

Propensity Score Methods, Models and Adjustment

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Key objective: causal conclusions from observational data

- Experimental studies:
 - Treatment assigned by the researcher, independent of confounding factors;
 - Causal statements possible.
- Observational studies:
 - Treatment assignment dependent on confounding factors;
 - Causal statements not possible ?

1. The need for adjustment: confounding in observational studies.
2. Manufacturing balance: the propensity score.
3. Statistical tools utilizing the propensity score.
4. Examples and extensions.
5. New directions.

- 1.1 The central causal question
- 1.2 Notation
- 1.3 Causal estimands
- 1.4 Basics of estimation
- 1.5 The Monte Carlo paradigm
- 1.6 Collapsibility
- 1.7 The randomized study
- 1.8 Confounding
- 1.9 Statistical modelling

- 2.1 Manufacturing balance
- 2.2 The propensity score for binary exposures
- 2.3 Matching via the propensity score
- 2.4 The Generalized Propensity Score
- 2.5 Propensity score regression
- 2.6 G-estimation
- 2.7 Adjustment by weighting
- 2.8 Augmentation and double robustness
- 2.9 Continuous treatments

- 3.1 Statistical tools
- 3.2 Key considerations
- 3.3 Examples

4.1 Longitudinal studies

4.2 The Marginal Structural Model (MSM)

- 5.1 New challenges
- 5.2 Bayesian approaches

Part 1

Introduction

The central causal question

In many research domains, the objective of an investigation is to quantify the effect on a measurable outcome of changing one of the conditions under which the outcome is measured.

- in a health research setting, we may wish to discover the benefits of a new therapy compared to standard care;
- in economics, we may wish to study the impact of a training programme on the wages of unskilled workers;
- in transportation, we may attempt to understand the effect of embarking upon road building schemes on traffic flow or density in a metropolitan area.

The central statistical challenge is that, unless the condition of interest is changed independently, the inferred effect may be subject to the influence of other variables.

Example: The effect of nutrition on health

In a large cohort, the relationship between diet and health status is to be investigated. Study participants are queried on the nutritional quality of their diets, and their health status in relation to key indicators is assessed via questionnaires.

For a specific outcome condition of interest, incidence of cardiovascular disease (CVD), the relation to a specific dietary component, vitamin E intake, is to be assessed.

In the study, both incidence of disease and vitamin E intake were dichotomized

- Exposure: Normal/Low intake of vitamin E.
- Outcome: No incidence/Incidence of CVD in five years from study initiation.

Example: The effect of nutrition on health

		Outcome	
		CVD	No CVD
Exposure	Normal	27	8020
	Low	86	1879

Question: does a diet lower in vitamin E lead to higher chance of developing CVD ? More specifically, is this a *causal* link ?

- that is, if we were to *intervene* to change an individual's exposure status, by how much would their risk of CVD change ?

The language of causal inference

We seek to quantify the effect on an *outcome* of changes in the value of an *exposure* or *treatment*.

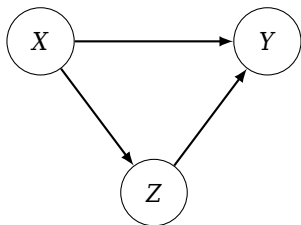
- Outcome: could be
 - binary;
 - integer-valued;
 - continuous-valued.
- Exposure: could be
 - binary;
 - integer-valued;
 - continuous-valued.
- Study: could be
 - cross-sectional (single time point);
 - longitudinal (multiple time points).

We consider an *intervention* to change exposure status.

We adopt the following notation: let

- i index individuals included in the study;
- Y_i denote the *outcome* for individual i ;
- Z_i denote the *exposure* for individual i ;
- X_i denote the values of other *predictors* (or *covariates*).

For a cross-sectional study, Y_i and Z_i will be scalar-valued; for the longitudinal case, Y_i and Z_i may be vector valued. X_i is typically vector-valued at each measurement time point.



Directed Acyclic Graph (DAG) for basic confounding set up in observational studies.

DAGs are commonly used to clarify causal thinking and assumptions.

Probability & Causal DAGs recap

- an inbound arrow indicates a causal relationship
 - X is a *direct cause* of Y and Z ;
 - Z is a direct cause of Y , but also a *mediator* of the *indirect cause* of X on Y ;
- a variable (node) that has no inbound arrows can be considered a '*founder*' variable;
- we must consider *paths* from the exposure Z to the outcome Y ; there are two
 - the *direct* path $Z \rightarrow Y$,
 - the *indirect* path $Z \rightarrow X \rightarrow Y$

We can think of the DAG as encapsulating the following equations:

$$Z = g_Z(X, \varepsilon_Z)$$

$$Y = g_Y(X, Z, \varepsilon_Y)$$

where ε_Z and ε_Y are independent random perturbations, and g_Z and g_Y are mapping functions.

That is,

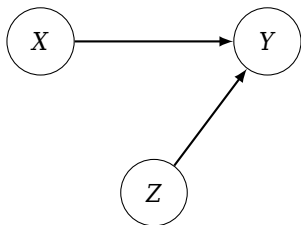
- we take X and ε_Z and combine them through g_Z to obtain Z ;
- we combine Z with X and ε_Y through g_Y to obtain Y .

For example

$$Z = X + \varepsilon_Z$$

$$Y = 2X + 5Z + 3XZ + \varepsilon_Y$$

Our goal is to understand the *unconfounded* effect of Z on Y, that is, where X is *not treated as a cause* of Z.



DAG with no confounding.

In the structural model, we imagine Z being fixed to some value, z say, not generated by its structural model.

$$Y = 2X + 5z + 3Xz + \varepsilon_Y$$

We denote by

$$Y_i(\mathbf{z})$$

the hypothetical outcome for individual i if we were to *intervene* to set exposure to \mathbf{z} .

$Y_i(\mathbf{z})$ is termed a *counterfactual* or *potential outcome*.

If exposure is binary, the pair of potential outcomes

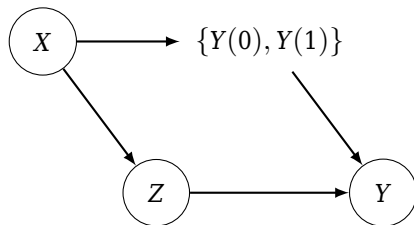
$$\{Y_i(0), Y_i(1)\}$$

represent the outcomes that would result for individual i if that subject was not exposed, or exposed, respectively.

The observed outcome, Y_i , may be written in terms of the potential outcomes and the observed exposure, Z_i , as

$$Y_i = (1 - Z_i)Y_i(0) + Z_iY_i(1).$$

That is, $Y(0)$ and $Y(1)$ are (potentially) caused by X , but not Z .



DAG with potential outcomes

If we know the value of X , then we know the distribution of both $Y(0)$ and $Y(1)$ without needing to know anything about the *actual* treatment Z .

If exposure is *multi-valued*, the potential outcomes

$$\{Y_i(z_1), Y_i(z_2), \dots, Y_i(z_d)\}$$

represent the outcomes that would result for individual i if that subject exposed to exposure level z_1, z_2, \dots, z_d respectively.

Then for the observed Y_i ,

$$Y_i = Y_i(z_j) \iff Z_i = z_j.$$

If exposure is *continuous-valued*, the potential outcomes

$$\{Y_i(\mathbf{z}), \mathbf{z} \in \mathcal{Z}\}$$

represent the outcomes that would result for individual i if that subject exposed to exposure level \mathbf{z} which varies in the set \mathcal{Z} .

Note 1.

It is rare that we can ever observe more than one of the potential outcomes for a given subject in a given study, that is, for binary exposures it is rare that we will be able to observe both

$$Y_i(0) \quad \text{and} \quad Y_i(1)$$

in the same study.

In the previous example, we cannot observe the CVD outcome under both the assumption that the subject *did* and simultaneously *did not* have a low vitamin E diet.

This is the first fundamental challenge of causal inference.

The central question of causal inference relates to comparing the (expected) values of different potential outcomes.

We consider the causal effect of exposure to be defined by *differences* in potential outcomes corresponding to *different* exposure levels.

Note 2.

This is a statistical, rather than necessarily mechanistic, definition of causality.

For a binary exposure, we define the causal effect of exposure by considering contrasts between $Y_i(0)$ and $Y_i(1)$; for example, we might consider

- Additive contrasts

$$Y_i(1) - Y_i(0)$$

- Multiplicative contrasts

$$Y_i(1)/Y_i(0)$$

For a continuous exposure, we might consider the path tracing how $Y_i(z)$ changes as z changes across some relevant set of values.

This leads to a *causal dose-response* function.

Example: Occlusion Therapy for Amblyopia

We might seek to study the effect of occlusion therapy (patching) on vision improvement of amblyopic children. Patching 'doses' are measured in terms of time for which the fellow (normal functioning) eye is patched.

As time is measured continuously, we may consider how vision improvement changes for any relevant dose of occlusion.

In general, we are interested in *population* causal effects based on *expected* potential outcomes

$$\mathbb{E}[Y_i(\mathbf{z})]$$

or contrasts of these quantities.

We might also consider *subgroup-specific* expected quantities

$$\mathbb{E}[Y_i(\mathbf{z})|i \in \mathcal{S}]$$

where \mathcal{S} is some stratum of interest in the general population.

Expected counterfactuals: binary exposure

For a binary exposure, we might consider the average effect of exposure (or *average treatment effect*, ATE) defined as

$$\mathbb{E}[Y_i(1) - Y_i(0)] = \mathbb{E}[Y_i(1)] - \mathbb{E}[Y_i(0)]$$

If the outcome is also binary, we note that

$$\mathbb{E}[Y_i(z)] \equiv \Pr[Y_i(z) = 1]$$

so may also consider odds or odds ratios quantities

$$\frac{\Pr[Y_i(z) = 1]}{\Pr[Y_i(z) = 0]} \quad \frac{\Pr[Y_i(1) = 1]/\Pr[Y_i(1) = 0]}{\Pr[Y_i(0) = 1]/\Pr[Y_i(0) = 0]}.$$

We may also consider quantities such as the

average treatment effect on the treated, ATT

defined as

$$\mathbb{E}[Y_i(1) - Y_i(0)|Z_i = 1]$$

although such quantities can be harder to interpret.

[JAMA Pediatr.](#) 2016 Feb;170(2):117-24. doi: 10.1001/jamapediatrics.2015.3356.

Antidepressant Use During Pregnancy and the Risk of Autism Spectrum Disorder in Children

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Example:

Antidepressants are quite widely prescribed for a variety of mental health concerns. However, pregnant women may be reluctant to embark on a course of antidepressants during pregnancy.

We might wish to investigate, in a population of users (and potential users) of antidepressants, the incidence of autism-spectrum disorder in early childhood and to assess the possibility of causal influence of antidepressant use on this incidence.

Example:

- Outcome: binary, recording the a diagnosis of autism-spectrum disorder in the child by age 5;
- Exposure: antidepressant use during 2nd or 3rd trimester of pregnancy.

Then we may wish to quantify

$$\mathbb{E}[Y_i(\text{antidepressant}) - Y_i(\text{no antidepressant}) | \text{Antidep. actually used}].$$

We wish to obtain estimates of causal quantities of interest based on the available data, which typically constitute a random sample from the target population.

Typically, we will use sample mean type quantities: for a random sample of size n , the sample mean

$$\frac{1}{n} \sum_{i=1}^n Y_i$$

is an estimator of the population mean and so on.

In a typical causal setting, we wish to perform estimation of

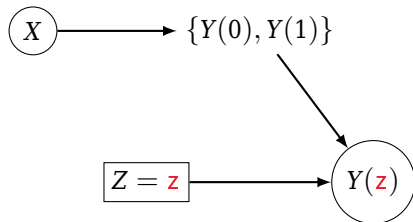
average potential outcome

(APO) values.

Consider first the situation where all subjects in a random sample receive a given exposure \mathbf{z} ; we wish to estimate

$$\mu(\mathbf{z}) = \mathbb{E}[Y(\mathbf{z})].$$

The intervention to set $Z = z$ is done independently of X , so the arrow $X \rightarrow Z$ is *removed*.



DAG with exposure intervention $Z = z$

As a mathematical calculation, we write the expected outcome as

$$\mathbb{E}[Y(\mathbf{z})] = \int y f_{Y(\mathbf{z})}(y) \, dy$$

where $f_{Y(\mathbf{z})}(y)$ is the distribution of the potential outcome $Y(\mathbf{z})$.

We read this calculation as

“average the collection of possible y values weighted by their probability of being observed”.

We may also write this as

$$\mathbb{E}[Y(\mathbf{z})] = \int y f_{Y(\mathbf{z}),X}(y, \mathbf{x}) \, dy \, d\mathbf{x}$$

which recognizes that in the population, the values of the predictors X also vary randomly according to some *joint* probability distribution.

We know from the DAG on p. 38 that

$$f_{Y(\mathbf{z}),X}(y, \mathbf{x}) = f_{Y(\mathbf{z})|X}(y|\mathbf{x})f_X(\mathbf{x})$$

Note that we may also write

$$\mathbb{E}[Y(\mathbf{z})] = \int y \mathbb{1}_{\{\mathbf{z}\}}(\mathbf{z}) f_{Y(\mathbf{z}),X}(y, \mathbf{x}) \, dy \, d\mathbf{z} \, d\mathbf{x}$$

assuming an exposure distribution that sets $z = \mathbf{z}$ with probability one.

- the data are considered to be sampled from the distribution

$$\mathbb{1}_{\{\mathbf{z}\}}(\mathbf{z}) f_{Y(\mathbf{z}),X}(y, \mathbf{x}) = \mathbb{1}_{\{\mathbf{z}\}}(\mathbf{z}) f_{Y(\mathbf{z})|X}(y|\mathbf{x}) f_X(\mathbf{x}).$$

Thus, for the APO we have

$$\mathbb{E}[Y(\mathbf{z})] = \int y \mathbb{1}_{\{\mathbf{z}\}}(\mathbf{z}) f_{Y(\mathbf{z}),X}(y|\mathbf{x}) f_X(\mathbf{x}) \, dy \, d\mathbf{z} \, d\mathbf{x}.$$

Now, in our hypothetical sample, we have observed n data points

$$\{(x_i, y_i, z_i), i = 1, \dots, n\}$$

from the joint distribution

$$\mathbb{1}_{\{z\}}(z) f_{Y(z),X}(y|x) f_X(x)$$

so that $z_i = z$ for all i . We may *estimate* the relevant APO $\mathbb{E}[Y(z)]$ by

$$\widehat{\mathbb{E}}[Y(z)] = \frac{1}{n} \sum_{i=1}^n y_i = \bar{y}.$$

Note 3.

To estimate functions of the sample mean, we may use simple transformations of the estimator; for example, if the outcome is binary, we estimate the odds

$$\frac{\Pr[Y_i(\mathbf{z}) = 1]}{\Pr[Y_i(\mathbf{z}) = 0]} \quad \text{by} \quad \frac{\bar{y}}{1 - \bar{y}}.$$

Causal quantities are typically *average* measures across a given population which we write as *integrals* with respect to probability distributions.

For any function $g(\cdot)$, we have mathematically that

$$\mathbb{E}[g(Y)] = \int g(y) f_Y(y) \, dy$$

Rather than performing this calculation using integration, we approximate it numerically using *Monte Carlo*.

Monte Carlo calculations proceed as follows:

- generate a sample of size n from the density

$$f_Y(\mathbf{y})$$

to yield $\mathbf{y}_1, \dots, \mathbf{y}_n$; there are standard techniques to achieve this.

- approximate $\mathbb{E}[g(Y)]$ by

$$\widehat{\mathbb{E}}[g(Y)] = \frac{1}{n} \sum_{i=1}^n g(\mathbf{y}_i).$$

- For large n , $\widehat{\mathbb{E}}[g(Y)]$ provides a good approximation to $\mathbb{E}[g(Y)]$.

Note 4.

This calculation is *at the heart of frequentist methods in statistics*:

- we collect a sample of *data* of size n ,
- form and *estimates* based on this sample (eg sample averages),
- if our sample is large enough, the estimate will be close to the true expected value.

Importance sampling is based on forming *weighted* averages

- we *re-weight* obtained samples from another distribution f_Y^* so that we can estimate quantities relating to f_Y
- this is like '*standardization*' (eg standardized mortality rate) in epidemiology.

Monte Carlo recap

Many of the causal measures described above are *marginal* measures.

That is, they involve *averaging* over the distribution of X : as we have seen

$$\mathbb{E}[Y(\mathbf{z})] = \int y f_{Y|Z,X}(y|\mathbf{z}, x) f_X(x) \, dy \, dx.$$

This is sometimes known as a *G-computation* formula. It essentially arises by assuming X and Z are *independent*, and then studying the *marginal* (over X) distribution

$$f_{Y|Z}(y|\mathbf{z}) = \int f_{Y|Z,X}(y|\mathbf{z}, x) f_X(x) \, dx.$$

Marginal measures are not typically the same as the equivalent measure defined for the *conditional* model

$$f_{Y|Z,X}(y|z, x).$$

Marginal measures that do not have the same interpretation in the conditional model are termed *non-collapsible*.

The approach that intervenes to set exposure equal to z for all subjects, however, does not facilitate comparison of APOs for different values of z .

Therefore consider a study design based on *randomization*; consider from simplicity the binary exposure case. Suppose that a random sample of size $2n$ is obtained, and split into two equal parts.

- the *first* group of n are assigned the exposure and form the '*exposed*' or '*treated*' sample,
- the *second* group are left '*untreated*'.

For both the treated and untreated groups we may use the previous logic, and estimate the ATE

$$\mathbb{E}[Y_i(1) - Y_i(0)] = \mathbb{E}[Y_i(1)] - \mathbb{E}[Y_i(0)]$$

by the difference in means in the two groups, that is

$$\frac{1}{n} \sum_{i=1}^n y_i - \frac{1}{n} \sum_{i=n+1}^{2n} y_i.$$

The key idea here is that the two halves of the original sample are *exchangeable* with respect to their properties:

- they only differ *due to exposure assignment*.

The randomized study

In a slightly modified design, suppose that we obtain a random sample of size n from the study population, but then assign exposure *randomly* to subjects in the sample: subject i receives treatment with probability p .

In the final sample, the number actually treated, n_1 , is a realization of a random variable N_1 where

$$N_1 \sim \text{Binomial}(n, p).$$

We may write

$$N_{\mathbf{z}} = \sum_{i=1}^n \mathbb{1}_{\{\mathbf{z}\}}(Z_i).$$

as the count of the number of individuals receiving $Z = \mathbf{z}$.

This suggests the estimators^[1]

$$\hat{\mathbb{E}}[Y(z)] = \frac{\sum_{i=1}^n \mathbb{1}_{\{z\}}(Z_i) Y_i}{N_z} \quad z = 0, 1 \quad (1)$$

that is

$$\hat{\mathbb{E}}[Y(0)] = \frac{1}{N_0} \sum_{i=1}^n (1 - Z_i) Y_i \quad \hat{\mathbb{E}}[Y(1)] = \frac{1}{N_1} \sum_{i=1}^n Z_i Y_i.$$

^[1] Formula (1) just says to take the mean in each treatment group !

Note that for the denominators,

$$N_0 \sim \text{Binomial}(n, 1 - p) \quad N_1 \sim \text{Binomial}(n, p)$$

so we may consider replacing the denominators by their expected values

$$np \quad \text{and} \quad n(1 - p)$$

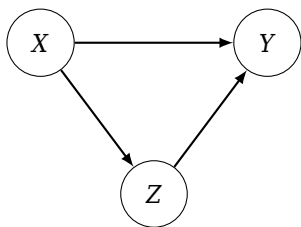
respectively for $z = 0, 1$. This yields the estimators

$$\widehat{\mathbb{E}}[Y(0)] = \frac{1}{n(1 - p)} \sum_{i=1}^n (1 - Z_i) Y_i \quad \widehat{\mathbb{E}}[Y(1)] = \frac{1}{np} \sum_{i=1}^n Z_i Y_i. \quad (2)$$

The second main challenge of causal inference is that for *observational* (or *non-experimental*) studies, *exposure is not necessarily assigned independently of other variables*.

