

STATS 571/671 Causal Inference Winter 2026

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Guest Lecture: Time-varying confounding and treatments

April 9, 2026

Overview

- 1 Graphical models
 - Graphs and semantics
 - Probabilistic DAG
 - Causal DAG
- 2 Single treatment
- 3 Time-varying treatments
 - Time-varying confounder
 - Marginal structural model

Graphical models

Single treatment
Time-varying treatments

Graphs and semantics
Probabilistic DAG
Causal DAG

Graphical models

Statistical graphs

A statistical graph is a graph over a vertex set V with one or more types of edges.
It is a compact (and intuitive!) form for encoding and reasoning about **dependencies**.

① Probabilistic graphical models.

absence of edge between $u, v \implies$ some form of independence between X_u and X_v
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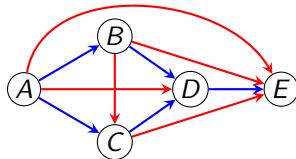
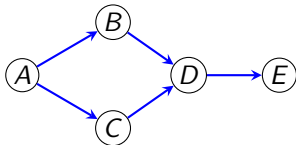
Statistical graphs

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1 Probabilistic graphical models.

absence of edge between $u, v \implies$ some form of **independence** between X_u and X_v

👉 For example, in this **Directed Acyclic Graph (DAG)**



The missing ' $B \rightarrow C$ ' posits

$$P(C \mid A, \textcolor{red}{B}) = P(C \mid A) \iff \boxed{B \perp\!\!\!\perp C \mid A}$$

Statistical graphs

A statistical graph is a graph over a vertex set V with one or more types of edges. It is a compact (and intuitive!) form for encoding and reasoning about **dependencies**.

① Probabilistic graphical models.

absence of edge between $u, v \implies$ some form of **independence** between X_u and X_v

- Undirected Graph (UG)
- Directed Acyclic Graph / Bayesian Network (DAG)
- Completed Partially Directed Acyclic Graph / Essential Graph (CPDAG)
- Partial Ancestral Graph (PAG)
- Local Independence Graph

👉 They represent a set of distributions over $(X_v : v \in V)$.

Statistical graphs

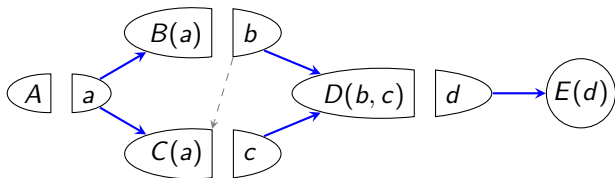
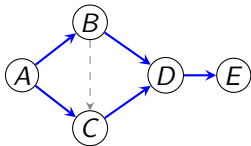
② Causal graphical models.

absence of $u \rightarrow v \implies$ intervening on X_u has no direct effect on X_v

Statistical graphs

② Causal graphical models.

absence of $u \rightarrow v \implies$ intervening on X_u has **no direct effect** on X_v



SWIG/FFRCISTG model: The absence of ' $B \rightarrow C$ ' encodes that $C(a, b) = C(a)$, i.e., C ignores any input from b .

Statistical graphs

② Causal graphical models.

absence of $u \rightarrow v \implies$ intervening on X_u has **no direct effect** on X_v

- Directed Acyclic Graph / Bayesian Network (DAG)
- Acyclic Directed Mixed Graph (ADMG)

👉 They represent a set of distributions over all the counterfactuals $X(\cdot)$.
 $\hookrightarrow X(\cdot) = (X_v(x_I) : v \in V, I \subseteq V, x_I \in \mathcal{X}_I)$
 $X(\cdot)$ contains $X(\emptyset)$, the **naturally occurring** random variables.

Semantics

A DAG can be either a probabilistic graphical model or a causal graphical model, depending on the **semantics** you use to interpret it.

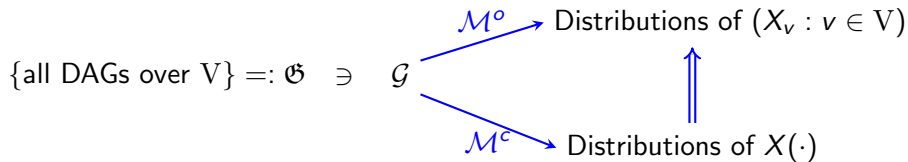
👉 A statistical graph has no intrinsic meaning until you interpret it with certain semantics!

