

PLSC 30600

Week 3: MAR estimation, reweighting, and imputation

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Science table: MAR and regression estimation

i	$X_{[1]i}$	$X_{[2]i}$	$Y_i(0)$	R_i	$Y_i^*(0)$
1	A	0	0	1	0
2	A	0	?	0	-99
3	B	0	1	1	1
4	B	0	?	0	-99
5	A	1	0	1	0
6	A	1	?	0	-99
7	B	1	1	1	1
8	B	1	?	0	-99
9	A	0	1	1	1
10	B	1	?	0	-99

Regression estimation under MAR

- Under MAR, for all $\mathbf{x} \in \text{Supp}[X_i]$:

$$E[Y_i \mid R_i = 0, \mathbf{X}_i = \mathbf{x}] = E[Y_i^* \mid R_i = 1, \mathbf{X}_i = \mathbf{x}] = E[Y_i \mid \mathbf{X}_i = \mathbf{x}].$$

- In our case, with two covariates by MAR:

$$E[Y_i \mid X_{[1]i}, X_{[2]i}] = E[Y_i^* \mid R_i = 1, X_{[1]i}, X_{[2]i}].$$

- Assume a functional form for the CEF, e.g.

$$E[Y_i \mid X_{[1]i}, X_{[2]i}] = \beta_0 + \beta_1 \mathbf{1}\{X_{[1]i} = B\} + \beta_2 X_{[2]i}.$$

- Use regression to estimate, predict for all i , then average.

Science table: MAR and regression estimation

i	$X_{[1]i}$	$X_{[2]i}$	$Y_i(0)$	R_i	$Y_i^*(0)$
1	A	0	0	1	0
2	A	0	?	0	$\hat{E}[Y_i X_{[1]i} = x_{[1]1}, X_{[2]i} = x_{[2]2}]$
3	B	0	1	1	1
4	B	0	?	0	$\hat{E}[Y_i X_{[1]i} = x_{[1]1}, X_{[2]i} = x_{[2]2}]$
5	A	1	0	1	0
6	A	1	?	0	$\hat{E}[Y_i X_{[1]i} = x_{[1]1}, X_{[2]i} = x_{[2]2}]$
7	B	1	1	1	1
8	B	1	?	0	$\hat{E}[Y_i X_{[1]i} = x_{[1]1}, X_{[2]i} = x_{[2]2}]$
9	A	0	1	1	1
10	B	1	?	0	$\hat{E}[Y_i X_{[1]i} = x_{[1]1}, X_{[2]i} = x_{[2]2}]$

Science table: MAR regression plug-in

i	$X_{[1]i}$	$X_{[2]i}$	$Y_i(0)$	R_i	$Y_i^*(0)$
1	A	0	0	1	0
2	A	0	?	0	$\hat{\beta}_0$
3	B	0	1	1	1
4	B	0	?	0	$\hat{\beta}_0 + \hat{\beta}_2$
5	A	1	0	1	0
6	A	1	?	0	$\hat{\beta}_0 + \hat{\beta}_3$
7	B	1	1	1	1
8	B	1	?	0	$\hat{\beta}_0 + \hat{\beta}_2 + \hat{\beta}_3$
9	A	0	1	1	1
10	B	1	?	0	$\hat{\beta}_0 + \hat{\beta}_2 + \hat{\beta}_3$

$$E[Y_i | X_{[1]i}, X_{[2]i}] = \beta_0 + \beta_2 1\{X_{[1]i} = B\} + \beta_3 X_{[2]i}.$$

Code: regression plug-in under MAR

```
> df <- data.frame(  
+   X_1 = c("A", "A", "B", "B", "A", "A", "B", "B", "A", "B"),  
+   X_2 = c(0, 0, 0, 0, 1, 1, 1, 1, 0, 1),  
+   R    = c(1, 0, 1, 0, 1, 0, 1, 0, 1, 0),  
+   Ystar = c(0, -99, 1, -99, 0, -99, 1, -99, 1, -99)  
+ )  
> df$X_1 <- factor(df$X_1)  
> (fit <- lm(Ystar ~ X_1 + X_2, data = df, subset = R == 1))
```

Call:

```
lm(formula = Ystar ~ X_1 + X_2, data = df, subset = R == 1)
```

Coefficients:

(Intercept)	X_1B	X_2
0.4286	0.7143	-0.2857

Code: regression plug-in under MAR

```
> df$yhat <- df$Ystar
> df$yhat[which(df$R == 0)] <-
+   predict(fit, newdata = df[which(df$R == 0), ])
> round(df$yhat, 3)

[1] 0.000 0.429 1.000 1.143 0.000 0.143 1.000 0.857 1.000 0.857

> mean(df$yhat)

[1] 0.6428571
```

Science table: strong ignorability and regression estimation

i	$X_{[1]i}$	$X_{[2]i}$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i
1	A	0	0	?	0	0
2	A	0	?	1	1	1
3	B	0	1	?	0	1
4	B	0	?	1	1	1
5	A	1	0	?	0	0
6	A	1	?	1	1	1
7	B	1	1	?	0	1
8	B	1	?	0	1	0
9	A	0	1	?	0	0
10	B	1	?	1	1	1

Regression estimation under strong ignorability

- Under strong ignorability, for all $x \in \text{Supp}[X_i]$:

$$E[Y_i(d) \mid X_i = x] = E[Y_i \mid D_i = d, X_i = x], \quad d \in \{0, 1\}.$$

- We need a treatment indicator in the regression model.
- Example CEF specification:

$$E[Y_i \mid D_i, X_{[1]i}, X_{[2]i}] = \beta_0 + \beta_1 D_i + \beta_2 1\{X_{[1]i} = B\} + \beta_3 X_{[2]i}.$$

- Predict $\hat{Y}_i(0)$ and $\hat{Y}_i(1)$, then average differences.