- it may be that exposure is assigned dependent on one or more of the measured predictors;
- if these predictors also predict outcome, then there is the possibility of *confounding* of the causal effect of exposure by those other variables;
- this is the set up in the DAG on p. 15.

The challenge of confounding



X is a confounder

- X predicts outcome Y in the presence of Z:

$$f_{Y|Z,X}(y|z, x) \neq f_{Y|Z}(y|z)$$

- X predicts exposure Z:

$$f_{Z|X}(z|x) \neq f_Z(z)$$

Example: The effect of nutrition on health: revisited

The relationship between low vitamin E diet and CVD incidence may be confounded by socio-economic status (SES); poorer individuals may have worse diets, and also may have higher risk of cardiovascular incidents via mechanisms other than those determined by diet:

- smoking;
- pollution;
- access to preventive measures/health advice.

Confounding is a central challenge as it renders the observed sample unsuitable for causal comparisons unless adjustments are made:

- in the binary case, if confounding is present, the treated and untreated groups are *not directly comparable*;
- the effect of confounder X on outcome is potentially *different* in the treated and untreated groups.
- direct comparison of sample means *does not* yield valid insight into average treatment effects;

Causal inference is fundamentally about comparing exposure subgroups on an *equal footing*, where there is no residual influence of the other predictors. This is possible in the randomized study as randomization breaks the association between Z and X .

It is *not* directly possible in the presence of confounding.

Note 5.

Confounding is not the same as non-collapsibility.

- Non-collapsibility concerns the measures of effect being reported, and the parameters being estimated; parameters in a marginal model do not in general correspond to parameters in a conditional model.

Non-collapsibility is a property of the model, not the study design. It may be present even for a randomized study.

- Confounding concerns the inter-relationship between outcome, exposure and confounder. It is not model-dependent, and does depend on the study design.

Simple confounding example

Suppose that Y, Z and X are all binary variables. Suppose that the true (structural) relationship between Y and (Z, X) is given by

$$\mathbb{E}[Y|Z = z, X = x] = \Pr[Y = 1|Z = z, X = x] = 0.2 + 0.2z - 0.1x$$

with $\Pr[X = 1] = q$. Then, by iterated expectation

$$\mathbb{E}[Y(z)] = 0.2 + 0.2z - 0.1q$$

and

$$\mathbb{E}[Y(1) - Y(0)] = 0.2.$$

Suppose also that in the population from which the data are drawn

$$\begin{aligned}\Pr[Z = 1|X = x] &= \begin{cases} p_0 & x = 0 \\ p_1 & x = 1 \end{cases} \\ &= (1 - x)p_0 + xp_1\end{aligned}$$

so that

$$\Pr[Z = 1] = (1 - q)p_0 + qp_1.$$

It can be shown that ATE estimator

$$\widehat{\mathbb{E}}[Y(1)] - \widehat{\mathbb{E}}[Y(0)] = \frac{\sum_{i=1}^n Z_i Y_i}{\sum_{i=1}^n Z_i} - \frac{\sum_{i=1}^n (1 - Z_i) Y_i}{\sum_{i=1}^n (1 - Z_i)}$$

has expectation

$$0.2 - 0.1q \left\{ \frac{p_1}{p} - \frac{1 - p_1}{1 - p} \right\}$$

and therefore the unadjusted estimator based on (2) is *biased*.

Example

The bias is caused by the fact that the two observed subsamples with

$$Z = 0 \quad \text{and} \quad Z = 1$$

are *not directly comparable* - they have a different profile in terms of X .

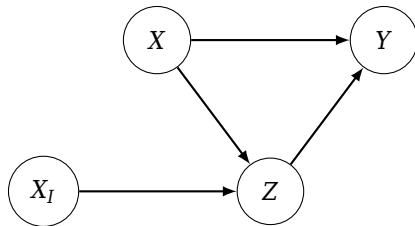
By *Bayes theorem*

$$\Pr[X = 1|Z = 1] = \frac{p_1 q}{p} \quad \Pr[X = 1|Z = 0] = \frac{(1 - p_1)q}{1 - p}$$

so, here, conditioning on $Z = 1$ and $Z = 0$ in turn in the computation of (2), leads to a different composition of X values in the two subsamples.

As X influences Y , the resulting Y values *not directly comparable*.

If predictor X_I predicts Z , but does not predict Y in the presence of Z , then X_I is termed an *instrument*.



DAG with instrument X_I : X_I predicts Z , but is not associated with outcome Y if we know Z .

Example: Non-compliance

In a randomized study of a binary treatment, if Z records the treatment actually *received*, suppose that there is *non-compliance* with respect to the treatment; that is, if X_I records the treatment *assigned* by the experimenter, then possibly

$$x_I \neq z.$$

Instruments are *not* confounders as they do not predict outcome once the influence of the exposure has been accounted for.

Suppose in the previous confounding example, we had

$$\mathbb{E}[Y|Z = z, X = 0] = \Pr[Y = 1|Z = z, X = 1] = 0.2 + 0.2z$$

for the structural model, but

$$\Pr[Z = 1|X] = (1 - X)p_0 + Xp_1.$$

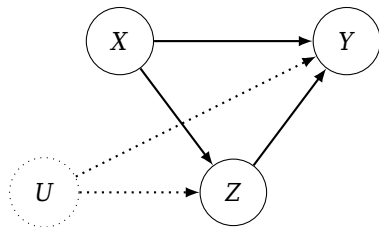
Then X influences Z , and there is still an imbalance in the two subgroups indexed by Z with respect to the X values, *but* as X does not influence Y , there is *no bias* if the ATE estimator based on (2) is used.

An important assumption that is commonly made is that of

No unmeasured confounding

that is, the measured predictors X include (possibly as a subset) all variables that confound the effect of Z on Y .

Critical Assumption



DAG with unmeasured confounder U.

We must assume that all variables that simultaneously influence exposure and outcome have been measured in the study.

- This is a strong (and possibly unrealistic) assumption in practical applications;
- It is the assumption made in standard regression analysis !
- It may be relaxed, and the influence of unmeasured confounders studied in sensitivity analyses.

So far, estimation based on the data via (1) and (2) has proceeded in a *non-parametric* or model-free fashion.

- models such as

$$f_{Y(\mathbf{z}),X}(y, \mathbf{x})$$

have been considered, but not modelled parametrically.

We now consider *semiparametric* specifications, where *parametric* models for example for

$$\mathbb{E}[Y(\mathbf{z})|X]$$

are considered but no distributional assumptions are made.

Suppose that the *true outcome mean* is given by

$$\mathbb{E}[Y|X, Z] = \mu(X, Z)$$

which may be parametric in nature, say

$$\mathbb{E}[Y|X, Z; \theta] = \mu(X, Z; \theta)$$

The importance of ‘no unmeasured confounders’

An important consequence of the no unmeasured confounders assumption is that we have the *equivalence* of the conditional mean *structural* and *observed-data* outcome models, that is

$$\mathbb{E}[Y(\mathbf{z})|X] \quad \text{and} \quad \mathbb{E}[Y|X, Z = \mathbf{z}]$$

when this model is *correctly specified*.

We might (optimistically) assume that the model $\mathbb{E}[Y|Z, X]$ is *correctly specified*, and captures the true relationship.

If this is, in fact, the case, then

No special techniques are needed to estimate the causal effect.

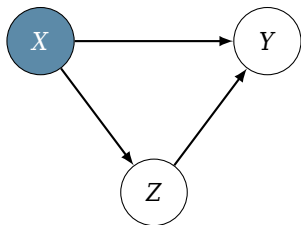
We may simply use *regression* of Y on (X, Z) using mean model $\mathbb{E}[Y|X, Z]$.

To estimate the APO, we simply set

$$\widehat{\mathbb{E}}[Y(\mathbf{z})] = \frac{1}{n} \sum_{i=1}^n \mu(X_i, \mathbf{z}) \quad (3)$$

and derive other estimates from this: if $\mu(x, z)$ correctly captures the relationship of the outcome to the exposure and confounders, then the estimator of the APO in (3) is *consistent* (gives the correct answer as the sample size increase to infinity).

By conditioning on X in the regression model, we *block* the indirect (confounding) path between Z and Y :



*DAG with confounding path $Z \rightarrow X \rightarrow Y$ **blocked** by conditioning on X*

The third challenge of causal inference is that

correct specification cannot be guaranteed;

- we may not capture the relationship between Y and (Z, X) correctly,
- we may mistakenly use a model $m(x, z)$ instead of $\mu(x, z)$.

We seek statistical methods that can overcome this.

Part 2

The Propensity Score

Constructing a balanced sample

Recall the randomized trial setting in the case of a binary exposure.

- we obtain a random sample of size n of individuals from the target population, and measure their X values;
- according to some random assignment procedure, we *intervene* to assign treatment Z to individuals, and measure their outcome Y ;
- the link between X and Z is *broken* by the random allocation.

Recall that this procedure led to the valid use of the estimators of the ATE based on (1) and (2).

The important feature of the randomized study is that we have, for confounders X (indeed all predictors)

$$f_{X|Z}(x|1) \equiv f_{X|Z}(x|0) \quad \text{for all } x,$$

or equivalently, in the case of a binary confounder,

$$\Pr[X = 1|Z = 1] = \Pr[X = 1|Z = 0].$$

The distribution of X is *balanced* across the two exposure groups; this renders direct comparison of the outcomes possible.

Probabilistically, X and Z are *independent*.

Constructing a balanced sample

In an *observational* study, there is a possibility that the two exposure groups are systematically *not balanced*

$$f_{X|Z}(x|1) \neq f_{X|Z}(x|0) \quad \text{for some } x,$$

or in the binary case

$$\Pr[X = 1|Z = 1] \neq \Pr[X = 1|Z = 0].$$

If X influences Y also, then this imbalance renders direct comparison of outcomes in the two groups impossible.

Whilst *global* balance may not be present, it may be that '*local*' balance, within certain *strata* of the sample, may be present.

- Let \mathcal{S} be some identified stratum in the sample space for X ;
- suppose for $x \in \mathcal{S}$, we have *balance*; that is, within \mathcal{S} , X is independent of Z ;

$$f_{X|Z:\mathcal{S}}(x|1 : x \in \mathcal{S}) = f_{X|Z}(x|0 : x \in \mathcal{S});$$

- for individuals who have X values in \mathcal{S} , there is the possibility of *direct comparison* of the treated and untreated groups.

We might then restrict attention to causal statements within stratum \mathcal{S} .

Note 6.

In an extreme yet trivial case, consider a confounder X that takes only a single value, x_0 say, for all individuals.

Then it is clear that any systematic differences in outcomes *must* be due to exposure.

Constructing a balanced sample

For *discrete* confounders, we can

- define strata where the X values are *precisely matched*, then
- compare the outcomes for treated and untreated individuals *within* those strata, then
- perform this comparison to *multiple* strata, and combine.

Consider matching strata $\mathcal{S}_1, \dots, \mathcal{S}_K$. We would then be able to compute the ATE by noting that

$$\mathbb{E}[Y(1) - Y(0)] = \sum_{k=1}^K \mathbb{E}[Y(1) - Y(0)|X \in \mathcal{S}_k] \Pr[X \in \mathcal{S}_k]$$

- $\mathbb{E}[Y(1) - Y(0)|X \in \mathcal{S}_k]$ may be estimated non-parametrically from the data by using (1) or (2) for data restricted to have $x \in \mathcal{S}_k$.
- $\Pr[X \in \mathcal{S}_k]$ may be estimated using the empirical proportion of x that lie in \mathcal{S}_k .

For *continuous* confounders, we again consider matching strata $\mathcal{S}_1, \dots, \mathcal{S}_K$. The formula for combining strata still holds, but

- we must assume a model for how $\mathbb{E}[Y(1) - Y(0)|X \in \mathcal{S}_k]$ varies with x for $x \in \mathcal{S}_k$.

In both cases, inference is restricted to the set of X space covered by the strata.

Constructing a balanced sample

In the continuous case, the above calculations depend on the assumption that the treatment effect is similar for x values that lie '*close together*' in predictor (confounder) space. However

- I. Unless we can achieve *exact* matching, then the term 'close together' needs careful consideration.
- II. If X is *moderate* or *high-dimensional*, there may be insufficient data to achieve adequate matching to facilitate the estimation of

$$\mathbb{E}[Y(1) - Y(0)|X \in \mathcal{S}_k];$$

recall that we need a large enough sample of treated and untreated subjects in stratum \mathcal{S}_k .

Nevertheless, matching in this fashion is an important tool in causal comparison.

We now introduce the important concept of the propensity score that facilitates causal comparison via a balancing approach.

Recall that our goal is to mimic the construction of the randomized study that facilitates direct comparison between treated and untreated groups. We may not be able to achieve this globally, but possibly can achieve it locally in strata of X space.

The question is how to define these strata.

Recall that in the binary exposure case, balance corresponds to being able to state that within \mathcal{S} , X is *independent* of Z :

$$f_{X|Z:\mathcal{S}}(x|1 : x \in \mathcal{S}) = f_{X|Z}(x|0 : x \in \mathcal{S})$$

This can be achieved if \mathcal{S} is defined in terms of a *statistic*, $e(X)$ ^[2] say. That is, we consider the conditional distribution

$$f_{X|Z, e(X)}(x|z, e)$$

so that, *given* $e(X) = e$, Z is *independent of* X , so that within strata of $e(X)$, the treated and untreated groups are directly comparable.

^[2] note the sans serif font $e(\cdot)$, distinct from e which indicates a numerical value.

For conditional independence, we require that

$$f_{X|Z,e(X)}(x|z, e) = f_{Z|e(X)}(z|e) \quad \text{for all } x, z, e. \quad (4)$$

Now, as Z is binary, we must be able to write

$$f_{Z|e(X)}(z|e) = p(e)^z(1 - p(e))^{1-z} \quad z \in 0, 1$$

where $p(e)$ is a probability, and a function of the fixed value e .

But $e(X)$ is a function of X , so automatically we have that

$$f_{Z|X, e(X)}(z|x, e) \equiv f_{Z|X}(z|x) \quad \text{provided } e = e(x).$$

Therefore, we require that

$$f_{Z|X}(z|x) = f_{Z|X, e(X)}(z|x, e) = p(e)^z(1 - p(e))^{1-z}$$

for all relevant z, x , with $e = e(x)$.

This can be achieved by choosing the statistic^[3]

$$e(x) = f_{Z|X}(1|x) = \Pr_{Z|X}[Z = 1|X = x]$$

and setting $p(\cdot)$ to be the identity function, so that

$$f_{Z|X}(z|x) = e^z(1 - e)^{1-z} \quad z = 0, 1, e = e(x).$$

The random variable $e(X)$ defines the strata via which the causal calculation can be considered.

^[3] Choosing $e(x)$ to be some monotone transform of $f_{Z|X}(1|x)$ would also achieve the same balance.

Balance via the propensity score

The function $e(x)$ defined in this way is the *propensity score*^[4]. It has the following important properties:

- (i) it is a balancing score; conditional on $e(X)$, X and Z are independent;
- (ii) it is a *scalar* quantity, irrespective of the dimension of X ;
- (iii) in noting that for balance we require that

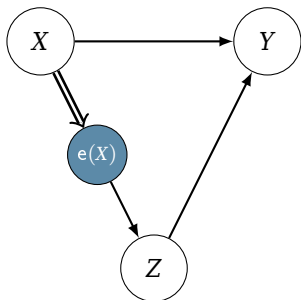
$$f_{Z|X}(z|x) \equiv f_{Z|e(X)}(z|e),$$

the above construction demonstrates that if $\tilde{e}(X)$ is another balancing score, then $e(X)$ is a function of $\tilde{e}(X)$;

- that is, $e(X)$ is the '*coarsest*' balancing score.

^[4] see Rosenbaum & Rubin (1983), Biometrika

Balance via the propensity score



DAG with confounding path $Z \rightarrow X \rightarrow Y$ **blocked** by conditioning on $e(X)$.
Double arrow $X \Rightarrow e(X)$ indicates a deterministic relationship.

To achieve balance we must ensure that

$$e(X) = \Pr[Z = 1|X]$$

is *correctly specified*.

- If X comprises entirely *discrete* components, then we may be able to estimate $\Pr[Z = 1|X]$ entirely non-parametrically, and satisfactorily if the sample size is large enough.
- If X has *continuous* components, it is common to use parametric modelling, with

$$e(X; \alpha) = \Pr[Z = 1|X; \alpha].$$

Balance then depends on *correct specification* of this model.

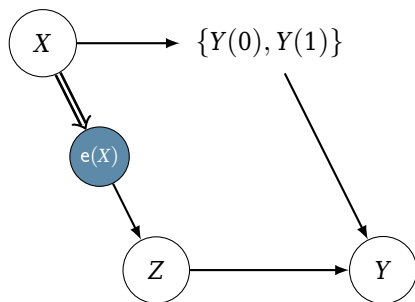
The assumption of ‘no unmeasured confounders’ amounts to assuming that the potential outcomes are jointly *independent* of exposure assignment given the confounders, that is

$$\{Y(0), Y(1)\} \perp Z \mid X$$

that is, in terms of densities

$$\begin{aligned} f_{Y(z), Z|X}(y, z|x) &= f_{Y(z)|X}(y|x)f_{Z|X}(z|x) \\ &= f_{Y|Z, X}(y|z, x)f_{Z|X}(z|x). \end{aligned}$$

Unconfoundedness given the propensity score



Directed Acyclic Graph (DAG) with potential outcomes and $e(X)$

It is clear from the DAG that

$$Y(z) \perp Z \mid e(X) \quad \text{for all } z.$$

We now consider the same stratified estimation strategy as before, but using $e(X)$ instead X to stratify.

Consider strata $\mathcal{S}_1, \dots, \mathcal{S}_K$ defined via $e(X)$. In this case, recall that

$$0 < e(X) < 1$$

so we might consider an equal quantile partition, say using quintiles.

Then we have

$$\mathbb{E}[Y(1) - Y(0)] = \sum_{k=1}^K \mathbb{E}[Y(1) - Y(0) | e(X) \in \mathcal{S}_k] \Pr[e(X) \in \mathcal{S}_k]$$

still holds approximately if the \mathcal{S}_k are small enough.

This still requires us to be able to estimate

$$\mathbb{E}[Y(1) - Y(0) | e(X) \in \mathcal{S}_k]$$

so we need a sufficient number of treated and untreated individuals with $e(X) \in \mathcal{S}_k$ to facilitate direct comparison within this stratum.

If the expected responses are constant across the stratum, the formulae (1) and (2) may be used.

The derivation of the propensity score indicates that it may be used to construct *matched* individuals or groups that can be compared directly.

- if two individuals have *precisely the same value* of $e(x)$, then they are exactly matched;
- if one of the pair is treated and the other untreated, then their outcomes can be *compared directly*, as any imbalance between their measured confounder values has been removed by the fact that they are matched on $e(x)$;
- this is conceptually identical to the standard procedure of matching in two-group comparison.

For an *exactly* matched pair (i_1, i_0) , treated and untreated respectively,

$$y_{i_1} - y_{i_0}$$

is an unbiased estimate of the ATE

$$\mathbb{E}[Y(1) - Y(0)];$$

more typically we might choose m such matched pairs, usually with different $e(x)$ values across pairs, and use the estimate

$$\frac{1}{m} \sum_{i=1}^m (y_{i_1} - y_{i_0})$$

Exact matching is difficult to achieve, therefore we more commonly attempt to achieve approximate matching

- May match one treated to M untreated (1 : M matching)
- caliper matching;
- nearest neighbour/kernel matching;
- matching with replacement.

Most standard software packages have functions that provide automatic matching using a variety of methods.

The theory developed above extends beyond the case of binary exposures.

Recall that we require *balance* to proceed with causal comparisons; essentially, with strata defined using X or $e(X)$, the distribution of X should not depend on Z .