Semantics

A DAG can be either a probabilistic graphical model or a causal graphical model, depending on the **semantics** you use to interpret it.

👉 A statistical graph has no intrinsic meaning until you interpret it with certain semantics!

► Consider a DAG $\mathcal{G}$ over a finite vertex set V .



- $\mathcal{M}^o(\mathcal{G})$ is a probabilistic model (aka Markov properties)
- $\mathcal{M}^c(\mathcal{G})$ is a causal model
- $\mathcal{M}^c(\mathcal{G}) \implies P(\{X_v(\emptyset) : v \in V\}) \in \mathcal{M}^o$

👉 **causal discovery**

DAG as a probabilistic model

Let the probabilistic semantics of a DAG be

$$\begin{aligned}\mathcal{M}^o(\mathcal{G}) &:= \{P : p(X) \text{ factorizes according to } \mathcal{G}\} \\ &= \left\{ P : p(X_v : v \in V) = \prod_{v \in V} p(X_v \mid X_{\text{Pa}(v)}) \right\}.\end{aligned}$$

Theorem Factorization $\iff$ Global Markov, where

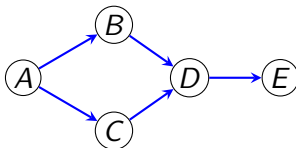
► Global Markov property: For disjoint $A, B, C \subset V$,

$$A \perp\!\!\!\perp B \mid C \implies X_A \perp\!\!\!\perp X_B \mid X_C [P], \quad P \in \mathcal{M}^o(\mathcal{G}).$$

👉 ' $A \perp\!\!\!\perp B \mid C$ ' means C blocks all the d-connecting paths between A and B .

DAG as a probabilistic model: Generating data

We can easily generate data by sequentially drawing from $p(X_v \mid X_{\text{Pa}(v)})$.



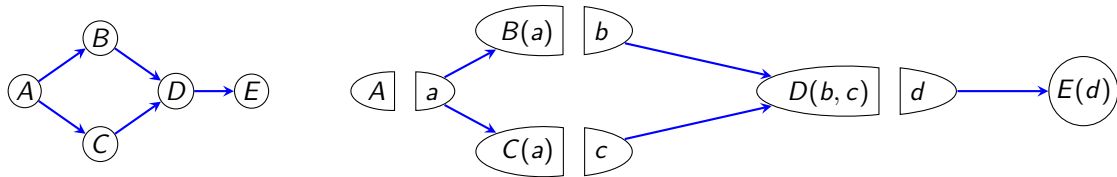
Following the topological ordering $A \prec B \prec C \prec D \prec E$,

- 1 Draw $A \sim P(A)$
- 2 Draw $B \sim P(B \mid A)$, $C \sim P(C \mid A)$
- 3 Draw $D \sim P(D \mid B, C)$
- 4 Draw $E \sim P(E \mid D)$

 Causal model: an alternative way of generating data.

DAG as a causal model (I): One-step-ahead counterfactuals

► Let $\mathcal{M}^c$ be the **FFRCISTG/SWIG causal model** (J. Robins, 1986; Richardson & Robins, 2013).



1 Draw $A \sim P(A)$

2 Independent of A, draw

👉 $A \perp\!\!\!\perp B(a), C(a)$ for every a

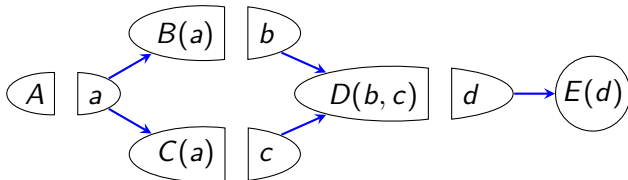
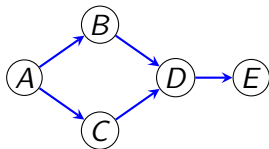
$B(a) \sim P(B \mid A = a), \quad C(a) \sim P(C \mid A = a), \quad \text{for every } a.$

