_{j=1}^{i-1} \sum_{\boldsymbol{s} \in \mathcal{S}_j} \pi_{\boldsymbol{s}} \mathbb{P}_{\boldsymbol{s}}(\boldsymbol{v}_{i,l}) = \sum_{\boldsymbol{s} \in \mathcal{S}_i} \pi_{\boldsymbol{s}} \mathbb{P}_{\boldsymbol{s}}(\boldsymbol{v}_{i,l})$$
(3)

6 By varying $v^{l} \in V_{N+1}$ in Equation 3, obtain a linear system and solve it using techniques similar to base case.

 $\mathbb{P}_{mix}(\boldsymbol{V}) = \sum_{\boldsymbol{s}_i} \sum_{v} \pi_{\boldsymbol{s}_i \cup \{v\}} \mathbb{P}_{\boldsymbol{s}_i \cup \{v\}}(\boldsymbol{V})$ (2)





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Simulation Results

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Crispr/cas9 can mediate high-efficiency off-target mutations in mice in vivo.

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