We seek a scalar statistic such that, conditional on the value of that statistic, X and Z are independent. In the case of general exposures, we must consider balancing scores that are functions of *both* Z and X .

For a balancing score $b(Z, X)$ ^[5], we require that

$$X \perp Z \mid b(Z, X).$$

We denote $B = b(Z, X)$ for convenience.

Consider the conditional distribution $f_{Z|X,B}(z|x, b)$: we wish to demonstrate that

$$f_{Z|X,B}(z|x, b) = f_{Z|B}(z|b) \quad \text{for all } z, x, b.$$

That is, we require that B completely characterizes the conditional distribution of Z given X .

^[5] note the sans serif font $b(\cdot)$, distinct from b which indicates a numerical value.

This can be achieved by choosing the statistic

$$b(z, x) = f_{Z|X}(z|x)$$

in line with the choice in the binary case.

The balancing score defined in this way is termed the

Generalized Propensity Score

which is a balancing score for general exposures.

Note, however, that this choice that mimics the binary exposure case is not the only one that we might make. The requirement

$$f_{Z|X,B}(z|x, b) = f_{Z|B}(z|b)$$

for all relevant z , x is met if we define $b(Z, X)$ to be *any* sufficient statistic that characterizes the conditional distribution of Z given X .

It may be possible, for example, to choose functions purely of X .

Example: Normally distributed exposures

Suppose that continuous valued exposure Z is distributed as

$$Z|X = x \sim \text{Normal}(x\alpha, \sigma^2)$$

for row-vector confounder X . We have that

$$f_{Z|X}(z|x) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left\{ -\frac{1}{2\sigma^2} (z - x\alpha)^2 \right\}$$

Example: Normally distributed exposures

We might therefore choose

$$b(Z, X) = \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left\{ -\frac{1}{2\sigma^2} (Z - X\alpha)^2 \right\}.$$

However, the linear predictor

$$b(X; \alpha) = X\alpha$$

also characterizes the conditional distribution of Z given X ; if we know that $x\alpha = b$, then

$$Z|X = x \equiv Z|B = b \sim \text{Normal}(b, \sigma^2).$$

In both cases, parameters α are to be estimated.

The generalized propensity score inherits all the properties of the standard propensity score;

- it induces balance;
- if the potential outcomes and exposure are independent given X under the unconfoundedness assumption, they are also independent given $b(Z, X)$.

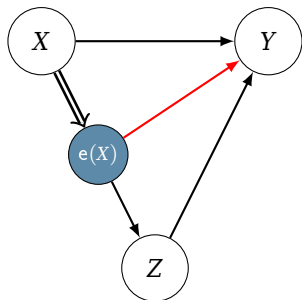
However, how exactly to use the generalized propensity score in causal adjustment for continuous exposures is not clear.

Up to this point we have considered using the propensity score for stratification, that is, to produce directly comparable groups of treated and untreated individuals.

Causal comparison can also be carried out using regression techniques: that is, we consider building an estimator of the APO by *regressing* the outcome on a function of the exposure and the propensity score.

Regressing on the propensity score is a means of controlling the confounding.

Propensity Score Regression



*Conditioning on $e(X)$ achieved using **regression***

We may build a regression model

$$\mathbb{E}_{Y|X,Z}[Y|X, e(X), Z]$$

which, as

$$X \perp\!\!\!\perp Z \mid e(X)$$

has the advantage that it will be more robust to possible mis-specification when a parametric model is proposed.

For example, we may specify

$$\mathbb{E}[Y|X, \mathbf{e}(X), Z] = \beta_0 + \psi_0 Z + \phi_0 \mathbf{e}(X)$$

and carry out OLS estimation to estimate ψ_0 as the ATE parameter.

If we have the *true* conditional mean^[6] is

$$\mathbb{E}[Y|X = x, Z = z, \mathbf{b}(Z, X) = b] = \mu(x, z, b)$$

then by the unconfoundedness result that

$$\mathbb{E}[Y(z)] = \mathbb{E}_X[\mathbb{E}[Y|X, Z = z, \mathbf{b}(z, X)]] = \mathbb{E}_X[\mu(X, z, \mathbf{b}(z, X))].$$

^[6] this is very particular assumption!

That is, to estimate the APO, we might

- fit the balancing model $b(Z, X)$ by regressing Z on X ;
- fit the model $\mu(x, z, b)$ incorporating the fitted values $\hat{b}(z_i, x_i)$;
- for each z of interest, estimate the APO by

$$\frac{1}{n} \sum_{i=1}^n \mu(x_i, z, \hat{b}(z, x_i)).$$

Example: Binary exposure

- $e(x; \alpha) = \Pr[Z = 1|X = x; \alpha]$ then regress Z on X to obtain $\hat{\alpha}$ and fitted values $\hat{e}(x) \equiv e(x; \hat{\alpha})$.
- For $\mu(x, z, e; \theta)$, estimate θ by regressing y_i on z_i and $e_i = \hat{e}(x_i)$.

For example, if $\theta = (\beta_0, \psi_0, \phi_0)$

$$\mathbb{E}[Y|X_i = x_i, Z = z_i, e(X_i) = e_i; \theta] = \beta_0 + \psi_0 z_i + \phi_0 e_i.$$

We then average the model predictions to obtain the APO estimate

$$\hat{\mathbb{E}}[Y(z)] = \frac{1}{n} \sum_{i=1}^n \mu(x_i, z, \hat{e}(x_i); \hat{\theta}).$$

Example: Continuous exposure

We propose a parametric probability density for the exposure

$$b(z, x; \alpha) = f_{Z|X}(z|x; \alpha)$$

for which we estimate α by regressing Z on X to obtain $\hat{\alpha}$ and fitted values $\hat{b}(z, x) \equiv b(z, x; \hat{\alpha})$. Then we specify

$$\mathbb{E}[Y|X = x, Z = z, b(Z, X) = b; \theta] = \mu(x, z, b; \theta)$$

and estimate this model by regressing y on z and $\hat{b}(z, x)$.

Example: Continuous exposure

We then compute the predictions under this model, and average them to obtain the APO estimate

$$\hat{\mathbb{E}}[Y(\mathbf{z})] = \frac{1}{n} \sum_{i=1}^n \mu(x_i, \mathbf{z}, \hat{\mathbf{b}}(\mathbf{z}, x_i); \hat{\theta}).$$

Note that here the propensity terms that enter into μ are computed at the target \mathbf{z} values

not the observed exposure values.

These procedures require us to make two modelling choices:

- the propensity model, $b(z, x)$ or $b(x)$;
- the outcome mean model $\mu(x, z, b)$.

For consistent inference for the ATE, we need

- the propensity model, *and*
- the dependence of the outcome mean model on z

to be correctly specified.

Example: Binary exposure

Suppose that the true (data generating) conditional mean can be written

$$\mathbb{E}[Y|X = x, Z = z] = \mu(x, z) = \mu_0(x) + z\mu_1(x)$$

but that the propensity score regression model

$$\mathbb{E}[Y|X = x, Z = z, e(X) = e] = m_0(x) + z\mu_1(x) + e\mu_1(x)$$

is used.

Example: Binary exposure

This is sufficient to give consistent estimation of the ATE

$$\mathbb{E}[Y(1) - Y(0)] = \mathbb{E}_X[\mu_1(X)].$$

That is, we may mis-specify the ‘treatment-free’ component

$$\mu_0(x)$$

provided we correctly specify the propensity model $e(x)$.

If we believe there is a treatment/predictor *interaction*, say

$$\mathbb{E}[Y|X, Z] = \beta_0 + Z(\psi_0 + \psi_1 X_1)$$

we should fit the propensity score regression model

$$\mathbb{E}[Y|X, e(X), Z] = \beta_0 + Z(\psi_0 + \psi_1 X_1) + e(X)(\phi_0 + \phi_1 X_1)$$

- for every term in Z , we include a *corresponding* term in $e(X)$;
- we use predictions from this model in order to estimate the ATE.

PSR Example

In the binary treatment case, if the data generating model is

$$\mathbb{E}[Y|X = x, Z = z] = \mathbf{x}_0\beta_{\text{TRUE}} + z\mathbf{x}_2\psi = \mu(x, z; \beta_{\text{TRUE}}, \psi)$$

for row vectors \mathbf{x}_0 and \mathbf{x}_2 , then the propensity score regression model

$$m(x, z; \beta, \psi, \phi) = \mathbf{x}_1\beta + z\mathbf{x}_2\psi + e(x)\mathbf{x}_2\phi$$

for row vector \mathbf{x}_1 will return a consistent estimator of ψ even if the *treatment-free mean model* $\mathbf{x}_1\beta$ is mis-specified.

Consider the OLS estimation of (β, ψ, ϕ) : we solve

$$\sum_{i=1}^n \begin{pmatrix} \mathbf{x}_{i1}^\top \\ z_i \mathbf{x}_{i2}^\top \\ e(x_i) \mathbf{x}_{i2}^\top \end{pmatrix} (y_i - \mathbf{x}_{i1} \beta - z_i \mathbf{x}_{i2} \psi - e(x_i) \mathbf{x}_{i2} \phi) = \mathbf{0}$$

analytically using the usual approaches.

If $\mathbf{x}_1 = \mathbf{x}_0$ then the treatment-free model is correctly specified, and we still recover the correct ATE.

If the mean model is *mis-specified*, but

- (i) the propensity score model $e(x)$ is *correctly specified*;
- (ii) the random quantity

$$\varepsilon_i = (Y_i - \mathbf{X}_{i1}\beta - Z_i \mathbf{X}_{i2}\psi - e(X_i)\mathbf{X}_{i2}\phi)$$

is *independent* of Z_i , so that the effect of Z_i is correctly captured via

$$Z_i \mathbf{X}_{i2}\psi.$$

the solutions to the resulting estimating equation are still *consistent* for the true values.

We simply rearrange the OLS estimating equations to

$$\sum_{i=1}^n \begin{pmatrix} \mathbf{x}_{i1}^\top \\ z_i \mathbf{x}_{i2}^\top \\ (z_i - e(x_i)) \mathbf{x}_{i2}^\top \end{pmatrix} (y_i - \mathbf{x}_{i1} \beta - z_i \mathbf{x}_{i2} \psi - e(x_i) \mathbf{x}_{i2} \phi) = \mathbf{0}$$

to see this.

Inference for ψ is correct if *at least one* of

- the mean model, *or*
- the propensity score model

is correctly specified, *provided* the treatment effect model is correctly specified.

This is known as *double robustness*.

We may consider the reduced form

$$\sum_{i=1}^n \begin{pmatrix} \mathbf{x}_{i1}^\top \\ (z_i - e(x_i))\mathbf{x}_{i2}^\top \end{pmatrix} (y_i - \mathbf{x}_{i1}\beta - z_i \mathbf{x}_{i2}\psi) = \mathbf{0}.$$

This form still leads to double robustness.

Estimation based on this system is known as *G-estimation*.

The most basic form of the G-estimating equation arises from the model that omits the treatment-free component:

$$\sum_{i=1}^n (z_i - e(x_i)) \mathbf{x}_{i2}^\top (y_i - z_i \mathbf{x}_{i2} \psi) = 0$$

and in the simplest case with ψ one-dimensional

$$\sum_{i=1}^n (z_i - e(x_i))(y_i - z_i \psi_0) = 0$$

say.

In this case we can solve explicitly to obtain

$$\hat{\psi}_0 = \frac{\sum_{i=1}^n (z_i - e(x_i)) y_i}{\sum_{i=1}^n z_i (z_i - e(x_i))}$$

with corresponding estimator

$$\frac{\sum_{i=1}^n (Z_i - e(X_i)) Y_i}{\sum_{i=1}^n Z_i (Z_i - e(X_i))}.$$

These results extend to more complicated settings: for example, the *doubly robust* G-estimator takes the form

$$\frac{\sum_{i=1}^n (Z_i - e(X_i))(Y_i - \mathbf{X}_{i1}\hat{\beta})}{\sum_{i=1}^n Z_i(Z_i - e(X_i))}.$$

We focus on the APO

$$\mu(\mathbf{z}) = \mathbb{E}[Y(\mathbf{z})] = \int y f_{Y(\mathbf{z}),X}(y, \mathbf{x}) \, dy \, d\mathbf{x}$$

and utilize the propensity model in a different fashion;

Instead of accounting for confounding by balancing through matching or regression, we aim to achieve balance via *weighting*.

Recall that intervening to set $Z = \mathbf{z}$ leads to the calculation

$$\mathbb{E}[Y(\mathbf{z})] = \int y \mathbb{1}_{\{\mathbf{z}\}}(\mathbf{z}) f_{Y(\mathbf{z}),X}(y, x) dy dz dx.$$

We take a random sample from the population with density

$$\mathbb{1}_{\{\mathbf{z}\}}(\mathbf{z}) f_{Y(\mathbf{z}),X}(y, x) \equiv \mathbb{1}_{\{\mathbf{z}\}}(\mathbf{z}) f_{Y|Z,X}(y|\mathbf{z}, x) f_X(x).$$

and construct the usual estimator

$$\widehat{\mathbb{E}}[Y(\mathbf{z})] = \frac{1}{n} \sum_{i=1}^n Y_i$$

as $Z_i = \mathbf{z}$ for all i .

In a randomized (*experimental*) study, suppose that exposure $Z = \mathbf{z}$ is assigned with probability determined by $f_Z(\mathbf{z})$.

Then we have the estimators

$$\hat{\mathbb{E}}[Y(\mathbf{z})] = \frac{\sum_{i=1}^n \mathbb{1}_{\{\mathbf{z}\}}(Z_i) Y_i}{\sum_{i=1}^n \mathbb{1}_{\{\mathbf{z}\}}(Z_i)} \quad \text{or} \quad \hat{\mathbb{E}}[Y(\mathbf{z})] = \frac{1}{nf_Z(\mathbf{z})} \sum_{i=1}^n \mathbb{1}_{\{\mathbf{z}\}}(Z_i) Y_i.$$

Let \mathcal{E} indicate the *experimental* design density

$$f_{X,Y,Z}^{\mathcal{E}}(x, y, z) = f_{Y|Z,X}^{\mathcal{E}}(y|z, x) f_Z^{\mathcal{E}}(z) f_X^{\mathcal{E}}(x).$$

We have that

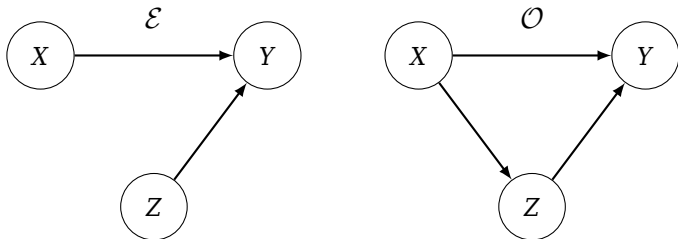
$$\mathbb{E}[Y(z)] \equiv \mathbb{E}_{Y|Z}^{\mathcal{E}}[Y|Z = z] = \frac{\mathbb{E}_{X,Y,Z}^{\mathcal{E}}[\mathbf{1}_{\{z\}}(Z)Y]}{\mathbb{E}_{X,Y,Z}^{\mathcal{E}}[\mathbf{1}_{\{z\}}(Z)]}$$

However, the data arise from the *observational* (non-experimental) distribution \mathcal{O} with density

$$f_{X,Y,Z}^{\mathcal{O}}(x, y, z) = f_{Y|Z,X}^{\mathcal{O}}(y|z, x)f_{Z|X}^{\mathcal{O}}(z|x)f_X^{\mathcal{O}}(x).$$

and in order to perform estimation, we must re-write the expectations in terms of this density.

Average potential outcome: Observational study



DAGs for Experimental (\mathcal{E}) and Observational (\mathcal{O}) distributions

$$\mathcal{E} : f_{X,Y,Z}^{\mathcal{E}}(x, y, z) = f_{Y|Z,X}^{\mathcal{E}}(y|z, x) f_Z^{\mathcal{E}}(z) f_X^{\mathcal{E}}(x)$$

$$\mathcal{O} : f_{X,Y,Z}^{\mathcal{O}}(x, y, z) = f_{Y|Z,X}^{\mathcal{O}}(y|z, x) f_{Z|X}^{\mathcal{O}}(z|x) f_X^{\mathcal{O}}(x)$$

We may use re-weighting (importance sampling logic) to re-write

$$\mathbb{E}[Y(\mathbf{z})] = \frac{\mathbb{E}_{X,Y,Z}^{\mathcal{O}}[\mathbf{1}_{\{\mathbf{z}\}}(Z)Y w(X, Y, Z)]}{\mathbb{E}_{X,Y,Z}^{\mathcal{O}}[\mathbf{1}_{\{\mathbf{z}\}}(Z) w(X, Y, Z)]}$$

where

$$w(x, y, z) = \frac{f_{Y|Z,X}^{\mathcal{E}}(y|z, x)f_Z^{\mathcal{E}}(z)f_X^{\mathcal{E}}(x)}{f_{Y|Z,X}^{\mathcal{O}}(y|z, x)f_{Z|X}^{\mathcal{O}}(z|x)f_X^{\mathcal{O}}(x)}.$$

The function $w(x, y, z)$ can be re-written

$$\frac{f_{Y|Z,X}^{\mathcal{E}}(y|z, x)f_Z^{\mathcal{E}}(z)f_X^{\mathcal{E}}(x)}{f_{Y|Z,X}^{\mathcal{O}}(y|z, x)f_{Z|X}^{\mathcal{O}}(z|x)f_X^{\mathcal{O}}(x)} = \frac{f_{Y|Z,X}^{\mathcal{E}}(y|z, x)}{f_{Y|Z,X}^{\mathcal{O}}(y|z, x)} \times \frac{f_Z^{\mathcal{E}}(z)}{f_{Z|X}^{\mathcal{O}}(z|x)} \times \frac{f_X^{\mathcal{E}}(x)}{f_X^{\mathcal{O}}(x)}$$

- for the first term, we have that

$$\frac{f_{Y|Z,X}^{\mathcal{E}}(y|z, x)}{f_{Y|Z,X}^{\mathcal{O}}(y|z, x)} = 1 \quad \text{for all } y, z, x;$$

under the *no unmeasured confounders* assumption.

- the third term equals 1 by assumption.

The second term

$$\frac{f_Z^{\mathcal{E}}(z)}{f_{Z|X}^{\mathcal{O}}(z|x)}$$

constitutes a *weight* that appears in the integral that yields the desired APO; the term

$$\frac{1}{f_{Z|X}^{\mathcal{O}}(z|x)}$$

accounts for the *imbalance* that influences the confounding and measures the difference between the *observed* sample and a hypothetical idealized *randomized* sample.

This suggests the (non-parametric) estimators

$$\widehat{\mathbb{E}}[Y(\mathbf{z})] = \frac{1}{n} \sum_{i=1}^n \frac{\mathbb{1}_{\{\mathbf{z}\}}(Z_i) Y_i}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i)} \quad (\text{IPW0})$$

which is unbiased, or

$$\widehat{\mathbb{E}}[Y(\mathbf{z})] = \frac{\sum_{i=1}^n \frac{\mathbb{1}_{\{\mathbf{z}\}}(Z_i) Y_i}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i)}}{\sum_{i=1}^n \frac{\mathbb{1}_{\{\mathbf{z}\}}(Z_i)}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i)}} \quad (\text{IPW})$$

which is consistent, each provided $f_{Z|X}^{\mathcal{O}}(\cdot|\cdot)$ *correctly specifies* the conditional density of Z given X for all (\mathbf{z}, \mathbf{x}) .

Note 7.

Inverse weighting constructs a pseudo-population in which there are no imbalances on confounders between the exposure groups. The pseudo-population is balanced, as required for direct comparison of treated and untreated groups.

Note 8.

The term in the denominator, $f_{Z|X}^O(z_i|x_i)$, is the *exposure model*. If Z_i is binary, this essentially reduces to

$$e(x_i)^{z_i}(1 - e(x_i))^{1-z_i}$$

where $e(\cdot)$ is the propensity score as defined previously.