3 Independent of previously drawn, draw

$D(b, c) \sim P(D \mid B = b, C = c), \quad \text{for every } b, c.$

4 Independent of previously drawn, draw

DAG as a causal model (II): Recursive substitution



Under **no intervention**, the **observed distribution** follows from

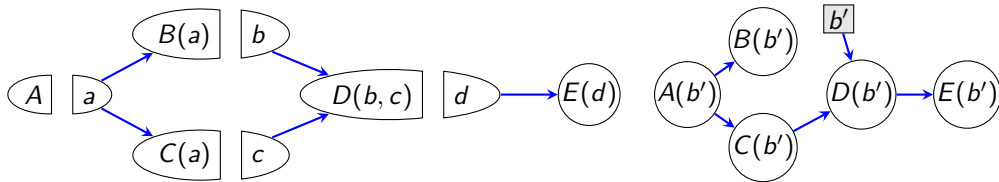
- 1 $A = A$,
- 2 $B = B(A)$, $C = C(A)$,
- 3 $D = D(B, C)$,
- 4 $E = E(D)$.

► Clearly, $(A, B, C, D, E) \sim P$

DAG as a causal model (III): Intervention

- Consider an **intervention** that imposes value b' to B . We want to generate **counterfactuals**

$$A(b'), B(b'), C(b'), D(b'), E(b').$$

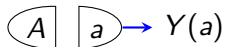


- 1 $A(b') = A$,
- 2 $B(b') = B(A(b')) = B(A)$ and $C(b') = C(A(b')) = C(A)$
👉 $B(b')$ is the **naturally occurring** value of B
- 3 $D(b') = D(b', C(b'))$,
- 4 $E(b') = E(D(b'))$.
👉 $P((A, B, C, D, E)(b')) \equiv P(A, B, C, D, E \mid \text{do}(B = b'))$.

Single treatment

Single treatment, randomized

- $A = 1$: treated; $A = 0$: control.



- 👉 From the SWIG, we can read off

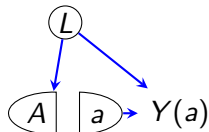
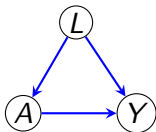
$$A \perp\!\!\!\perp Y(a),$$

so

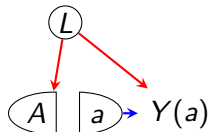
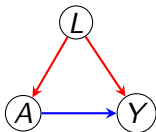
$$\mathbb{E} Y(a) = \mathbb{E}[Y \mid A = a], \quad a = 0, 1.$$

👉 association = causation

Single treatment, conditionally randomized



Single treatment, conditionally randomized



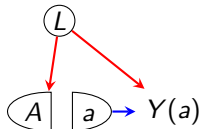
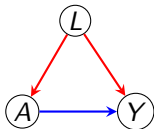
👉 L is an observed confounder between A and Y , so $\mathbb{E} Y(a) \neq \mathbb{E}[Y \mid A = a]$.

► association $\neq$ causation

There is no unobserved confounding.

👉 We can use L to identify $\mathbb{E} Y(a)$ through **standardization/adjustment** or **IPW** (inverse probability weighting).

Single treatment, conditionally randomized: Standardization



👉 **Standardization:** From the SWIG, we see that

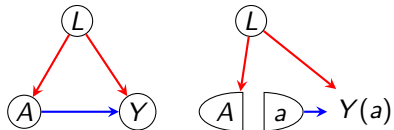
$$A \perp\!\!\!\perp Y(a) \mid L,$$

i.e., A is randomized within **every stratum** of L .

- 1 Within stratum $L = l$, we have $\mathbb{E}[Y(a) \mid L = l] = \mathbb{E}[Y \mid A = a, L = l]$.
- 2 Averaging over l to get the whole population:

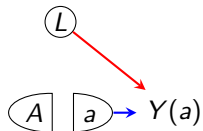
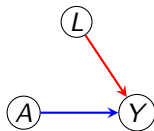
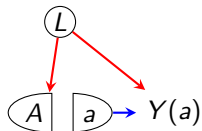
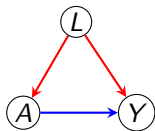
$$\mathbb{E} Y(a) = \sum_l \mathbb{E}[Y(a) \mid L = l]P(L = l) = \boxed{\sum_l \mathbb{E}[Y \mid A = a, L = l]P(L = l)}.$$

Single treatment, conditionally randomized: IPW



$$p(L = l)p(A = a \mid L = l)p(Y \mid A = a, L = l)$$

Single treatment, conditionally randomized: IPW



$$p(L = l)p(A = a \mid L = l)p(Y \mid A = a, L = l)$$

$$p(L = l)\cancel{p(A = a \mid L = l)}p(Y \mid A = a, L = l) \\ \times q(A = a) / \cancel{p(A = a \mid L = l)},$$

where q is an arbitrary distribution of A .