Note 9.

We must have

$$f_{Z|X}^O(z|x) > 0$$

for all x, z .

This is termed the *positivity* assumption or

experimental treatment assignment

assumption.

We may write

$$\mathbb{E}[Y(\mathbf{z})] = \mathbb{E}[Y(\mathbf{z}) - \mu(\mathbf{X}, \mathbf{z})] + \mathbb{E}[\mu(\mathbf{X}, \mathbf{z})]$$

where $\mu(x, \mathbf{z}) = \mathbb{E}[Y|X = x, Z = \mathbf{z}]$ is the data generating conditional outcome mean.

We then have the alternate estimator

$$\widehat{\mathbb{E}}[Y(\mathbf{z})] = \frac{1}{n} \sum_{i=1}^n \frac{\mathbb{1}_{\{\mathbf{z}\}}(Z_i)(Y_i - \mu(X_i, Z_i))}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i)} + \frac{1}{n} \sum_{i=1}^n \mu(X_i, \mathbf{z}) \quad (\text{AIPW})$$

This is termed the *augmented IPW* (AIPW) estimator.

Then, if both

$$f_{Z|X}^{\mathcal{O}}(z|x) \quad \text{and} \quad \mu(x, z)$$

are correctly specified, we have

$$\text{Var}_{\text{AIPW}} \leq \text{Var}_{\text{IPW}}.$$

Furthermore, (AIPW) is *doubly robust*

- *consistent* even if one of $f_{Z|X}^{\mathcal{O}}(z|x)$ and $\mu(x, z)$ is *mis-specified*.

Suppose that (possibly mis-specified) models

$$f(z|x) \quad m(x, z).$$

are used to form the estimator

$$\widehat{\mathbb{E}}[Y(z)] = \frac{1}{n} \sum_{i=1}^n \frac{\mathbb{1}_{\{z\}}(Z_i)(Y_i - m(X_i, Z_i))}{f(Z_i|X_i)} + \frac{1}{n} \sum_{i=1}^n m(X_i, z) \quad (5)$$

Then the *bias* of the estimator is is

$$\mathbb{E} \left[\frac{(f(\mathbf{z}|X) - f_{Z|X}^{\mathcal{O}}(\mathbf{z}|X))(m(X, \mathbf{z}) - \mu(X, \mathbf{z}))}{f(\mathbf{z}|X)} \right] \quad (6)$$

which is zero if

$$f_{Z|X}^{\mathcal{O}} \equiv f \quad \text{or} \quad \mu(x, \mathbf{z}) \equiv m(x, \mathbf{z}).$$

Asymptotically, for estimators that are sample averages, the variance of the estimator converges to zero under standard conditions.

Therefore in large samples it is the magnitude of the bias as given by (6) that determines the quality of the estimator.

- equation (6) demonstrates how mis-specification in the functions $\mu(x, z)$ and $f_{Z|X}^{\mathcal{O}}$ contributes to the bias.

We proceed by assuming that $\mu(x, z)$ is represented by model $m(x, z)$, but that the propensity model $f_{Z|X}^{\mathcal{O}}(z|x)$ is correctly specified.

In the formulation, parametric models for

$$f_{Z|X}^{\mathcal{O}}(z|x; \alpha) \quad m(x, z; \beta)$$

are typically used.

Parameters (α, β) are estimated from the observed data by regressing

- Stage I: Z on X using $(z_i, x_i), i = 1, \dots, n,$
- Stage II: Y on (Z, X) using $(y_i, z_i, x_i), i = 1, \dots, n$

and using plug-in version of (IPW) and (AIPW).

Note 10.

It is possible to conceive of situations where the propensity-type model

$$f_{Z|X}^{\mathcal{O}}(z|x) \quad \text{or} \quad f_{Z|X}^{\mathcal{O}}(z|x; \alpha)$$

is known precisely and does not need to be estimated.

It can be shown that using *estimated* quantities

$$\widehat{f}_{Z|X}^{\mathcal{O}}(z|x) \quad \text{or} \quad f_{Z|X}^{\mathcal{O}}(z|x; \widehat{\alpha})$$

yields *lower variances* for the resulting estimators than if the *known* quantities are used.

We may write the estimating equation yielding (5) as

$$\sum_{i=1}^n \frac{\mathbb{1}_{\{\mathbf{z}\}}(Z_i)}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i)} (Y_i - m(X_i, Z_i)) + \sum_{i=1}^n \{m(X_i, \mathbf{z}) - \mu(\mathbf{z})\} = 0$$

The first summation is a component of the score obtained when performing OLS regression for Y with mean function

$$m(x, z) = m_0(x, z) + \phi \frac{\mathbb{1}_{\{z\}}(z)}{f_{Z|X}^O(z|x)}$$

and $m_0(x, z)$ is a conditional mean model, and ϕ is a regression coefficient associated with the derived predictor^[7]

$$\frac{\mathbb{1}_{\{z\}}(z)}{f_{Z|X}^O(z|x)}.$$

[7] This predictor is sometimes called the '*clever covariate*'

Therefore, an estimator equivalent to (5) can be obtained by regressing Y on (X, Z) for fixed \mathbf{z} using $m(\mathbf{x}, \mathbf{z})$, and forming the estimator

$$\frac{1}{n} \sum_{i=1}^n \left\{ m_0(X_i, Z_i) + \hat{\phi} \frac{\mathbf{1}_{\{\mathbf{z}\}}(Z_i)}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i)} \right\}.$$

In a parametric model setting, this becomes

$$\frac{1}{n} \sum_{i=1}^n \left\{ m_0(X_i, Z_i; \hat{\beta}) + \hat{\phi} \frac{\mathbf{1}_{\{\mathbf{z}\}}(Z_i)}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i; \hat{\alpha})} \right\}$$

where α is estimated from Stage (I), and β is estimated along with ϕ in the secondary regression.

The equivalent to (AIPW) for estimating the ATE for binary treatment

$$\mathbb{E}[Y(1)] - \mathbb{E}[Y(0)]$$

is merely $\widehat{\mathbb{E}}[Y(1)] - \widehat{\mathbb{E}}[Y(0)]$ or

$$\frac{1}{n} \sum_{i=1}^n \left[\frac{\mathbf{1}_1(Z_i)}{f_{Z|X}^O(1|X_i)} - \frac{\mathbf{1}_0(Z_i)}{f_{Z|X}^O(0|X_i)} \right] (Y_i - m(X_i, Z_i)) + \frac{1}{n} \sum_{i=1}^n \delta(X_i)$$

where

$$\delta(x) = m(x, 1) - m(x, 0).$$

Therefore we can repeat the above argument and base the contrast estimator on the regression of Y on (X, Z) using the mean specification

$$m(x, z) = m_0(x, z) + \phi \left[\frac{\mathbb{1}_1(z)}{f_{Z|X}^{\mathcal{O}}(1|x)} - \frac{\mathbb{1}_0(z)}{f_{Z|X}^{\mathcal{O}}(0|x)} \right]$$

or

$$m(x, z) = m_0(x, z) + \left[\phi_1 \frac{\mathbb{1}_1(z)}{f_{Z|X}^{\mathcal{O}}(1|x)} - \phi_0 \frac{\mathbb{1}_0(z)}{f_{Z|X}^{\mathcal{O}}(0|x)} \right].$$

For continuous treatments, if necessary we may carry out adjustment via the conditional *expectation*

$$b(X) = \mathbb{E}_{Z|X}^{\circlearrowleft}[Z|X]$$

rather than (for example) the propensity score which is based on the conditional *probability* model

$$f_{Z|X}^{\circlearrowleft}(Z|X).$$

The data generating model

$$Y = Z\psi + \mu_0(\mathbf{X}; \beta) + \varepsilon$$

which forms the basis of the G-estimation procedure can be utilized if Z is *continuous*.

This relies on the construction of a model for $\mathbb{E}_{Z|X}^{\circlearrowleft}[Z|X]$ which can be achieved using a linear model.

In the continuous setting we can consider other functions of Z in the treatment effect model, for example

$$\mathbf{x}_0\beta + \psi_0Z + \psi_1Z^2$$

or, in an *interaction* model

$$\mathbf{x}_0\beta + \psi_0Z + \psi_1Z^2 + \psi_2ZX_1 + \psi_3Z^2X_1$$

In general, we need to construct models for all the terms in Z : for example

$$b_1(X) = \mathbb{E}_{Z|X}[Z|X] \quad \text{model for } Z$$

$$b_2(X) = \mathbb{E}_{Z|X}[Z^2|X] \quad \text{model for } Z^2$$

etc.

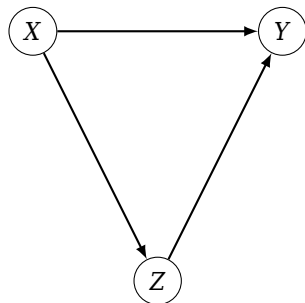
In propensity score regression, we again use the balancing scores to block the backdoor paths. For the model

$$\mathbf{x}_0\beta + \psi_0Z + \psi_1Z^2$$

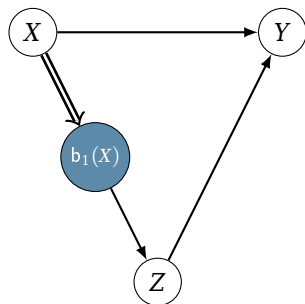
it is sufficient to use the PSR model

$$\beta_0 + \psi_0Z + \psi_1Z^2 + \phi_0\mathbf{b}_1(\mathbf{X})$$

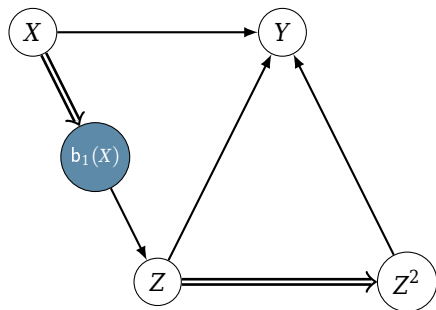
as there is only one backdoor path.



Confounding DAG



Confounding DAG with balancing score $b_1(X)$



Inclusion of quadratic term: confounding path still blocked by $b_1(X)$

However, for the model

$$\mathbf{x}_0\beta + \psi_0Z + \psi_1Z^2 + \psi_2ZX_1 + \psi_3Z^2X_1$$

we must block *both* paths through the interactions using

$$\phi_0\mathbf{b}_1(X) + \phi_1\mathbf{b}_1(X)X_1 + \phi_2\mathbf{b}_2(X) + \phi_3\mathbf{b}_2(X)X_1$$

that includes *both* $\mathbf{b}_1(X)$ and $\mathbf{b}_2(X)$.

For IPW estimation, in principle the construction in equation (IPW0)

$$\hat{\mu}_{\text{IPW}}(\mathbf{z}) = \frac{1}{n} \sum_{i=1}^n \frac{\mathbb{1}_{\{\mathbf{z}\}}(Z_i) Y_i}{f_{Z|X}^{\circ}(Z_i|X_i)}$$

works in the continuous case, as again

$$\mathbb{E}_{X,Y,Z}^{\circ} \left[\frac{\mathbb{1}_{\{\mathbf{z}\}}(Z) Y}{f_{Z|X}^{\circ}(Z|X)} \right] = \mu(\mathbf{z}).$$

We may also use the *standardized weight* estimator in equation (IPW).

We have as usual

$$\mathbb{E}_{X,Z}^{\mathcal{O}} \left[\frac{\mathbb{1}_{\{\mathbf{z}\}}(Z)}{f_{Z|X}^{\mathcal{O}}(Z|X)} \right] = 1.$$

In the continuous setting, for any fixed \mathbf{z} , the estimator includes those data for which

$$\mathbb{1}_{\{\mathbf{z}\}}(z_i) = 1$$

that is, when $z_i = \mathbf{z}$. When Z is treated as continuous, we will get at most one data point meeting the criterion for each \mathbf{z} .

Therefore in practice we typically need to use an estimator based on

$$\frac{\mathbb{1}_{\{A_z\}}(Z)}{f_{Z|X}^O(z|X)}$$

where, for some small $d > 0$,

$$A_z = (z - d, z + d)$$

is a d -neighbourhood of z .

It is sometimes recommended to use the *stabilized* weight based on the (estimated) marginal distribution $f_Z(z)$, that is

$$\frac{f_Z^{\circ}(z)}{f_{Z|X}^{\circ}(z|X)}.$$

That is, say

$$\frac{1}{n} \sum_{i=1}^n \frac{\mathbb{1}_{\{A_z\}}(Z_i) f_Z^{\circ}(Z_i)}{f_{Z|X}^{\circ}(Z_i|X_i)} Y_i$$

These estimators do not rely on a mean model, but as before can be augmented with a proposed mean model

$$m(x, z)$$

such as

$$\hat{\mu}_{\text{AIPW}}(\mathbf{z}) = \sum_{i=1}^n W_{i\mathbf{z}}(Y_i - m(X_i, Z_i)) + \frac{1}{n} \sum_{i=1}^n m(X_i, \mathbf{z}).$$

This can also be fitted using the augmented outcome regression (AOR) approach based on augmented model

$$m(X_i, Z_i) + \phi_0 \frac{\mathbb{1}_{\{A_z\}}(Z_i)}{f_{Z|X}^{\mathcal{O}}(Z_i|X_i)}$$

fitted using least squares.

In weighted least squares (WLS), estimation is carried out according to a proposed mean model, with minimization of a weighted least square objective function.

For example, the mean model $m(x, z) \equiv m(z) = \beta_0 + \psi_0 z$ might be fitted according to the WLS objective function

$$\sum_{i=1}^n w(x_i, z_i) (y_i - \beta_0 - \psi_0 z_i)^2$$

This model assumes a linear dependence on Z .

Note: need to take care with *positivity* violations

- cannot have that X predicts Z too precisely
- can check by inspecting the weights: should have average near 1.

Part 3

Implementation and Computation

Causal inference typically relies on reasonably standard statistical tools:

1. **Standard distributions:**

- Normal;
- Binomial;
- Time-to-event distributions (Exponential, Weibull etc.)

2. **Regression tools:**

- linear model/ordinary least squares;
- generalized linear model, typically linear regression;
- survival models.

Could also consider advanced modelling methods for

- the outcome mean model

$$\mu(x, z) = \mathbb{E}_{Y|X,Z}[Y|X = x, Z = z]$$

- the propensity or balancing score

$$e(x) = \Pr[Z = 1|X = x] \quad b(x) = \mathbb{E}_{Z|X}[Z|X = x]$$

In either case we can utilize

- linear/generalized linear models
- flexible models (eg splines)
- prediction approaches (eg machine learning methods, regression trees, neural networks)
- ensemble methods (eg model averaging, boosting)

to construct fitted versions of each model.

Potential pitfalls:

1. The quantification of *uncertainty*;
 - no ready analytic answers,
 - typically relies on bootstrap;
 - large computational burden
2. *Positivity violations*.
 - prediction (of treatment mechanism) is not the fundamental goal;
 - can be overcome using methods that target balance or overlap explicitly.

Variance estimation can be carried out using the so-called ‘robust’ *sandwich* estimation procedure.

- based on large-sample (semiparametric) theory;
- `sandwich` package in R for standard R classes;
- some causal packages have built-in robust variance estimation; see for example `drgee`.
- need to account for estimation of *nuisance* parameters;
- for propensity score regression or G-estimation, estimation of nuisance parameters has a minimal effect on the variance estimate.

Bootstrap methods can also be used for regression or IPW approaches.

For a survival outcome, *pooled logistic regression* is often used.

The usual continuous survival time outcome is replaced by a discrete, binary outcome;

- this is achieved by partitioning the outcome space into intervals,

$$(0, t_1], (t_1, t_2], \dots$$

and assuming that the failure density is approximately constant in each interval.

- using a hazard parameterization, we have that

$$\Pr[\text{Failure in } (t_{j-1}, t_j] | \text{No failure before } t_{j-1}] = q_j$$

which converts each single failure time outcome into a series of binary responses, with 0 and 1 recording 'no failure' and 'failure'.

Semiparametric models based on *estimating equations* are typically used:

- such models make no parametric assumptions about the distributions of the various quantities, but instead make moment restrictions;
- resulting estimators inherit good asymptotic properties;
- variance of estimators typically estimated in a 'robust' fashion using the sandwich estimator of the asymptotic variance.

In light of the previous discussions, in order to facilitate causal comparisons, there are several key considerations that practitioners must take into account.

1. **The importance of no unmeasured confounding.**

When considering the study design, it is essential for valid conclusions to have measured and recorded all confounders.

2. **Model construction for the outcome regression.**

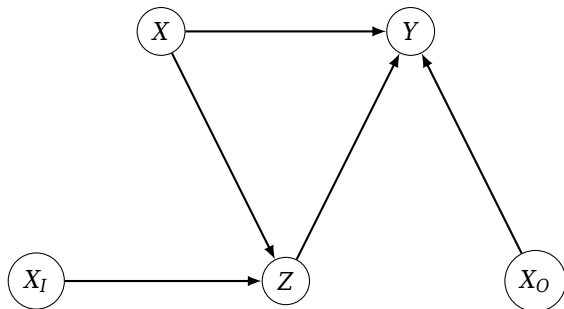
- ideally, the model for the expected value of Y given Z and X , $\mu(x, z)$, should be correctly specified, that is, correctly capture the relationship between outcome and the other variables.
- if this can be done, then no causal adjustments are necessary.
- conventional variable selection techniques can be used; this will prioritize predictors of outcome and therefore will select all confounders;
- however, in finite sample, this method may omit weak confounders that may lead to bias.

3. **Model construction for the propensity score.**

The model for the balancing score should correctly capture the relationship between the exposure and the confounders. We focus on

- identifying the *confounders*;
- *ignoring* the *instruments*: instruments do not predict the outcome, therefore cannot be a source of bias (unless there is unmeasured confounding) - however they can increase the variability of the resulting propensity score estimators.
- the need for the propensity model to induce *balance*;
- *positivity* (or *overlap*): propensity score strata must contain sufficient data to facilitate comparison;
- effective model selection.

Key considerations



DAG with predictors classified by their effects: X are *confounders*; X_I are *instruments*; X_O are *pure predictors of outcome*.

Note 11.

Conventional model selection techniques (stepwise selection, selection via information criteria, sparse selection) *should not be used* when constructing the propensity score.

This is because such techniques prioritize the accurate prediction of exposure conditional on the other predictors; however, this is *not* the goal of the analysis.

These techniques may merely select strong instruments and omit strong predictors of outcome that are only weakly associated with exposure.

Note 12.

An apparently conservative approach is to build rich (highly parameterized) models for both $\mu(x, z)$ and $e(x)$.

This approach prioritizes

bias elimination

at the cost of

variance inflation.

4. **The required measure of effect.**

Is the causal measure required

- a risk difference ?
- a risk ratio ?
- an odds ratio ?
- an ATT, ATE or APO ?

Example: NHANES Analysis

See knitr sheet.

Example: Simulation study

Comparison of different adjustment methods.

Part 4

Extensions

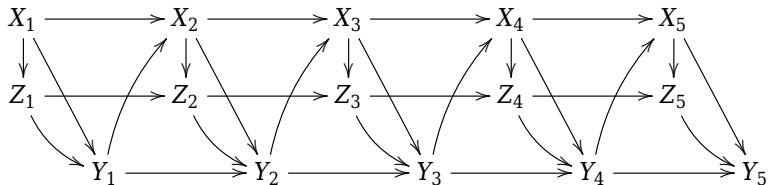
It is common for studies to involve multiple longitudinal measurements of exposure, confounders and outcomes.

In this case, the possible effect of confounding of the exposure effect by the confounders is more complicated.