👉 **IPW**: Weighting by

$$1/p(A \mid L) \quad \blacktriangleright \quad q(A = 0) = q(A = 1) = 1/2$$

or

$$p(A)/p(A \mid L) \quad \blacktriangleright \quad q(A) = p(A), \text{ stabilized weight}$$

gives a trial where A is **randomized** (does not depend on L).

▶ **association = causation**

Single treatment, conditionally randomized



IPW:

$$\mathbb{E}[Y(a)] = \mathbb{E} \left\{ \frac{\mathbb{I}_{A=a} Y}{P(A=a | L)} \right\} / \mathbb{E} \left\{ \frac{\mathbb{I}_{A=a}}{P(A=a | L)} \right\} = \mathbb{E} \left\{ \frac{\mathbb{I}_{A=a} Y}{P(A=a | L)} \right\}.$$

Stabilized IPW has the same target

$$\mathbb{E} \left\{ \frac{\mathbb{I}_{A=a} \cancel{P(A=a)}}{P(A=a | L)} Y \right\} / \mathbb{E} \left\{ \frac{\mathbb{I}_{A=a} \cancel{P(A=a)}}{P(A=a | L)} \right\} = \mathbb{E} \left\{ \frac{\mathbb{I}_{A=a} Y}{P(A=a | L)} \right\}.$$

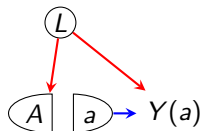
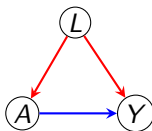
👉 But it makes a difference when fitting marginal structural models with estimated weights...

Single treatment, conditionally randomized

► **Standardization** and **IPW** target the **same population quantity**:

$$\underbrace{\mathbb{E} \left\{ \frac{\mathbb{I}_{A=a} Y}{P(A=a | L)} \right\}}_{\text{IPW}} = \mathbb{E} \left\{ \frac{\mathbb{E}[\mathbb{I}_{A=a} Y | L]}{P(A=a | L)} \right\} = \mathbb{E} \left\{ \frac{P(A=a | L) \mathbb{E}[Y | A=a, L]}{P(A=a | L)} \right\} = \underbrace{\mathbb{E} \{ \mathbb{E}[Y | A=a, L] \}}_{\text{standardization}}$$

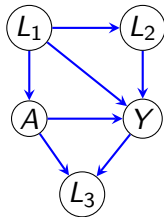
👉 Both standardization and IPW are **adjusting for L** : We use L to block all the **non-causal paths** (paths not in the shape $A \rightarrow \dots \rightarrow Y$).



👉 Non-causal ('backdoor') path $A \leftarrow L \rightarrow Y$ is blocked by L (i.e., not d-connected given L).

Quiz

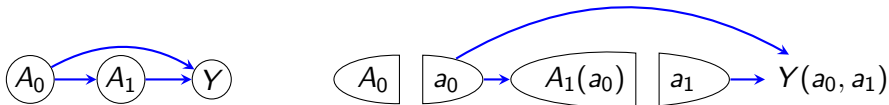
In the setting below, which strategies can correctly identify $\mathbb{E} Y(a)$?



Time-varying treatments

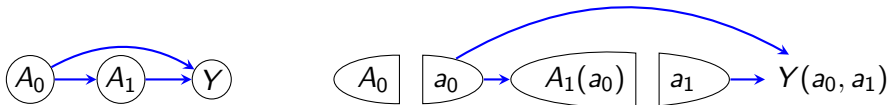
Two treatments, randomized

- 1 Time 0: randomly assign A_0 (1: treated; 0: control)
- 2 Time 1: randomly assign A_1 (1: treated; 0: control) depending on A_0 .
- 3 Time 2: measure outcome Y



Two treatments, randomized

- 1 Time 0: randomly assign A_0 (1: treated; 0: control)
- 2 Time 1: randomly assign A_1 (1: treated; 0: control) **depending on A_0** .
- 3 Time 2: measure outcome Y