Furthermore, we may be interested in different types of effect:

- the *direct* effect: the effect of exposure in any given interval on the outcome in that interval, or the final observed outcome;
- the *total* effect: the effect of exposure aggregated across intervals final observed outcome;

Possible structure across five intervals:



- The effect of exposure on later outcomes may be *mediated* through variables measured at intermediate time points
 - for example, the effect of exposure Z_1 may have a direct effect on Y_1 that is confounded by X_1 ; however, the effect of Z_1 on Y_2 may also be non-negligible. This effect is mediated via X_2 .
- There may be *time-varying* confounding;

The propensity score may be generalized to the multivariate setting. We consider for $j = 1, \dots, m$,

- exposure: $\tilde{Z}_{ij} = (Z_{i1}, \dots, Z_{ij})$;
- outcome: $\tilde{Y}_{ij} = (Y_{i1}, \dots, Y_{ij})$;
- confounders: $\tilde{X}_{ij} = (X_{i1}, \dots, X_{ij})$.

Sometimes the notation

$$Z_{1:m} = (Z_1, \dots, Z_m)$$

will be useful.

We consider vectors of potential outcomes corresponding to these observed quantities, that is, we consider a potential sequence of interventions up to time j

$$\tilde{\mathbf{z}}_{ij} = (\mathbf{z}_{i1}, \dots, \mathbf{z}_{ij})$$

and then the corresponding sequence of potential outcomes

$$\tilde{Y}(\tilde{\mathbf{z}}_{ij}) = (Y(\mathbf{z}_{i1}), \dots, Y(\mathbf{z}_{ij})).$$

We define the *multivariate (generalized) propensity score* by

$$b_j(z, x) = f_{Z_j|X_j, \tilde{Z}_{j-1}, \tilde{X}_{j-1}}(z|x, \tilde{z}_{j-1}, \tilde{x}_{j-1})$$

that is, using the conditional distribution of exposure at interval j , given the confounder at interval j , and the historical values of exposures and confounders.

Under the sequential generalizations of the *no unmeasured confounders* and *positivity* assumptions, this multivariate extension of the propensity score provides the required balance, and provides a means of estimating the *direct effect* of exposure.

The multivariate generalization above essentially builds a joint model for the sequence of exposures, and embeds this in a full joint distribution for all measured variables.

An alternative approach uses *mixed* (or *random effect*) models to capture the joint structure.

- such an approach is common in longitudinal data analysis;
- here we consider building a model for the longitudinal exposure data that encompasses a random effect.

Suppose first we have a continuous exposure: we consider the mixed effect model where for time point j

$$Z_{ij} = \tilde{X}_{ij}\alpha + \tilde{Z}_{i,j-1}\vartheta + \xi_i + \epsilon_{ij}$$

where

- $\tilde{X}_{ij}\alpha$ captures the fixed effect contribution of past and current confounders;
- $\tilde{Z}_{i,j-1}\vartheta$ captures the fixed effect contribution of past exposures;
- ξ_i is a subject specific *random effect*;
- ϵ_{ij} is a residual error.

The random effect ξ_i helps to capture unmeasured time-invariant confounding.

The distributional assumption made about ϵ_{ij} determine the precise form of a generalized propensity score that can again be used to estimate the direct effect of exposure.

For binary or other discrete exposures, the random effect model is built on the linear predictor scale, with say

$$\eta_{ij} = \tilde{X}_{ij}\alpha + \tilde{Z}_{i,j-1}\vartheta + \xi_i$$

determining the required conditional mean for the exposure at interval j .

Full-likelihood based inference may be used, but also generalized estimating approaches may be developed.

The estimation of the total effect of exposure is more complicated as the need to acknowledge mediation and time-varying confounding renders standard likelihood-based approaches inappropriate.

The *Marginal Structural Model* is a semiparametric inverse weighting methodology designed to estimate total effects of functions of aggregate exposures that generalizes conventional inverse weighting.

We observe for each individual i a sequence of exposures

$$Z_{i1}, Z_{i2}, \dots, Z_{im}$$

and confounders

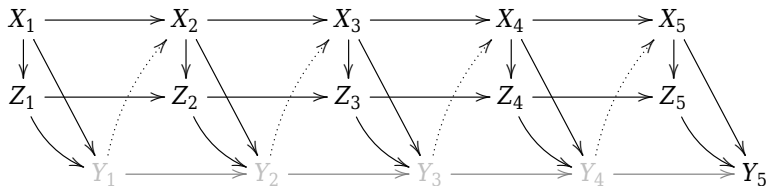
$$X_{i1}, X_{i2}, \dots, X_{im}$$

along with outcome $Y_i \equiv Y_{im}$ measured at the end of the study.

Intermediate outcomes $Y_{i1}, Y_{i2}, \dots, Y_{i,m-1}$ also possibly available.

The Marginal Structural Model

For example, with $m = 5$:



Common example: pooled logistic regression

- discrete time survival outcome
- outcome is binary, intermediate outcomes monotonic
- length of follow-up is random, or event time is censored.

We seek to quantify the causal effect of exposure pattern

$$\tilde{\mathbf{z}} = (z_1, z_2, \dots, z_m)$$

on the outcome. If the outcome is binary, we might consider^[8]

$$\log \left(\frac{\Pr(Y_{im} = 1 | \tilde{\mathbf{z}}; \beta_0, \psi)}{\Pr(Y_{im} = 0 | \tilde{\mathbf{z}}; \beta_0, \psi)} \right) = \beta_0 + \psi \sum_{j=1}^m z_j$$

as the (structural) *marginal* model.

^[8] We might also consider structural models in which the influence of covariates/confounders is recognized.

However, this model is expressed for data presumed to be collected under an *experimental* design, \mathcal{E} .

In reality, it is necessary to adjust for the influence of

- *time-varying confounding* due to the observational nature of exposure assignment
- *mediation* as past exposures may influence future values of the confounders, exposures and outcome.

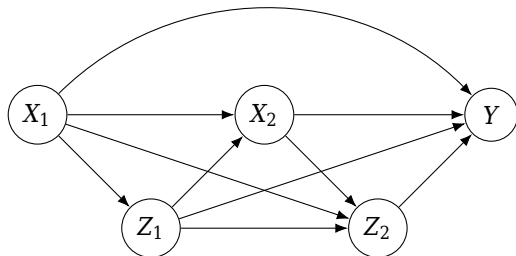
The adjustment can be achieved using *inverse weighting* via a *marginal structural model*.

The Marginal Structural Model: The logic

- Inference is required under *hypothetical* population \mathcal{E} ;
 - in population \mathcal{E} , the *conditional independence* $z_{ij} \perp \tilde{x}_{ij} \mid \tilde{z}_{i(j-1)}$ holds true.
- Samples from *observational* population \mathcal{O} are available.
- The weights w_i convey information on how much \mathcal{O} resembles \mathcal{E} : this information is contained in the parameters γ .
- \mathcal{E} has the *same marginal exposure assignment distribution* as \mathcal{O} .

Two time points

For a two time point setting:



In this formulation, the time ordering

$$X_1 \longrightarrow Z_1 \longrightarrow X_2 \longrightarrow Z_2 \longrightarrow Y$$

delimits the possible causal pathways.

We can consider the expected counterfactual outcomes associated with treatment *patterns*

$$\mathbb{E}[Y(\mathbf{z}_1, \mathbf{z}_2)]$$

or equivalently

$$\mathbb{E}_{Y|Z_1, Z_2}^{\mathcal{E}}[Y|Z_1 = \mathbf{z}_1, Z_2 = \mathbf{z}_2]$$

where the experimental distribution \mathcal{E} assumes randomized treatments.

To learn about the APOs for different treatment patterns from observational data is not straightforward.

- Z_1 has a *direct* effect on Y , and a *mediated* effect via X_2 and Z_2 ;
- Z_2 has a *direct* effect on Y , but it is *confounded* by X_2 ; to remove this confounding we need to condition on X_2 ;
- However, conditioning on X_2 *blocks the directed path* from Z_1 to Y and hence affects the causal effect.

We cannot break the confounding by blocking paths by conditioning to get at the aggregate effect.

We may use *inverse weighting* to break the confounding as in the single interval case. For example, for APO

$$\mu(\mathbf{z}_1, \mathbf{z}_2) = \mathbb{E}_{Y|Z_1, Z_2}^{\mathcal{E}} [Y | Z_1 = \mathbf{z}_1, Z_2 = \mathbf{z}_2]$$

we may use the estimator

$$\tilde{\mu}(\mathbf{z}_1, \mathbf{z}_2) = \frac{1}{n} \sum_{i=1}^n \frac{\mathbb{1}_{\{\mathbf{z}_1\}}(Z_{1i}) \mathbb{1}_{\{\mathbf{z}_2\}}(Z_{2i})}{f_{Z_1, Z_2 | X_1, X_2}^{\mathcal{O}}(Z_{1i}, Z_{2i} | X_{1i}, X_{2i})} Y_i$$

Each outcome data point is re-weighted by the IPW weight across the whole treatment sequence.

In the re-weighted data, *model-based* analysis can also be used: for example, we could propose a marginal model

$$\mathbb{E}_{Y|Z_1, Z_2}^{\mathcal{E}}[Y|Z_1 = \mathbf{z}_1, Z_2 = \mathbf{z}_2] = \beta_0 + \psi_1 \mathbf{z}_1 + \psi_2 \mathbf{z}_2$$

or, using the *total* treatment

$$\mathbb{E}_{Y|Z_1, Z_2}^{\mathcal{E}}[Y|Z_1 = \mathbf{z}_1, Z_2 = \mathbf{z}_2] = \beta_0 + \psi_0(\mathbf{z}_1 + \mathbf{z}_2)$$

and then perform a *weighted least squares analysis* (WLS) to estimate (ψ_1, ψ_2) or ψ_0 .

Such a model is termed a *marginal structural model* (MSM).

That is for example

$$(\hat{\beta}_0, \hat{\psi}_1, \hat{\psi}_2) = \arg \min_{(\beta_0, \psi_1, \psi_2)} \sum_{i=1}^n w_i (y_i - \beta_0 - \psi_1 z_{1i} - \psi_2 z_{2i})^2$$

where

$$w_i = \frac{1}{f_{Z_1, Z_2 | X_1, X_2}^{\mathcal{O}}(z_{1i}, z_{2i} | x_{1i}, x_{2i})}$$

where

$$f_{Z_1, Z_2 | X_1, X_2}^{\mathcal{O}}(z_1, z_2 | x_1, x_2) = f_{Z_1 | X_1}^{\mathcal{O}}(z_1 | x_1) f_{Z_2 | X_1, X_2, Z_1}^{\mathcal{O}}(z_2 | x_1, x_2, z_1).$$

An alternative weight

$$w_i = \frac{f_{Z_1, Z_2}^{\circ}(z_{1i}, z_{2i})}{f_{Z_1, Z_2 | X_1, X_2}^{\circ}(z_{1i}, z_{2i} | x_{1i}, x_{2i})}$$

could be used, where

$$f_{Z_1, Z_2}^{\circ}(z_{1i}, z_{2i}) = f_{Z_1}^{\circ}(z_1) f_{Z_2 | Z_1}^{\circ}(z_2 | z_1).$$

This generalizes the earlier form of IPW estimator.

If a *non-parametric* model for $f_{Z_1, Z_2}^{\circ}(z_{1i}, z_{2i})$ is adopted, then the new weight essentially reduces to the original weight.

Using a *parametric* model,

$$w_i = \frac{f_{Z_1, Z_2}^{\circ}(\mathbf{z}_{1i}, \mathbf{z}_{2i}; \hat{\alpha})}{f_{Z_1, Z_2 | X_1, X_2}^{\circ}(\mathbf{z}_{1i}, \mathbf{z}_{2i} | \mathbf{x}_{1i}, \mathbf{x}_{2i}; \hat{\gamma})}$$

where

- $\alpha = (\alpha_1, \alpha_2)$ is estimated from the model

$$f_{Z_1, Z_2}^{\circ}(\mathbf{z}_1, \mathbf{z}_2; \alpha) = f_{Z_1}^{\circ}(\mathbf{z}_1; \alpha_1) f_{Z_2 | Z_1}^{\circ}(\mathbf{z}_2 | \mathbf{z}_1; \alpha_2)$$

- $\gamma = (\gamma_1, \gamma_2)$ is estimated from the model

$$\begin{aligned} f_{Z_1, Z_2 | X_1, X_2}^{\circ}(\mathbf{z}_1, \mathbf{z}_2 | \mathbf{x}_1, \mathbf{x}_2; \gamma) &= f_{Z_1 | X_1}^{\circ}(\mathbf{z}_1 | \mathbf{x}_1; \gamma_1) \\ &\quad \times f_{Z_2 | X_1, X_2, Z_1}^{\circ}(\mathbf{z}_2 | \mathbf{x}_1, \mathbf{x}_2, \mathbf{z}_1; \gamma_2) \end{aligned}$$

It is also possible to carry out a *conditional* analysis given baseline predictors X_1 which are not subject to the influence of any treatment: for example

$$\mathbb{E}_{Y|Z_1, Z_2, X_1}^{\mathcal{E}} [Y | Z_1 = \mathbf{z}_1, Z_2 = \mathbf{z}_2, X_1 = \mathbf{x}_1] = \beta_0 + \mathbf{x}_1 \beta_1 + \psi_1 \mathbf{z}_1 + \psi_2 \mathbf{z}_2$$

for which the so-called *stabilized* weights

$$w_i = \frac{f_{Z_1, Z_2 | X_1}^{\mathcal{O}}(\mathbf{z}_{1i}, \mathbf{z}_{2i} | \mathbf{x}_{1i})}{f_{Z_1, Z_2 | X_1, X_2}^{\mathcal{O}}(\mathbf{z}_{1i}, \mathbf{z}_{2i} | \mathbf{x}_{1i}, \mathbf{x}_{2i})}$$

should be used.

Separate models are needed for numerator and denominator

- Denominator:

$$f_{Z_1, Z_2 | X_1, X_2}^{\circ}(z_1, z_2 | x_1, x_2) = f_{Z_1 | X_1}^{\circ}(z_1 | x_1) f_{Z_2 | X_1, X_2, Z_1}^{\circ}(z_2 | x_1, x_2, z_1)$$

- Numerator:

$$f_{Z_1, Z_2 | X_1, X_2}^{\circ}(z_1, z_2 | x_1) = f_{Z_1 | X_1}^{\circ}(z_1 | x_1) f_{Z_2 | X_1, Z_1}^{\circ}(z_2 | x_1, z_1)$$

parameterized by α and γ respectively, say.

That is, after cancelling terms,

$$w_i = \frac{f_{Z_2|X_1,Z_1}^{\mathcal{O}}(z_2|x_1, z_1; \hat{\alpha})}{f_{Z_2|X_1,X_2,Z_1}^{\mathcal{O}}(z_2|x_1, x_2, z_1; \hat{\gamma})}$$

This weight may be less extreme than the unstabilized counterpart.

Note that conditioning on X_1 in the outcome model is necessary to account for possible confounding.

Note

The term 'stabilized' is slightly misleading; the introduction of the numerator term *changes the estimand*, so the original and stabilized versions of the MSM estimate *different* quantities.

In many cases the stabilized weights will be more uniform, and this has the effect of reducing estimator variance, but the estimation target is changed.

MSM Example

Part 5

New Challenges and Approaches

The main challenge for causal adjustments using the propensity score is the nature of the observational data being recorded.

The data sets and databases being collected are increasingly complex and typically originate from different sources. The benefits of 'Big Data' come with the costs of more involved computation and modelling.

There is always an important trade off between the sample size n and the dimension of the confounder (and predictor) set.

Examples

- pharmacoepidemiology;
- electronic health records and primary care decision making;
- real-time health monitoring;

For observational databases, the choice of inclusion/exclusion criteria for analysis can have profound influence on the ultimate results:

- different databases can lead to different conclusions for the same effect of interest purely because of the methodology used to construct the raw data, irrespective of modelling choices.
- the key task of the statistician is to report uncertainty in a coherent fashion, ensuring that all sources of uncertainty are reflected. This should include uncertainty introduced due to lack of compatibility of data sources.

Modern quantitative health research also has conventional challenges:

- *missing data*: many causal procedures are adapted forms of procedures developed for handling *informative missingness* (especially inverse weighting);
- *length-bias and left truncation in prevalent case studies*: selection of prevalent cases is also a form of ‘selection bias’ that causes bias in estimation if unadjusted;
- *non-compliance*: in randomized and observational studies there is the possibility of non- or partial compliance which is again a potential source of selection bias.

The *Bayesian* paradigm also provides a framework for decision-making under uncertainty.

Much of the reasoning on causal inference, and many of the modelling choices we must make for causal comparison and adjustment, are identical under Bayesian and classical (frequentist, semiparametric) reasoning.

With increasingly complex data sets in high dimensions, Bayesian methods can be useful as they

- provide a means of informed and coherent decision making in the presence of uncertainty;
- yield interpretable variability estimates in finite sample at the cost of interpretable modelling assumptions;
- allow the statistician to impose structure onto the inference problem that is helpful when information is sparse;
- naturally handle prediction, hierarchical modelling, data synthesis, and missing data problems.

Typically, these advantages come at the cost of more involved computation.

- D.B. Rubin formulated the modern foundations for causal inference from a largely Bayesian (missing data) perspective:
 - revived potential outcome concept to define causal estimand
 - inference through Bayesian predictive formulation
 - focus on matching
- Semiparametric frequentist formulation dominant from mid 80s
- Bayesian approaches can adopt a semiparametric approach

- Full Bayes: full likelihood in two parametric models
 - needs correct specification;
 - two component models are treated independently.
- Quasi-Bayes: use semiparametric estimating equation approach for Stage II, with Stage I parameters treated in a fully Bayesian fashion.
 - possibly good frequentist performance;
 - difficult to understand frequentist properties.
- Pseudo-Bayes: use amended likelihood to avoid feedback between Stage I and Stage II
 - not fully Bayesian, no proper probability model

1. The causal contrast
2. Do we really need potential outcomes ?
3. 'Observables' implies 'Prediction'
4. The Fundamental Theory of Bayesian Inference.
5. The Bayesian Causal Specification

A rapidly developing field ...

Part 6

Conclusions

- Causal inference methods provide answers to important questions concerning the impact of hypothetical exposures;
- Causal graphs are useful in formulating inference;
- Standard statistical methods are used;
- Balance is the key to accounting for confounding;
- The propensity score is a tool for achieving balance;
- The propensity score can be used for
 - matching,
 - weighting, and
 - as part of regression modelling.

Key remaining challenges

- Flexible representations of model components;
- Model selection;
- Scale and complexity of observational data;

- McGill: Erica Moodie, Michael Wallace, Marina Klein
- Toronto: Olli Saarela
- Imperial College London: Dan Graham, Emma McCoy



Reading List

- The propensity score
 - Rosenbaum and Rubin (1983): The introduction of the propensity score, gives basic definitions and properties.
- Applications
 - Austin (2011)
- Extensions beyond binary treatments
 - Hirano and Imbens (2004)
 - Imai and van Dyk (2004)
- Propensity score regression
 - Robins et al. (1992)
- Weighting
 - Lunceford and Davidian (2004)
 - Bang and Robins (2005)
- The marginal structural model

- Hernán et al. (2000)
- Hernán et al. (2001)
- Model selection
 - Brookhart et al. (2006)
- Longitudinal studies
 - Moodie and Stephens (2012)
 - Graham et al. (2014)
- High-dimensional settings
 - Schneeweiss et al. (2009)
- Bayesian methods
 - Rubin (1978)
 - McCandless et al. (2009)
 - An (2010)
 - Saarela et al. (2015)

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- Saarela, O., Stephens, D. A., Moodie, E. E. M., and Klein, M. B. (2015). On Bayesian estimation of marginal structural models. Biometrics **71**, 279–288.
- Schneeweiss, S., Rassen, J. A., Glynn, R. J., Avorn, J., Mogun, H., and Brookhart, M. A. (2009). High-dimensional propensity score adjustment in studies of treatment effects using health care claims data. Epidemiology **20**, 512–522. doi:10.1097/EDE.0b013e3181a663cc.

Appendix: Monte Carlo Methods

For any function $g(\cdot)$, we have

$$\begin{aligned}\mathbb{E}[g(Y)] &= \int g(y) f_Y(y) \, dy \\ &= \int g(y) f_{Y,X}(y, x) \, dy \, dx\end{aligned}$$

Rather than performing this calculation using integration, we approximate it numerically using *Monte Carlo*.

Back

Monte Carlo calculations proceed as follows:

- generate a sample of size n from the density

$$f_Y(\mathbf{y})$$

to yield y_1, \dots, y_n ; there are standard techniques to achieve this.

- approximate $\mathbb{E}[g(Y)]$ by

$$\widehat{\mathbb{E}}[g(Y)] = \frac{1}{n} \sum_{i=1}^n g(y_i).$$

- For large n , $\widehat{\mathbb{E}}[g(Y)]$ provides a good approximation to $\mathbb{E}[g(Y)]$.

We have that

$$\mathbb{E}[g(Y)] = \int g(y) f_Y(y) \, dy = \int g(y) \frac{f_Y(y)}{f_Y^*(y)} f_Y^*(y) \, dy$$

where $f_Y^*(y)$ is some other density. Thus

$$\mathbb{E}_{f_Y}[g(Y)] \equiv \mathbb{E}_{f_Y^*} \left[g(Y) \frac{f_Y(Y)}{f_Y^*(Y)} \right].$$

This is known as *importance sampling*: we

- generate a sample of size n from the density

$$f_Y^*(y)$$

to yield y_1, \dots, y_n ;

- approximate $\mathbb{E}[g(Y)]$ by

$$\widehat{\mathbb{E}}[g(Y)] = \frac{1}{n} \sum_{i=1}^n g(y_i) \frac{f_Y(y_i)}{f_Y^*(y_i)}.$$

This means that even if we do *not* have a sample from the distribution of interest, f_Y , we can still compute averages with respect to f_Y if we have access to a sample from a related distribution, f_Y^* .

Clearly, for the importance sampling computation to work, we need that

$$\frac{f_Y(y_i)}{f_Y^*(y_i)}$$

is *finite* for the required range of Y , which means that we must have

$$f_Y^*(y) > 0 \quad \text{whenever} \quad f_Y(y) > 0.$$

Importance sampling is based on forming *weighted* averages

- we re-weight samples from f_Y^* so that we can estimate quantities relating to f_Y
- this is like '*standardization*' (eg standardized mortality rate) in epidemiology.

Appendix: Confounding Bias Example

Simple confounding example

Suppose that Y, Z and X are all binary variables. Suppose that the true (structural) relationship between Y and (Z, X) is given by

$$\mathbb{E}[Y|Z = z, X = x] = \Pr[Y = 1|Z = z, X = x] = 0.2 + 0.2z - 0.1x$$

with $\Pr[X = 1] = q$. Then, by iterated expectation

$$\mathbb{E}[Y(z)] = 0.2 + 0.2 z - 0.1q$$

and

$$\mathbb{E}[Y(1) - Y(0)] = 0.2.$$

Suppose also that in the population from which the data are drawn

$$\Pr[Z = 1|X = x] = \begin{cases} p_0 & x = 0 \\ p_1 & x = 1 \end{cases} = (1 - x)p_0 + xp_1.$$

in which case

$$\Pr[Z = 1] = (1 - q)p_0 + qp_1.$$

Simple confounding example

If we consider the estimators in (2)

$$\widehat{\mathbb{E}}[Y(1)] = \frac{1}{np} \sum_{i=1}^n \mathbb{1}_{\{1\}}(Z_i) Y_i \quad \widehat{\mathbb{E}}[Y(0)] = \frac{1}{n(1-p)} \sum_{i=1}^n \mathbb{1}_{\{0\}}(Z_i) Y_i$$

and set $p = (1-q)p_0 + qp_1$, we see that for the first term

$$\begin{aligned} \mathbb{E}_{Y,Z,X}[\mathbb{1}_{\{1\}}(Z)Y] &= \mathbb{E}_{Z,X}[\mathbb{1}_{\{1\}}(Z)\mathbb{E}_{Y|Z,X}[Y|Z,X]] \\ &= \mathbb{E}_{Z,X}[\mathbb{1}_{\{1\}}(Z)(0.2 + 0.2Z - 0.1X)] \\ &= 0.2\mathbb{E}_X[\mathbb{E}_{Z|X}[\mathbb{1}_{\{1\}}(Z)|X]] \\ &\quad + 0.2\mathbb{E}_X[\mathbb{E}_{Z|X}[\mathbb{1}_{\{1\}}(Z)Z|X]] \\ &\quad - 0.1\mathbb{E}_X[X\mathbb{E}_{Z|X}[\mathbb{1}_{\{1\}}(Z)|X]] \end{aligned}$$

Simple confounding example

Now

$$\begin{aligned}\mathbb{E}_{Z|X}[\mathbf{1}_{\{1\}}(Z)|X] &= \mathbb{E}_{Z|X}[\mathbf{1}_{\{1\}}(Z)Z|X] \\ &\equiv \Pr[Z = 1|X] = (1 - X)p_0 + Xp_1\end{aligned}$$

and

$$\begin{aligned}\mathbb{E}_X[\mathbb{E}_{Z|X}[\mathbf{1}_{\{1\}}(Z)|X]] &= (1 - q)p_0 + qp_1 = p \\ \mathbb{E}_X[\mathbb{E}_{Z|X}[\mathbf{1}_{\{1\}}(Z)Z|X]] &= (1 - q)p_0 + qp_1 = p \\ \mathbb{E}_X[X\mathbb{E}_{Z|X}[\mathbf{1}_{\{1\}}(Z)|X]] &= qp_1\end{aligned}$$

and therefore

$$\mathbb{E}_{Y,Z,X}[\mathbf{1}_{\{1\}}(Z)Y] = 0.4p - 0.1qp_1.$$

Simple confounding example

$$\therefore \mathbb{E} \left[\frac{1}{np} \sum_{i=1}^n \mathbb{1}_{\{1\}}(Z_i) Y_i \right] = \frac{0.4p - 0.1p_1}{p}$$

By a similar calculation, as $\mathbb{1}_{\{0\}}(Z) = 1 - \mathbb{1}_{\{1\}}(Z)$,

$$\mathbb{E}_X[\mathbb{E}_{Z|X}[\mathbb{1}_{\{0\}}(Z)|X]] = 1 - p$$

$$\mathbb{E}_X[\mathbb{E}_{Z|X}[\mathbb{1}_{\{0\}}(Z)Z|X]] = 0$$

$$\mathbb{E}_X[X\mathbb{E}_{Z|X}[\mathbb{1}_{\{0\}}(Z)|X]] = q(1 - p_1)$$

so

$$\mathbb{E} \left[\frac{1}{n(1-p)} \sum_{i=1}^n \mathbb{1}_{\{0\}}(Z_i) Y_i \right] = \frac{0.2(1-p) - 0.1q(1-p_1)}{1-p}$$

Simple confounding example

Finally, therefore ATE estimator

$$\widehat{\mathbb{E}}[Y(1)] - \widehat{\mathbb{E}}[Y(0)]$$

has expectation

$$\frac{0.4p - 0.1qp_1}{p} - \frac{0.2(1-p) - 0.1q(1-p_1)}{1-p}$$

which equals

$$0.2 - 0.1q \left\{ \frac{p_1}{p} - \frac{1-p_1}{1-p} \right\}$$

and therefore the unadjusted estimator based on (2) is *biased*.

The bias is caused by the fact that the two subsamples with

$$Z = 0 \quad \text{and} \quad Z = 1$$

are *not directly comparable* - they have a different profile in terms of X .

By *Bayes theorem*

$$\Pr[X = 1|Z = 1] = \frac{p_1 q}{p} \quad \Pr[X = 1|Z = 0] = \frac{(1 - p_1)q}{1 - p}$$

so, here, conditioning on $Z = 1$ and $Z = 0$ in turn in the computation of (2), leads to a different composition of X values in the two subsamples.

As X influences Y , the resulting Y values *not directly comparable*.

Appendix: Probability & Causal Graphs

A *probabilistic model* for the data is a *joint* probability distribution

$$f_{X,Y,Z}(x, y, z)$$

which represents how the data are generated.

Back

This *joint* model automatically specifies

- the *marginal* distributions, $f_X(x)$, $f_Y(y)$ and $f_Z(z)$;
- the *conditional* distributions

$$f_{X|Y}(x|y) \quad f_{X|Z}(x|z) \quad f_{Y|X}(y|x) \quad \dots$$

and

$$f_{Y|X,Z}(y|x,z) \quad f_{Y,Z|X}(y,z|x)$$

etc.

that describe how the variables behave *individually*, or when one variable is *fixed* etc.

We have the *chain rule* decomposition

$$f_{X,Y,Z}(x, y, z) = f_X(x)f_{Z|X}(z|x)f_{Y|X,Z}(y|x, z)$$

but also

$$f_{X,Y,Z}(x, y, z) = f_Z(z)f_{Y|Z}(y|z)f_{X|Y,Z}(x|y, z)$$

and so on, for any ordering of the variables.

Two random variables X, Z are *independent*

$$X \perp\!\!\!\perp Z$$

if and only if, for all values (x, z) ,

$$f_{X,Z}(x, z) = f_X(x)f_Z(z)$$

$$f_{Z|X}(z|x) = f_Z(z)$$

$$f_{X|Z}(x|z) = f_X(x)$$

Knowledge about X does not influence our assessment of Z , and vice versa.

We can consider *conditional independence*: say

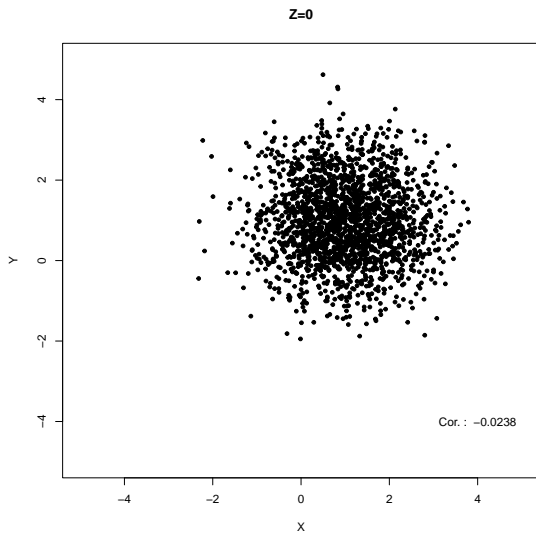
$$Y \perp\!\!\!\perp Z \mid X$$

if and only if, for all (x, z, y)

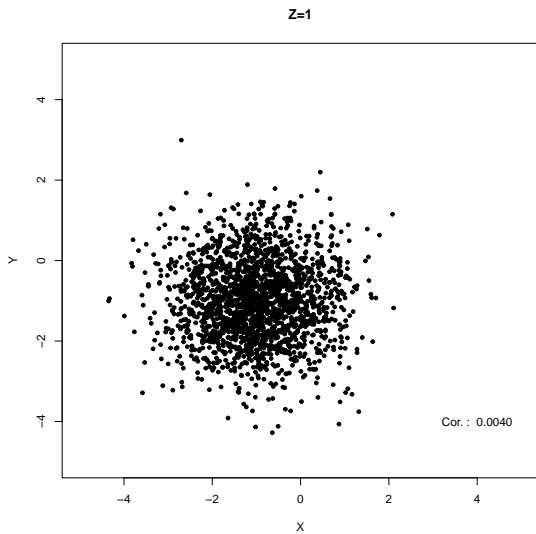
$$f_{Y,Z|X}(y, z|x) = f_{Z|X}(z|x)f_{Y|X}(y|x)$$

At every fixed value of X , knowledge concerning the value of Y does not influence our assessment of Z , and vice versa.

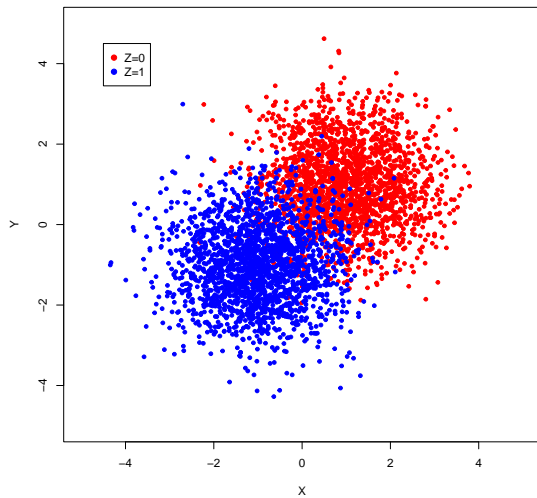
Example



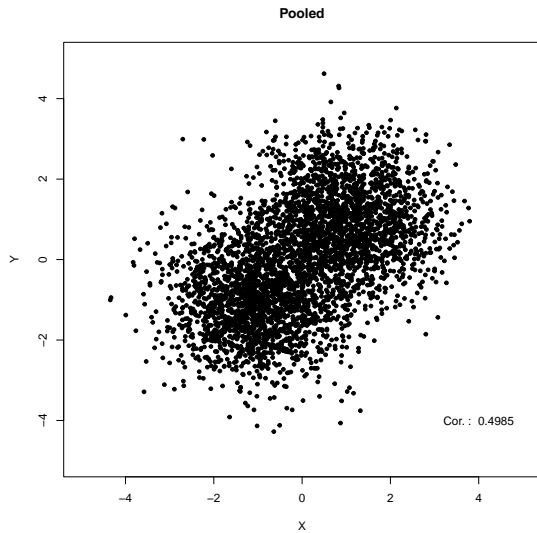
Example



Example



Example



We can compute the *expectation* or *expected value*

$$\mathbb{E}_Y[Y]$$

as a summary of the distribution. The *conditional* expectation

$$\mathbb{E}_{Y|X,Z}[Y|X = x, Z = z]$$

is a function of the two values (x, z) .

The *iterated expectation* result is a very useful tool: we have

$$\mathbb{E}_Y[Y] = \mathbb{E}_X [\mathbb{E}_{Y|X}[Y|X]]$$

and

$$\mathbb{E}_{Y|Z}[Y|Z] = \mathbb{E}_{X|Z} [\mathbb{E}_{Y|X,Z}[Y|X, Z]]$$

etc.

- $Y|X$ is the conditional model for Y given X ;
- $Y|Z$ is the conditional model for Y given Z ;
- $Y|X, Z$ is the conditional model for Y given X and Z .

If X and Z are *independent*, we can simplify

$$\mathbb{E}_{Y|Z}[Y|Z] = \mathbb{E}_{X|Z} [\mathbb{E}_{Y|X,Z}[Y|X, Z]]$$

to

$$\mathbb{E}_{Y|Z}[Y|Z] = \mathbb{E}_X [\mathbb{E}_{Y|X,Z}[Y|X, Z]]$$

In the causal problem, we can compute $\mathbb{E}_{Y|Z}[Y|Z = \mathbf{z}]$ by

- (i) fixing $Z = \mathbf{z}$ independently of X ,
- (ii) computing for each fixed x

$$\mathbb{E}_{Y|X,Z}[Y|X = x, Z = \mathbf{z}] = \mu(x, \mathbf{z})$$

say,

- (iii) averaging the result over the distribution $f_X(x)$

$$\mathbb{E}_X[\mu(X, \mathbf{z})].$$

This works provided X and Z are *independent*.

Recall the factorization from slide 256

$$f_{X,Y,Z}(x, y, z) = f_X(x)f_{Y|X}(y|x)f_{Z|X,Y}(z|x, y).$$

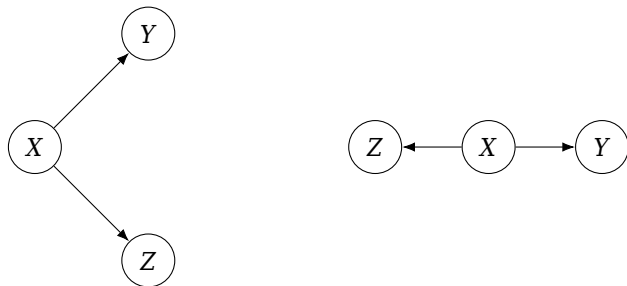
We might assume that

$$Z \perp\!\!\!\perp Y|X$$

so that $f_{Z|X,Y}(z|x, y) = f_{Z|X}(z|x)$ and

$$f_{X,Y,Z}(x, y, z) = f_X(x)f_{Y|X}(y|x)f_{Z|X}(z|x)$$

We can depict the conditional independence using a graph:



This type of graph is sometimes called a *fork*.

- Nodes \textcircled{X} , \textcircled{Y} , \textcircled{Z} denote the variables;
- Edges with *arrows* indicate the nature of dependence in the chain rule factorization;
- *Directed* arrows specify the conditional independence assumptions;

- Nodes without *incoming* edges are *founders*;

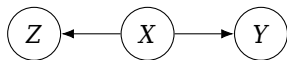


corresponds to

$$f_X(x)f_{Y|X}(y|x)$$

- Nodes with only *outgoing* edges act to *block* dependence.

For example, in



so that

$$f_{X,Y,Z}(x, y, z) = f_X(x)f_{Y|X}(y|x)f_{Z|X}(z|x)$$

it follows that

$$Y \perp\!\!\!\perp Z|X.$$

However, note that

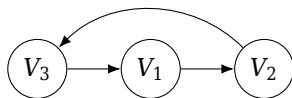
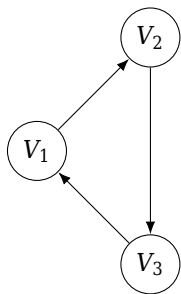
$$Y \not\perp\!\!\!\perp Z.$$

A (causal) graph G is described using the following elements:

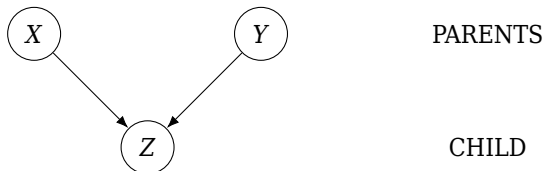
- A set of *nodes* or *vertices*, V_1, V_2, \dots , representing variables.
- A set of *edges*, E_1, E_2, \dots , representing dependencies.
- Two nodes are *adjacent* if there is an edge between them.
- Edges can be *directed*, denoted using arrows, or *undirected*; if all edges are directed, the graph is directed.
- The graph with the arrow directions removed is termed the *skeleton*.

- A *path* between two nodes V_1 and V_2 is a sequence of edges connecting those nodes;
 - a *directed* path is a path where the directions of arrows on edges are obeyed.
 - two nodes are *connected* if a path exists between them, and *disconnected* otherwise.

- In general, a graph may contain *cycles*, that is, directed paths that start and end at the same node.



A directed graph that has no cycles is termed a *directed acyclic graph* (DAG).



$$f_{X,Y,Z}(x, y, z) = f_X(x)f_Y(y)f_{Z|X,Y}(z|x, y)$$

In this DAG, we have $X \perp\!\!\!\perp Y$:

$$f_{X,Y}(x, y) = f_X(x)f_Y(y).$$

However, conditioning on $Z = z$

$$f_{X,Y|Z}(x, y|z) \neq f_X(x|z)f_Y(y|z)$$

in general. That is,

$$X \perp\!\!\!\perp Y$$

but

$$X \not\perp\!\!\!\perp Y \mid Z$$

Conditioning on Z *induces dependence*; the node Z is sometimes termed a *collider*.

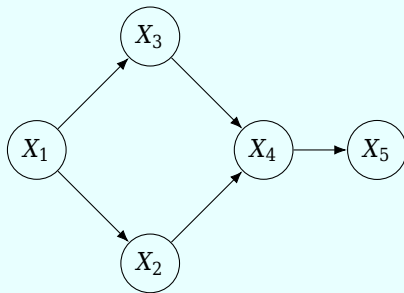
The probability distribution P is *compatible* with graph G if P admits the factorization implied by G .