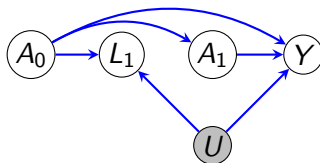
👉 (A_0, A_1) as a whole is **randomized**, so

$$\mathbb{E} Y(a_0, a_1) = \mathbb{E}[Y \mid A_0 = a_0, A_1 = a_1].$$

👉 association = causation

Two treatments: Example on HIV

- 1 Month 0: Assign therapy ($A_0 = 1$: treated; $A_0 = 0$: control) at the start of the follow-up. 👉 Suppose A_0 is randomly assigned.
- 2 Month 6: Measure blood CD4 counts L_1 and assign therapy ($A_1 = 1$: treated; $A_1 = 0$: control). 👉 Suppose A_1 's assignment depends only on A_0 but not L_1 .
- 3 Month 12: Measure the final health score Y .

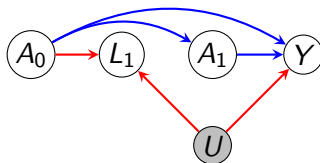


👉 U represents the unobserved health status that affects both L_1 and Y .

Can we identify $\mathbb{E} Y(0, 0)$?

Two treatments: Example on HIV

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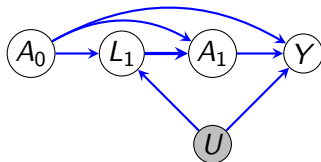
👉 U represents the unobserved health status that affects both L_1 and Y .

Can we identify $\mathbb{E} Y(0, 0)$?

Yes, non-causal path is not d-connected, unless we condition on L .

Two treatments, with time-varying confounder

- 1 Month 0: Assign therapy ($A_0 = 1$: treated; $A_0 = 0$: control) at the start of the follow-up.
👉 Suppose A_0 is randomly assigned.
- 2 Month 6: Measure blood CD4 counts L_1 and assign therapy ($A_1 = 1$: treated; $A_1 = 0$: control).
👉 Suppose A_1 's assignment depends on both A_0 and L_1 .
- 3 Month 12: Measure the final health score Y .



► Can we identify $\mathbb{E} Y(a_0, a_1)$?
👉 CD4 count is called a time-varying confounder

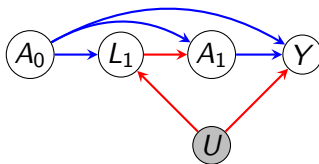
Graphical models
Single treatment
Time-varying treatments

Time-varying confounder
Marginal structural model

Dilemma

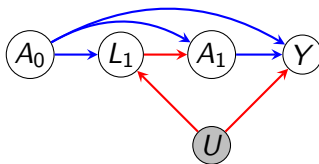
Dilemma

- 1 Not adjusting for L_1 .

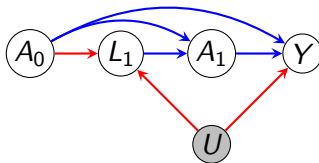


Dilemma

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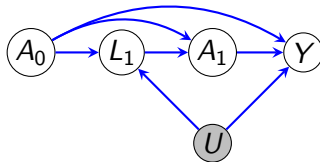


- 2 Adjusting for L_1 .

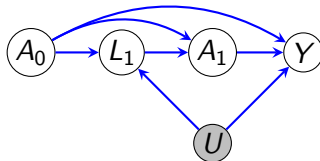


👉 Need something more sophisticated.

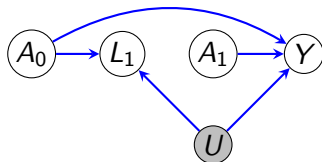
IPW: Removing A_1 's dependency on L_1



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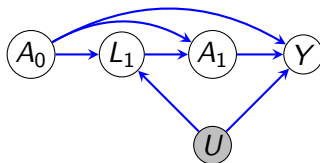


👉 IPW

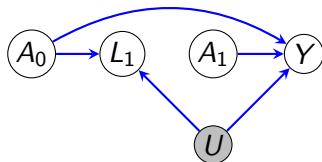


$$\text{weight} = 1/p(A_1 \mid A_0, L_1)$$

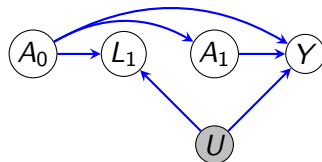
IPW: Removing A_1 's dependency on L_1



👉 IPW



weight = $1/p(A_1 \mid A_0, L_1)$



stabilized weight = $p(A_1 \mid A_0)/p(A_1 \mid A_0, L_1)$

👉 After reweighting, $\mathbb{E} Y(a_0, a_1) = \mathbb{E}[Y \mid A_0 = a_0, A_1 = a_1]$.