- note that G does not define P , merely the chain rule factorization that P admits;
- we may deduce from G that

$$f_{X,Y,Z}(x, y, z) = f_X(x)f_Y(y)f_{Z|X,Y}(z|x, y)$$

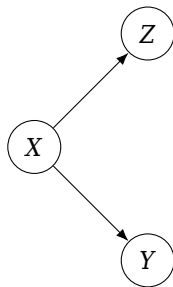
say, *but* we do not know the forms or values of the individual terms.

Example:



$$f_{X_1}(x_1)f_{X_2|X_1}(x_2|x_1)f_{X_3|X_1}(x_3|x_1)f_{X_4|X_2,X_3}(x_4|x_2,x_3)f_{X_5|X_4}(x_5|x_4)$$

When we write



what precisely does the symbol \longrightarrow mean ?

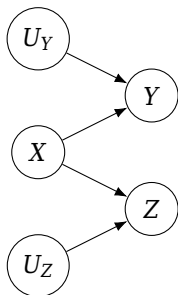
A *structural* interpretation states that we

- generate X independently,
- generate Y and Z independently as functions of the realized X , for example

$$Y = 3X$$

$$Z = 4X + 9$$

X, U_Z, U_Y
independent



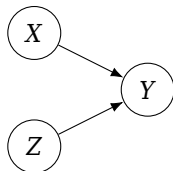
$$Y = g_1(X, U_Y)$$

$$Z = g_2(X, U_Z)$$

For example

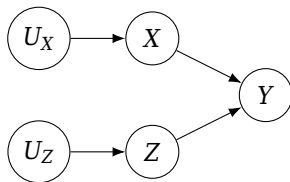
$$Y = X + U_Y$$

$$Z = X + U_Z$$



$$Y = g(X, Z)$$

If we fixed $X = x$ and $Z = z$, we would know $Y = g(x, z)$ *precisely*.



so that $X = g_1(U_X)$, $Z = g_2(U_Z)$, and

$$Y = g(X, Z).$$

If we know $X = x$ and $Z = z$, then we do not need to know the values of U_X and U_Z to determine Y . That is

$$Y \perp\!\!\!\perp (U_X, U_Z) \mid (X, Z)$$

We can interpret causation in terms of these functions.

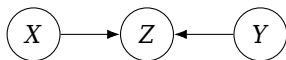
- X *causes* Y if it appears in the function, g , that assigns Y 's value;
- X *causes* Y if, in the graph representing the joint distribution, there is a *directed path* from X to Y ;
- X is a *direct cause* of Y if there is an arrow from X to Y .

To assess whether

$$X \perp\!\!\!\perp Y \mid Z$$

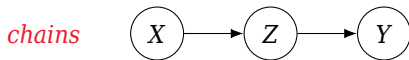
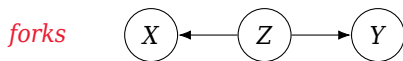
for any distribution compatible with the DAG, we must assess whether Z *'blocks'* paths from X to Y .

Consider the *collider* ('inverted fork') graph

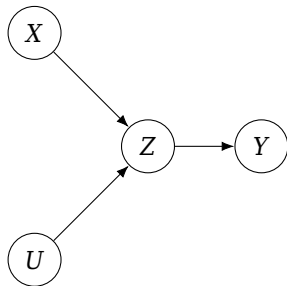


Z is a collider on this path.

A *directed path* from one node to another cannot contain a collider; all parts must be



The notion of being a collider is *path-specific*: for example



- Z is a *collider* on path $X \rightarrow Z \rightarrow U$
- Z is *not a collider* on path $X \rightarrow Z \rightarrow Y$.

A path is *unconditionally open* (or *unblocked*) if there is no collider on the path;

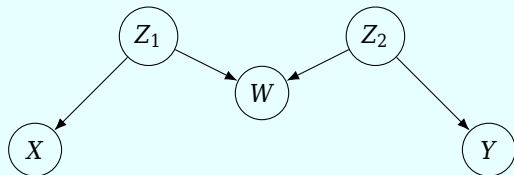
- if there is a collider, the path is *closed* (*blocked*).

Two variables X and Y are *d-separated* if there is *no open path between them*;

- if there is an open path, X and Y are *d-connected*.

Example: Diabetes example (Lash et al.)

- Z_1 family income
- Z_2 genetic risk
- W parental diabetes
- X low educational attainment
- Y diabetes of subject



Example: Diabetes example (Lash et al.)

X and Y are d-separated; there is one path between X and Y , but it is blocked by the collider W .

$$f_{Z_1}(z_1)f_{Z_2}(z_2)f_{W|Z_1,Z_2}(w|z_1,z_2)f_{X|Z_1}(x|z_1)f_{Y|Z_2}(y|z_2)$$

and X and Y are *independent*:

Modern Epidemiology, TL Lash, TJ Vanderweele, S. Haneuse, Kenneth J Rothman

Conditional d-separation

For a *non-collider* Z : consider *conditioning* on Z

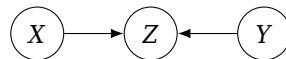


$$X \perp\!\!\!\perp Y \mid Z$$



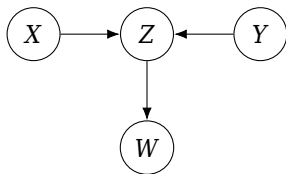
$$X \perp\!\!\!\perp Y \mid Z$$

For a *collider* Z : consider conditioning on Z



$$X \not\perp\!\!\!\perp Y \mid Z$$

Consider



$$f_X(x)f_Y(y)f_{Z|X,Y}(z|x,y)f_{W|Z}(w|z)$$

We have that X and Y are independent.

But

$$\begin{aligned}f_{X,Y,W}(x, y, w) &= f_X(x)f_Y(y) \int f_{Z|X,Y}(z|x, y)f_{W|Z}(w|z) dz \\ &= f_X(x)f_Y(y)f_{W|X,Y}(w|x, y)\end{aligned}$$

Therefore we have that



and so W *is a collider* in the reduced graph.

Therefore

- (i) conditioning on a *non-collider* Z *blocks* the path at Z ;
- (ii) conditioning on a *collider* Z or a *descendant* W of Z *opens* the path at Z ;

Suppose S is a set of variables.

- S *blocks* a path from X to Y if, after conditioning on S , the path is *closed*;
- S *unblocks* a path if after conditioning the path is *open*;
- If S *blocks every path* from X to Y , then X and Y are *d-separated* by S .

- If S d-separates X and Y , it renders them *conditionally independent*

$$X \perp\!\!\!\perp Y \mid S,$$

so that

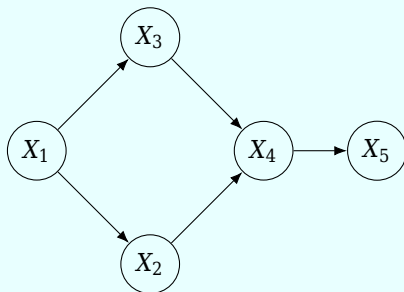
$$f_{X|Y,S}(x|y,s) \equiv f_{X|S}(x|s) \quad \forall(x,y,s).$$

- If S does not d-separate X and Y , then X and Y *may be dependent*, and

$$f_{X|Y,S}(x|y,s)$$

cannot be made independent of y in general.

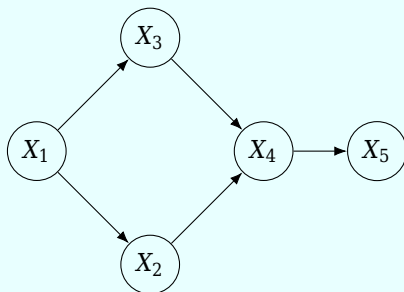
Example:



$\{X_2\}$ and $\{X_3\}$ are d-separated by $\{X_1\}$, and $X_2 \perp\!\!\!\perp X_3 \mid X_1$.

- there are two paths between X_2 and X_3 ;
 - $X_2X_1X_3$: blocked by conditioning on X_1 .
 - $X_2X_4X_3$: blocked by the collider at X_4 , and $X_4 \notin \{X_1\}$.

Example:



$\{X_2\}$ and $\{X_3\}$ are *not* d-separated by $\{X_1, X_5\}$:

- $X_2 \not\perp\!\!\!\perp X_3 \mid (X_1, X_5)$.
- X_5 is a descendant of collider X_4 ;

If X and Y are d-separated by S then

$$X \perp\!\!\!\perp Y \mid S$$

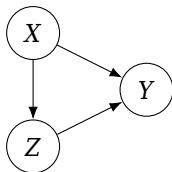
for *all* distributions compatible with G ; conversely, if they are not d-separated, then X and Y are *dependent* given S for at least one distribution compatible with G .

Intervening set the level of Z to z has the effect of

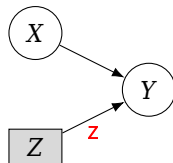
- removing all *incoming* arrows to Z
- switching the marginal for Z to the *degenerate distribution* $f_Z^*(\cdot)$

$$f_Z^*(z) = \mathbb{1}_{\{z\}}(z) \quad z \in \mathbb{R}.$$

In the earlier example

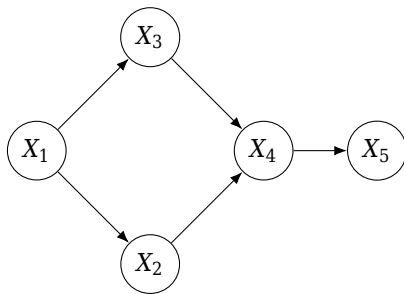


$$f_X(x)f_{Z|X}(z|x)f_{Y|X,Z}(y|x, z)$$



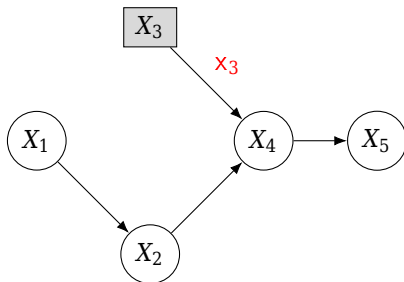
$$f_X(x)f_Z^*(z)f_{Y|X,Z}(y|x, z)$$

Consider the DAG



$$f_{X_1}(x_1)f_{X_2|X_1}(x_2|x_1)f_{X_3|X_1}(x_3|x_1)f_{X_4|X_2,X_3}(x_4|x_2,x_3)f_{X_5|X_4}(x_5|x_4)$$

Suppose we *intervene* to set $X_3 = \mathbf{x}_3$. The relevant DAG is



$$f_{X_1}(x_1)f_{X_2|X_1}(x_2|x_1)f_{X_3}^*(\mathbf{x}_3)f_{X_4|X_2,X_3}(x_4|x_2,\mathbf{x}_3)f_{X_5|X_4}(x_5|x_4)$$

where $f_{X_3}^*(\cdot)$ is a *degenerate* distribution at \mathbf{x}_3 . X_1 is *no longer a cause* of X_3 .

Note

We note the distinction between the distributions

$$f_{X_1, X_2, X_4, X_5 | X_3}(x_1, x_2, x_4, x_5 | x_3) = \frac{f_{X_1, X_2, X_3, X_4, X_5}(x_1, x_2, x_3, x_4, x_5)}{f_{X_3}(x_3)}$$

which arises from the *original* DAG, and

$$f_{X_1, X_2, X_4, X_5 | X_3}^*(x_1, x_2, x_4, x_5 | x_3) = \frac{f_{X_1, X_2, X_3, X_4, X_5}^*(x_1, x_2, x_3, x_4, x_5)}{f_{X_3}^*(x_3)}$$

which arises from the *intervention* DAG.

Note

In the causal literature, the distinction is sometimes acknowledged using the *'do' operator*

$$f_{X_1, X_2, X_4, X_5}(x_1, x_2, x_4, x_5 \mid \text{do}(X_3) = x_3)$$

is the same as

$$f_{X_1, X_2, X_4, X_5 | X_3}^*(x_1, x_2, x_4, x_5 \mid x_3)$$

This notation was introduced by J. Pearl.

We aim to understand the effect of Z on Y .

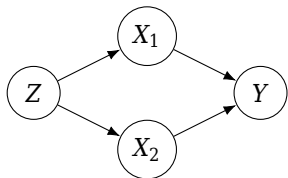
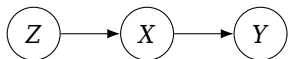
- An *open* undirected path between Z and Y allows for the *association* between Z and Y to be *modified* by the presence of other variables.

This is known as a *biasing* path.

- By '*association*', we typically mean some form of *correlation*.

Graphical representation of bias

- the *association* between Z and Y is *unconditionally unbiased* (or *marginally unbiased*) for the effect of Z on Y if the only open paths between them are *directed paths*.



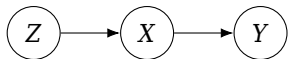
A set of nodes S is *sufficient* to control bias in the association between Z and Y if

- conditional on S , the *open* paths between Z and Y are precisely the *directed* paths between Z and Y .

S is *minimally sufficient* if it is the smallest sufficient set.

Conditioning on descendants of Z

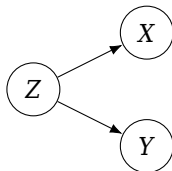
(i) *blocks* directed paths



$Z \perp\!\!\!\perp Y \mid X$ but $Z \not\perp\!\!\!\perp Y$

(ii) can *unblock* or *create* paths that lead to *biasing* of the effect of Z on Y.

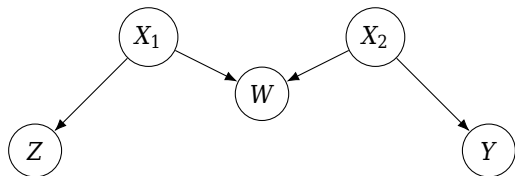
(iii) may be unnecessary in statistical terms: for example



Conditioning on X will not affect bias.

Graphical representation of bias

Undirected paths from Z to Y are termed '*backdoor*' paths (relative to Z) if they *start* with an arrow pointing *into* Z .



The only path from Z to Y is a backdoor path; however, it is not open because of the collider W .

Before conditioning

- *all biasing* paths in a DAG are backdoor paths, and
- all *open* backdoor paths are biasing paths.

To obtain an unbiased estimate of the effect of Z on Y , all backdoor paths between Z and Y must be *blocked*.

Consider a set of variables S . This set satisfies the *backdoor criterion* with respect to Z and Y if

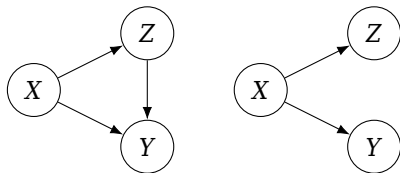
- (i) S *contains no descendant* of Z , and
- (ii) there is *no open backdoor path* from Z to Y after conditioning on S .

Conditioning on S allows identification of the causal effect of Z on Y .

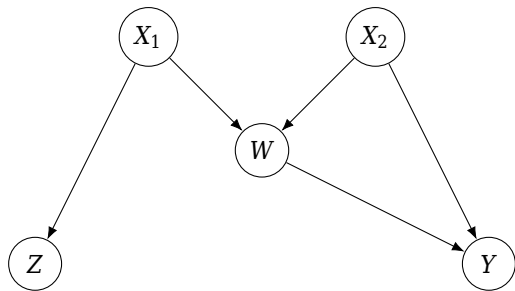
A *confounding path* between Z and Y is

- (i) a *biasing* path (that is, an *undirected open path*) that
- (ii) *ends* with an arrow into Y.

Variables on a confounding path are termed *confounders*.



X is a confounder in both cases.



W is a collider on the undirected path from Z to Y

Path 1: $Z \rightarrow X_1 \rightarrow W \rightarrow X_2 \rightarrow Y$

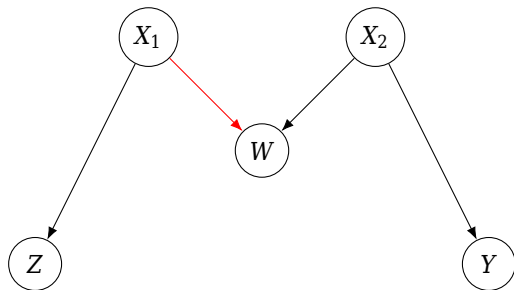
and hence this path is blocked.

However unconditional on W , the effect of Z on Y is confounded by the backdoor path

$$\text{Path 2: } Z \rightarrow X_1 \rightarrow W \rightarrow Y.$$

Conditioning on W alone opens Path 1, therefore to block both paths need to condition on

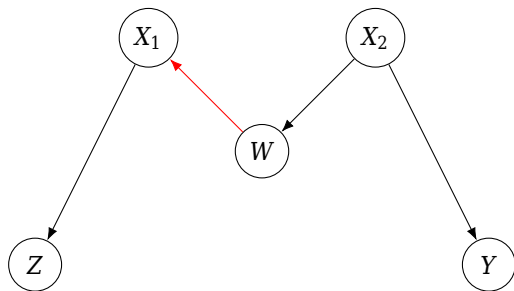
$$S \equiv \{W, X_2\}.$$



Conditioning on W *opens* the confounding path. Therefore $Z \not\perp\!\!\!\perp Y$ (as there is no open path between them), but

$$Z \not\perp\!\!\!\perp Y \mid W$$

Further conditioning on either $\{X_1\}$ or $\{X_2\}$ blocks the path.



Conditioning on W *blocks* the confounding path. Therefore conditioning on any one of

$$\{X_1\}, \{W\}, \{X_2\}$$

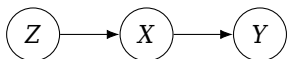
will block the path.

- *Direct effect*: A direct effect of Z on Y (relative to X) is the effect captured by a *directed* path from Z to Y that does not pass through X .
- *Indirect effect*: An indirect effect of X on Y that is captured by directed paths that pass through X .

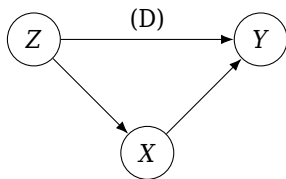
In this formulation, X is termed an *intermediate* or *mediator* variable.

Note that X may be ignored as a mediator, and merely treated as a third variable.

Direct and indirect effects

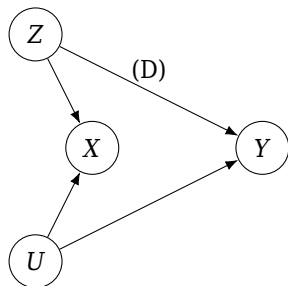


Indirect effect



Direct (D) & Indirect effect

Direct effect is confounded



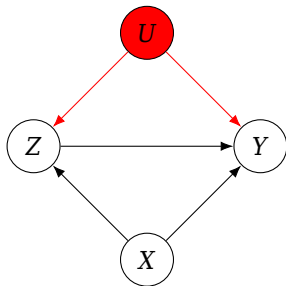
No indirect effect

Direct effect is not confounded

X is a collider, so there is no other open path from Z to Y .

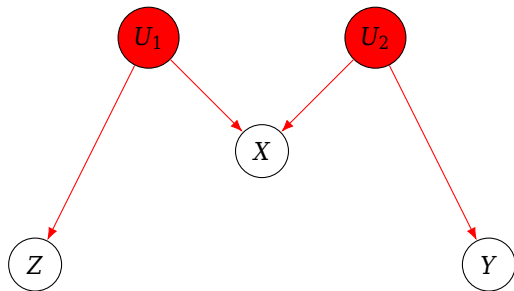
Unmeasured confounding

Suppose that in reality there is a further variable U that is a confounder, but is unmeasured in the observed data.



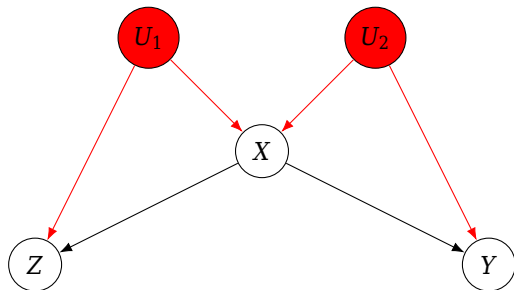
There is a hidden confounding path $Z \rightarrow U \rightarrow Y$. Conditioning on U is not possible, as we are unaware of its existence.