IPW: Identification

$$\mathbb{E} Y(a_0, a_1) = \mathbb{E} \left\{ \frac{Y \mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} / \mathbb{E} \left\{ \frac{\mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\}.$$

👉 Does it make a difference to use the stabilized weight $P(A_1 = a_1 \mid A_0 = a_0) / P(A_1 = a_1 \mid A_0 = a_0, L_1)$?

Quiz

Suppose A_0, L_1, A_1 are all binary. What is the estimate of $\mathbb{E} Y(0, 0)$ based on IPW?

n	A_0	L_1	A_1	$\mathbb{E}[Y \mid A_0, L_1, A_1]$
50	0	0	0	4
100	0	0	1	-1
100	0	1	0	2
50	0	1	1	-3
50	1	0	0	4
50	1	0	1	-2
100	1	1	0	7
200	1	1	1	11

👉 The first row means there are 50 subjects with $A_0 = 0, L_1 = 0, A_1 = 0$ and their average outcome is 4.

g-formula

The identification formula is called a **g-formula**

$$\mathbb{E} Y(a_0, a_1) = \mathbb{E} \left\{ \frac{Y \mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} / \mathbb{E} \left\{ \frac{\mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\},$$

where we first observe

$$\begin{aligned} \mathbb{E} \left\{ \frac{\mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} &= \mathbb{E} \left\{ \frac{P(A_1 = a_1, A_0 = a_0 \mid L_1)}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} \\ &= \mathbb{E} P(A_0 = a_0 \mid L_1) = P(A_0 = a_0). \end{aligned}$$

g-formula

Then, the formula can be rewritten as

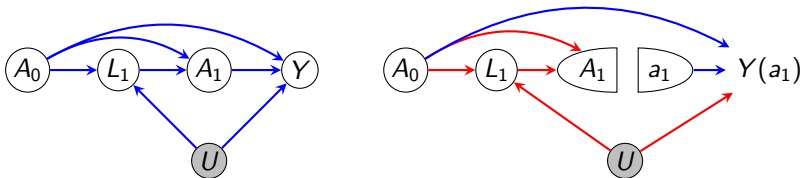
$$\begin{aligned}\mathbb{E} Y(a_0, a_1) &= \mathbb{E} \left\{ \frac{Y \mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} / \mathbb{E} \left\{ \frac{\mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} \\&= \mathbb{E} \left\{ \frac{Y \mathbb{I}_{A_0=a_0, A_1=a_1}}{P(A_0 = a_0) P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} \\&= \mathbb{E} \left\{ \frac{\mathbb{E}[Y \mathbb{I}_{A_0=a_0, A_1=a_1} \mid L_1]}{P(A_0 = a_0) P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} \\&= \mathbb{E} \left\{ \frac{\mathbb{E}[Y \mid A_0 = a_0, A_1 = a_1, L_1] P(A_1 = a_1, A_0 = a_0 \mid L_1)}{P(A_0 = a_0) P(A_1 = a_1 \mid A_0 = a_0, L_1)} \right\} \\&= \mathbb{E} \left\{ \frac{\mathbb{E}[Y \mid A_0 = a_0, A_1 = a_1, L_1] P(A_0 = a_0 \mid L_1)}{P(A_0 = a_0)} \right\} \\&= \boxed{\sum_{l_1} \mathbb{E}[Y \mid A_0 = a_0, A_1 = a_1, L_1 = l_1] P(L_1 = l_1 \mid A_0 = a_0),}\end{aligned}$$

in the form of **standardization/adjustment**.

g-formula: Intuition

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- 1 Consider $Y(a_1) := Y(A_0, a_1)$.



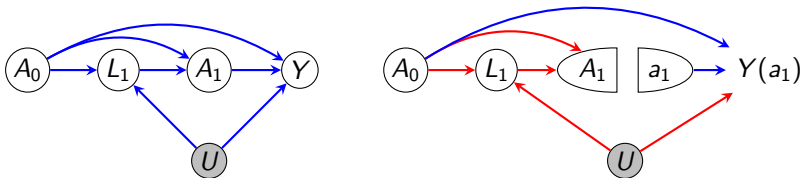
Within the stratum of (A_0, L_1) , A_1 is independent of $Y(a_1)$, so

(why?)

$$\mathbb{E}[Y(a_1) \mid A_0 = a_0, L_1 = l_1] = \mathbb{E}[Y \mid A_0 = a_0, A_1 = a_1, L_1 = l_1].$$

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- 2 Because A_0 is randomly assigned,

$$\mathbb{E}[Y(a_0, a_1)] = \mathbb{E}[Y(a_1) \mid A_0 = a_0] = \sum_{l_1} \mathbb{E}[Y(a_1) \mid A_0 = a_0, L_1 = l_1] P(L_1 = l_1 \mid A_0 = a_0).$$

Positivity

From the standardization / g-formula

$$\mathbb{E} Y(a_0, a_1) = \sum_l \mathbb{E}[Y \mid A_1 = a_1, A_0 = a_0, L_1 = l_1] P(L_1 = l_1 \mid A_0 = a_0),$$

to identify $\mathbb{E} Y(a_0, a_1)$, we must have

$$\forall l_1 : P(L_1 = l_1 \mid A_0 = a_0) > 0 \implies \text{data within } (a_0, a_1, l_1),$$

i.e.,

$$\forall l_1 : P(L_1 = l_1 \mid A_0 = a_0) > 0 \implies P(A_1 = a_1 \mid A_0 = a_0, L_1 = l_1) > 0.$$

Quiz

Suppose A_0, L_1, A_1 are all binary. What is the estimate of $\mathbb{E} Y(0, 0)$ based on standardization / g-formula?

n	A_0	L_1	A_1	$\mathbb{E}[Y \mid A_0, L_1, A_1]$
50	0	0	0	4
100	0	0	1	-1
100	0	1	0	2
50	0	1	1	-3
50	1	0	0	4
50	1	0	1	-2
100	1	1	0	7
200	1	1	1	11

👉 The first row means there are 50 subjects with $A_0 = 0, L_1 = 0, A_1 = 0$ and their average outcome is 4.

Generalization

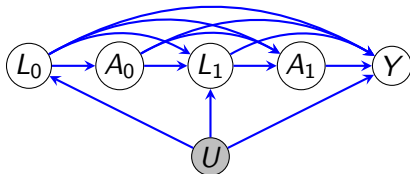
Let L_0, L_1 be CD4 counts at baseline and time 1.

► time-varying confounder

Let A_0, A_1 be antiretroviral therapy at baseline and time 1.

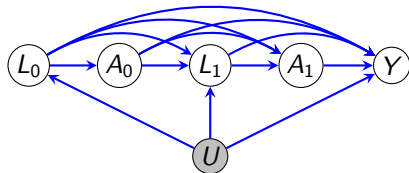
► time-varying treatment

- 1 Month 0: Assign therapy ($A_0 = 1$: treated; $A_0 = 0$: control) at the start of the follow-up.
👉 Suppose $Y(a_0, a_1) \perp\!\!\!\perp A_0 \mid L_0$ for baseline covariates L_0 .
- 2 Month 6: Measure blood CD4 counts L_1 and assign therapy ($A_1 = 1$: treated; $A_1 = 0$: control).
👉 Suppose $Y(a_0, a_1) \perp\!\!\!\perp A_1 \mid L_0, A_0, L_1$.
- 3 Month 12: Measure the final health score Y .



👉 These conditions are known as sequential ignorability.

Generalization



Under positivity and **sequential ignorability**

$$Y(a_0, a_1) \perp\!\!\!\perp A_0 \mid L_0,$$

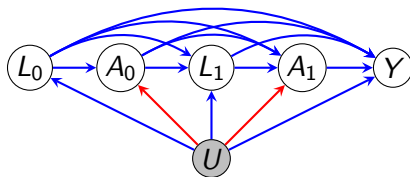
$$Y(a_0, a_1) \perp\!\!\!\perp A_1 \mid L_0, A_0, L_1,$$

$$\begin{aligned} \mathbb{E} Y(a_0, a_1) &= \sum_{l_0} \sum_{l_1} \mathbb{E}[Y \mid A_1 = a_1, A_0 = a_0, L_1 = l_1, L_0 = l_0] \\ &\quad \times P(L_1 = l_1 \mid A_0 = a_0, L_0 = l_0) P(L_0 = l_0). \end{aligned}$$

👉 Extends to more time points.