With two unmeasured confounders:



We have that X , Y and Z are *independent*; the (true but hidden) path between Z and Y is blocked at collider X .

However with the same unmeasured confounders:



In the modelled DAG, $Y \perp\!\!\!\perp Z \mid X$; however, conditioning on X *opens* the *hidden* path.

In a statistical formulation of a causal inference problem

1. We identify *treatment* Z and *outcome* Y
2. We form the *DAG* representing the relationships between Z and Y which contains other measured variables X .
3. The causal effect of Z on Y flows down *open* and *directed* paths from Z to Y ;
 - there may be a *direct* effect if there is an arrow from Z into Y ;
 - there may be *indirect* effects if a directed path passes through *mediating* variables.

4. If there are *undirected* paths from Z to Y that are open, then these paths may induce *bias* in estimation of the effect of Z on Y .
5. In order to obtain unbiased estimation, the open undirected (biasing) paths must be *blocked*; typically this is done by *conditioning* on variables on those paths.
6. A *collider* node blocks a path; however, conditioning on the collider *opens* the path at that node.

Appendix: Propensity Score Regression Example

Example:

In this example we have

- two confounders X_1 and X_2
- binary treatment Z

where the treatment effect model depends on Z only, or on both Z and X_1 .

Back

Example:

Suppose that we have the following data generating model:

- Confounders: $(X_1, X_2)^\top \sim \text{Normal}_2((1, 1)^\top, \Sigma)$ with

$$\Sigma = \begin{bmatrix} 0.1 & 0.0 \\ 0.0 & 0.5 \end{bmatrix} \begin{bmatrix} 1.0 & 0.8 \\ 0.8 & 1.0 \end{bmatrix} \begin{bmatrix} 0.1 & 0.0 \\ 0.0 & 0.5 \end{bmatrix}$$

- Treatment: $Z|X_1, X_2 \sim \text{Bernoulli}(e(X_1, X_2))$, where

$$e(x_1, x_2) = \frac{\exp\{1 + x_1 - 2x_2\}}{1 + \exp\{1 + x_1 - 2x_2\}}$$

- Outcome: $Y|X, Z \sim \text{Normal}(\mu(X, Z), 1)$, where

$$\mu(x, z) = (2 + 3x_1 + x_2 + x_1x_2) + z$$

Example:

We consider fitting the parametric model

$$m(x, z; \beta, \psi) = (\beta_0 + \beta_1 x_1) + z\psi_0$$

which is mis-specified due to the 'treatment-free' model specification.
The true values is $\psi_0 = 1$.

Example

```
#n=1000
#Correct specification
> round(coef(summary(lm(Y~X1+X2+X1:X2+Z))), 4)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.7134      0.6222   4.3608  0.0000
X1             2.2156      0.6869   3.2254  0.0013
X2             0.2882      0.4807   0.5996  0.5489
Z             1.0150      0.0674  15.0572  0.0000
X1:X2         1.7421      0.4721   3.6905  0.0002
```

```
#Incorrect specification
> round(coef(summary(lm(Y~X1+Z))), 4)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  -4.2613      0.4034 -10.5631    0
X1           11.4990      0.3888  29.5760    0
Z            0.6366      0.0762   8.3523    0
```

Example:

In the correctly specified model, we have

$$\hat{\psi}_0 : 1.0150 (0.0674)$$

however in the incorrectly specified model we have

$$\hat{\psi}_0 : 0.6366 (0.0762)$$

This effect persists at even larger sample sizes.

Example:

Now consider fitting the parametric model

$$m(x, z; \beta, \psi, \phi) = (\beta_0 + \beta_1 x_1) + z\psi_0 + e(x_1, x_2)\phi_0$$

which considers the additional propensity score term.

Initially, we will set

$$e(x_1, x_2) = \frac{\exp\{1 + x_1 - 2x_2\}}{1 + \exp\{1 + x_1 - 2x_2\}}$$

that is, using the true value.

```
#Propensity score regression
> round(coef(summary(lm(Y~X1+Z+eX))), 4)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	4.1718	0.5609	7.4377	0
X1	5.1662	0.4701	10.9907	0
Z	1.0172	0.0682	14.9069	0
eX	-4.6374	0.2430	-19.0815	0

Example:

We now have

$$\hat{\psi}_0 : 1.0172 (0.0682)$$

and so correct estimation of ψ_0 has been recovered.

Example:

Now suppose

$$\mu(x, z) = (2 + 3x_1 + x_2 + x_1x_2) + z(1 + x_1 + x_2)$$

and using the propensity score regression model

$$m(x, z; \beta, \psi, \phi) = (\beta_0 + \beta_1x_1) + z(\psi_0 + \psi_1x_1 + \psi_2x_2) + e(x_1, x_2)\phi_0$$

Example

```
#n=1000
#Correct specification
> round(coef(summary(lm(Y~X1+X2+X1:X2+Z+Z:X1+Z:X2))),4)
```

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.5674	0.9486	3.7609	0.0002
X1	1.2812	1.0109	1.2675	0.2053
X2	0.1155	0.6004	0.1923	0.8475
Z	-0.2023	0.9313	-0.2173	0.8281
X1:X2	1.9903	0.5672	3.5090	0.0005
X1:Z	2.3744	1.0558	2.2488	0.0247
X2:Z	0.8420	0.2091	4.0272	0.0001

Example

```
#Incorrect specification
> round(coef(summary(lm(Y~X1+Z+Z:X1+Z:X2))), 4)
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  -4.4874      0.5541  -8.0981    0
X1            11.7187      0.5363  21.8503    0
Z              6.4906      0.8778   7.3941    0
X1:Z          -6.5766      0.9644  -6.8196    0
Z:X2           2.8785      0.1642  17.5344    0
```

Example

```
#Propensity score regression
> round(coef(summary(lm(Y~X1+Z+Z:X1+Z:X2+eX))),4)
```

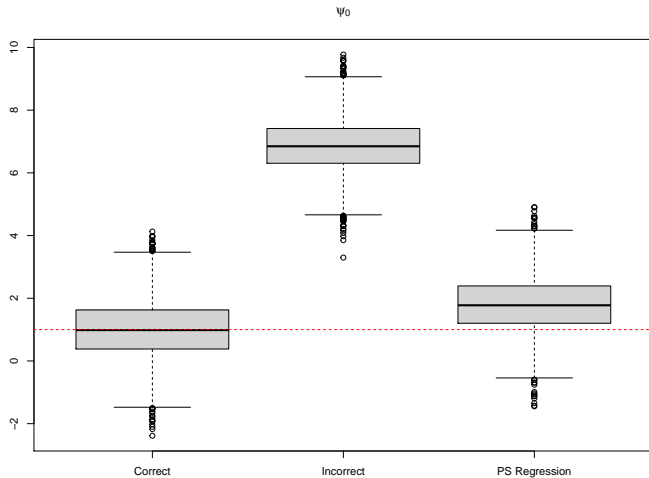
	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.9848	0.7752	5.1403	0.0000
X1	5.4002	0.6565	8.2252	0.0000
Z	1.4774	0.8716	1.6951	0.0904
eX	-4.7679	0.3313	-14.3913	0.0000
X1:Z	0.6533	1.0113	0.6460	0.5184
Z:X2	0.8889	0.2036	4.3664	0.0000

Example:

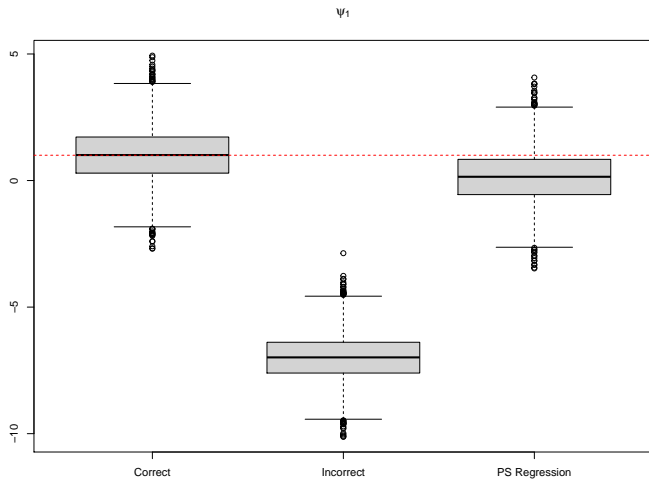
Hard to conclude anything due to the inherent variability, but it seems that including the propensity score does improve the estimation of (ψ_0, ψ_1, ψ_2) .

Need to do a larger simulation study: we perform 5000 replications, and inspect the boxplots of the estimates for the three parameters.

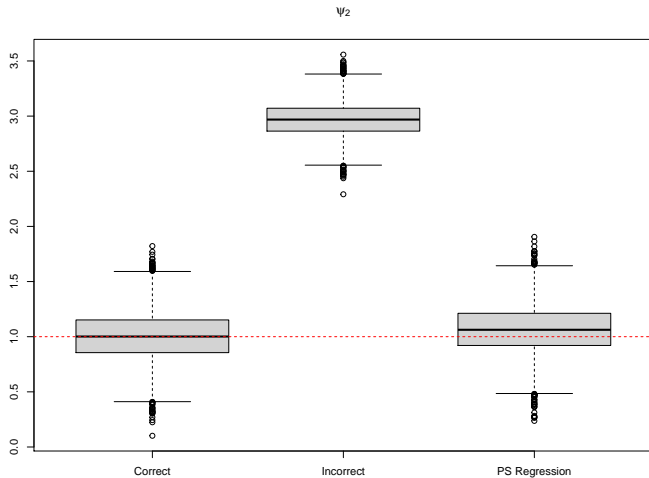
Example



Example



Example



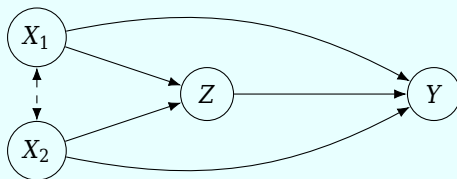
Example:

This confirms that including the propensity score *does* improve the estimation of (ψ_0, ψ_1, ψ_2) , even if the treatment-free model component is incorrectly specified.

However, it seems that there is still a small amount of bias.

Example:

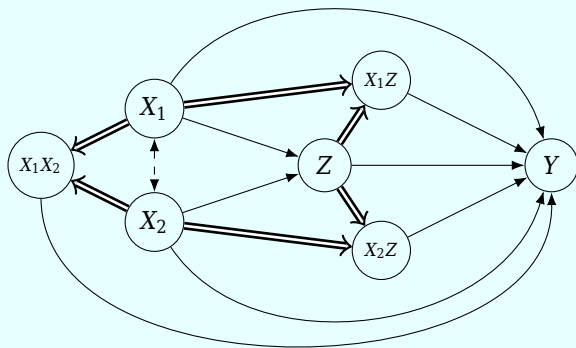
Here is a version of the DAG for the data generating model



Example

Example:

However, a more accurate DAG includes the *interactions*.



Example:

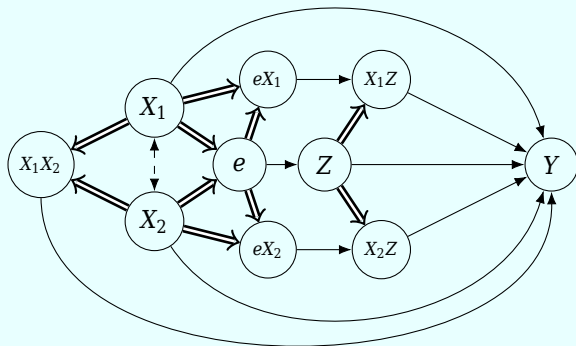
We need to block the open paths via the interactions. This can be achieved by using the model

$$m(x, z; \beta, \psi, \phi) = (\beta_0 + \beta_1 x_1) + z(\psi_0 + \psi_1 x_1 + \psi_2 x_2) \\ + e(x_1, x_2)(\phi_0 + \phi_1 x_1 + \phi_2 x_2)$$

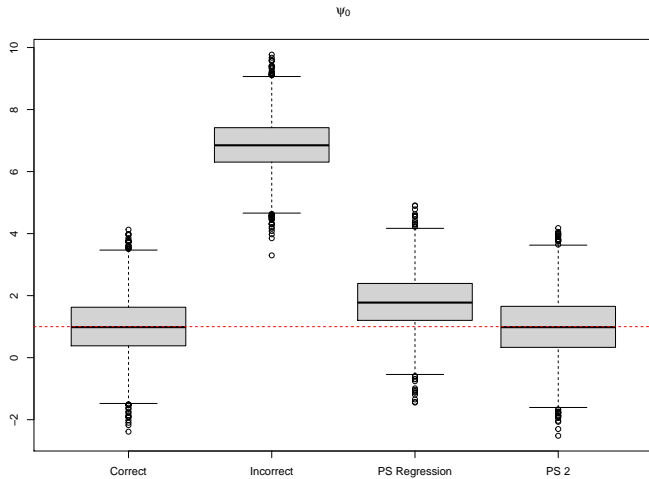
Conditioning on $e(X)$, $e(X)X_1$ and $e(X)X_2$ blocks the paths.

Example

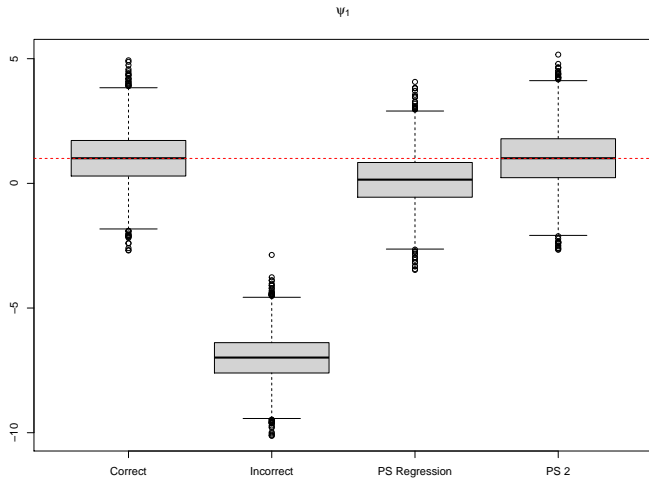
Example:



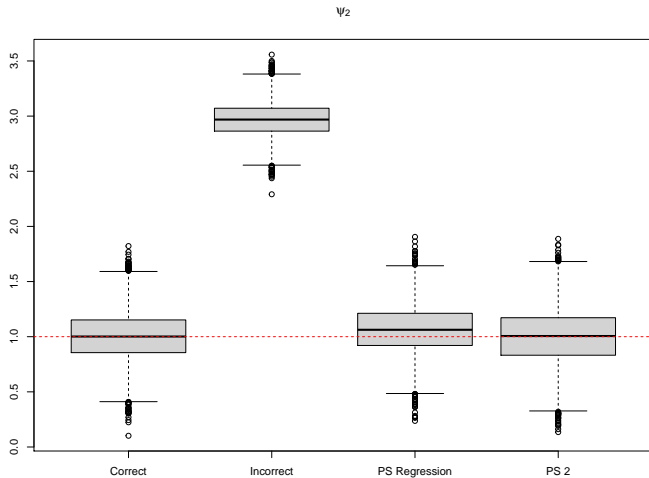
Example



Example



Example



Example:

The augmented propensity score regression model (PS 2) improves the performance.

Note, however, that the variances of the estimators from propensity score regression model are slightly *larger* than those arising from the correctly specified model.

- 10% to 20% larger in this simulation.

Example:

In this analysis, we may estimate the ATE by taking the average difference of the two fitted values under the proposed model, that is

$$\hat{\delta} = \frac{1}{n} \sum_{i=1}^n (\hat{\psi}_0 + \hat{\psi}_1 x_{i1} + \hat{\psi}_2 x_{i2}).$$

Example:

We need to take care in estimating the APO. In the data generating model, with

$$\mu(x, z) = (2 + 3x_1 + x_2 + x_1x_2) + z(1 + x_1 + x_2)$$

we have that

$$\mu(z) = 2 + 3\mathbb{E}[X_1] + \mathbb{E}[X_2] + \mathbb{E}[X_1X_2] + z(1 + \mathbb{E}[X_1] + \mathbb{E}[X_2]).$$

This cannot in general be estimated correctly using

$$\hat{\mu}(z) = \frac{1}{n} \sum_{i=1}^n m(x_i, z; \hat{\beta}, \hat{\psi}, \hat{\phi}).$$

Note

This type of adjustment works for a *linear* outcome model; however, for other types of model such as

- log-linear
- logistic

more care needs to be taken.

Appendix: Marginal Structural Model Example

Example: ART interruption in HIV/HCV co-infected individuals

See Saarela et al. 2015, *Biometrics*.

Antiretroviral therapy (ART) has reduced morbidity and mortality due to nearly all HIV-related illnesses, apart from mortality due to end-stage liver disease, which has increased since ART treatment became widespread.

In part, this increase may be due to improved overall survival combined with Hepatitis C virus (HCV) associated hepatic liver fibrosis, the progress of which is accelerated by immune dysfunction related to HIV-infection.

Example: ART interruption in HIV/HCV co-infected individuals

The Canadian Co-infection Cohort Study is one of the largest projects set up to study the role of ART on the development of end-stage liver disease in HIV-HCV co-infected individuals.

Given the importance of ART in improving HIV-related immunosuppression, it is hypothesized that liver fibrosis progression in co-infected individuals may be partly related to adverse consequences of ART interruptions.

Example: ART interruption in HIV/HCV co-infected individuals

Study comprised

- $N = 474$ individuals with at least one follow-up visit (scheduled at every six months) after the baseline visit,
- 2066 follow-up visits in total (1592 excluding the baseline visits).
- The number of follow-up visits m_i ranged from 2 to 16 (median 4).

Example: ART interruption in HIV/HCV co-infected individuals

We adopt a *pooled logistic regression* approach:

- a single binary outcome (death at study termination)
- longitudinal binary exposure (adherence to ART)
- possible confounders
 - *baseline covariates*: female gender, hepatitis B surface antigen (HBsAg) test and baseline APRI, as well as
 - *time-varying covariates*: age, current intravenous drug use (binary), current alcohol use (binary), duration of HCV infection, HIV viral load, CD4 cell count, as well as ART interruption status at the previous visit.
- need also a model for informative censoring.

Example: ART interruption in HIV/HCV co-infected individuals

- Analysis includes co-infected adults who were not on HCV treatment and did not have liver fibrosis at baseline.
- The outcome event was defined as aminotransferase-to-platelet ratio index (APRI), a surrogate marker for liver fibrosis, being at least 1.5 in any subsequent visit.
- Included visits where the individuals were either on ART or had interrupted therapy ($Z_{ij} = 1$), based on self-reported medication information, during the 6 months before each follow-up visit.

Example: ART interruption in HIV/HCV co-infected individuals

- Individuals suspected of having spontaneously cleared their HCV infection (based on two consecutive negative HCV viral load measurements) were excluded as they are not considered at risk for fibrosis progression.
- In the treatment assignment model all time-varying covariates (x_{ij}), including the laboratory measurements (HIV viral load and CD4 cell count), were lagged one visit.
- Individuals starting HCV medication during the follow-up were censored.

Example: ART interruption in HIV/HCV co-infected individuals

We considered the structural model

$$\log \left(\frac{f(Y_{ij} = 1 | \tilde{z}_{ij}; \theta)}{f(Y_{ij} = 0 | \tilde{z}_{ij}; \theta)} \right) = \theta_0 + \theta_1 z_j$$

θ_1 measures the total effect of exposure in the most recent interval, allowing for mediation.

Example: ART interruption in HIV/HCV co-infected individuals

Results:

Estimator	$\hat{\theta}_1$	SE	z
Unadjusted	4.616	0.333	13.853
MSM	0.354	0.377	0.937
Bootstrap	0.308	0.395	0.780

After adjustment for confounding and effects of mediation, we can conclude that the marginal effect of exposure is *non-significant*.