Out of luck

If **either red edge** is present, then $\mathbb{E} Y(a_0, a_1)$ cannot be identified.

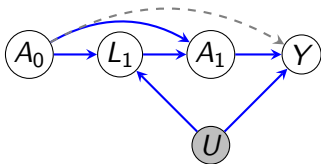


Verma constraint

When there can be latent confounding, a sharp null of no direct effect may not correspond to any independence or conditional independence in the observed distribution.

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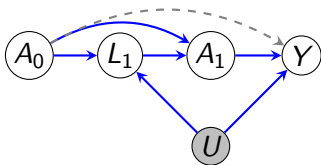


$$H_0 : Y(a_0, a_1) = Y(a'_0, a_1) \forall a_0, a'_0$$

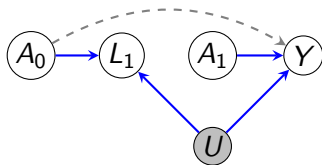
👉 H_0 does **not** correspond to any marginal or conditional independence on $P(A_0, L_1, A_1, Y)$.

Verma constraint

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$$H_0 : Y(a_0, a_1) = Y(a'_0, a_1) \forall a_0, a'_0$$



$$H_0 : A_0 \perp\!\!\!\perp Y \text{ under } \text{weight} = 1/p(A_1 | A_0, L_1)$$

👉 H_0 does **not** correspond to any marginal or conditional independence on $P(A_0, L_1, A_1, Y)$.

👉 Such a constraint on $P(A_0, L_1, A_1, Y)$ is called a **Verma constraint** or a **generalized conditional independence**. Described by the **nested Markov model** associated with ADMGs.

Marginal structural (mean) model

Consider two treatments A_0, A_1 .

👉 A marginal structural (mean) model (J. M. Robins et al., 2000) is to postulate

$$\mathbb{E}[Y(a_0, a_1)] = f(a_0, a_1; \theta).$$

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For example, when A_0, A_1 are both **binary** and Y is continuous:

- Saturated model

$$\mathbb{E}[Y(a_0, a_1)] = \alpha + \beta_0 a_0 + \beta_1 a_1 + \gamma a_0 a_1$$

- Main effect only

$$\mathbb{E}[Y(a_0, a_1)] = \alpha + \beta_0 a_0 + \beta_1 a_1$$

Fitting model with IPW

If (A_0, A_1) is randomized, we have $\mathbb{E}[Y(a_0, a_1)] = \mathbb{E}[Y \mid A_0 = a_0, A_1 = a_1]$, so the model can be simply fitted with least squares.

👉 Now under **time-varying confounding**, we can use **IPW to reweigh data** such that we can treat the data **as if A_0, A_1 are randomized**.

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👉 Now under **time-varying confounding**, we can use **IPW to reweigh data** such that we can treat the data **as if A_0, A_1 are randomized**.

To fit marginal structural mean model,

- 1 Estimate the propensity score $\hat{P}(a_1 \mid a_0, l_1)$ (e.g., with logistic regression)
- 2 Compute weights $\hat{w} = 1/\hat{P}(A_1 \mid A_0, L_1)$ or the stabilized weights

$$\hat{w}_s = \left(\sum_{l_1} \hat{P}(A_1 \mid A_0, l_1) \hat{P}(l_1 \mid A_0) \right) / \hat{P}(A_1 \mid A_0, l_1).$$

- 3 Fit least squares using $\hat{w}$ or $\hat{w}_s$ as weights.

👉 It makes a difference here.

Further reading

See Chapters 19, 20 and 21 of Hernán MA, Robins JM (2020). Causal Inference: What If. Boca Raton: Chapman & Hall/CRC.

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-  Richardson, T., & Robins, J. M. (2013). Single world intervention graphs (swigs): A unification of the counterfactual and graphical approaches to causality. *Center for the Statistics and the Social Sciences, University of Washington Series. Working Paper, 128(30)*, 2013.
-  Robins, J. (1986). A new approach to causal inference in mortality studies with a sustained exposure period—application to control of the healthy worker survivor effect. *Mathematical modelling*, 7(9-12), 1393–1512.
-  Robins, J. M., Hernan, M. A., & Brumback, B. (2000). Marginal structural models and causal inference in epidemiology.