Definition: regression estimator for causal inference

Definition (Regression Estimator for Causal Inference)

Let $Y_i(0)$, $Y_i(1)$, and D_i be random variables with $\text{Supp}[D_i] = \{0, 1\}$. Let $Y_i = Y_i(1) \cdot D_i + Y_i(0) \cdot (1 - D_i)$ and $\tau_i = Y_i(1) - Y_i(0)$, and let \mathbf{X}_i be a random vector. Given n i.i.d. observations of (Y_i, D_i, \mathbf{X}_i) , the regression estimator for $E[\tau_i]$ is

$$\hat{E}[\tau_i] = \frac{1}{n} \sum_{i=1}^n \hat{E}[Y_i \mid D_i = 1, \mathbf{X}_i] - \frac{1}{n} \sum_{i=1}^n \hat{E}[Y_i \mid D_i = 0, \mathbf{X}_i],$$

where $\hat{E}[Y_i \mid D_i = d, \mathbf{X}_i = \mathbf{x}]$ is an estimator of the CEF.

Science table: strong ignorability and regression imputation

i	$X_{[1]i}$	$X_{[2]i}$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i
1	A	0	0	$\hat{m}_1(x)$	0	0
2	A	0	$\hat{m}_0(x)$	1	1	1
3	B	0	1	$\hat{m}_1(x)$	0	1
4	B	0	$\hat{m}_0(x)$	1	1	1
5	A	1	0	$\hat{m}_1(x)$	0	0
6	A	1	$\hat{m}_0(x)$	1	1	1
7	B	1	1	$\hat{m}_1(x)$	0	1
8	B	1	$\hat{m}_0(x)$	0	1	0
9	A	0	1	$\hat{m}_1(x)$	0	0
10	B	1	$\hat{m}_0(x)$	1	1	1

$$\hat{m}_d(x) = \hat{\mathbb{E}} [Y_i \mid D_i = d, X_{[1]i} = x_{[1]}, X_{[2]i} = x_{[2]}], \quad d \in \{0, 1\}.$$

Science table: strong ignorability regression plug-in

i	$X_{[1]i}$	$X_{[2]i}$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i
1	A	0	0	$\hat{\beta}_0 + \hat{\beta}_1$	0	0
2	A	0	$\hat{\beta}_0$	1	1	1
3	B	0	1	$\hat{\beta}_0 + \hat{\beta}_1 + \hat{\beta}_2$	0	1
4	B	0	$\hat{\beta}_0 + \hat{\beta}_2$	1	1	1
5	A	1	0	$\hat{\beta}_0 + \hat{\beta}_1 + \hat{\beta}_3$	0	0
6	A	1	$\hat{\beta}_0 + \hat{\beta}_3$	1	1	1
7	B	1	1	$\hat{\beta}_0 + \hat{\beta}_1 + \hat{\beta}_2 + \hat{\beta}_3$	0	1
8	B	1	$\hat{\beta}_0 + \hat{\beta}_2 + \hat{\beta}_3$	0	1	0
9	A	0	1	$\hat{\beta}_0 + \hat{\beta}_1$	0	0
10	B	1	$\hat{\beta}_0 + \hat{\beta}_2 + \hat{\beta}_3$	1	1	1

$$E[Y_i \mid D_i, X_{[1]i}, X_{[2]i}] = \beta_0 + \beta_1 D_i + \beta_2 1\{X_{[1]i} = B\} + \beta_3 X_{[2]i}.$$

Code: regression plug-in under ignorability

```
> df <- data.frame(  
+   X_1 = c("A", "A", "B", "B", "A", "A", "B", "B", "A", "B"),  
+   X_2 = c(0, 0, 0, 0, 1, 1, 1, 1, 0, 1),  
+   D    = c(0, 1, 0, 1, 0, 1, 0, 1, 0, 1),  
+   Y    = c(0, 1, 1, 1, 0, 1, 1, 0, 0, 1)  
+ )  
> df$X_1 <- factor(df$X_1)  
> (fit_ign <- lm(Y ~ D + X_1 + X_2, data = df))
```

Call:

```
lm(formula = Y ~ D + X_1 + X_2, data = df)
```

Coefficients:

(Intercept)	D	X_1B	X_2
0.3143	0.3571	0.3571	-0.1429

Code: regression plug-in under ignorability

```
> df$yhat_1 <- df$Y
> df$yhat_0 <- df$Y
> df$yhat_1[which(df$D == 0)] <-
+   predict(fit_ign,
+           newdata = transform(df[which(df$D == 0), ], D = 1))
> df$yhat_0[which(df$D == 1)] <-
+   predict(fit_ign,
+           newdata = transform(df[which(df$D == 1), ], D = 0))
```

Code: regression plug-in under ignorability

```
> round(df[, c("yhat_0", "yhat_1")], 3)
```

	yhat_0	yhat_1
1	0.000	0.671
2	0.314	1.000
3	1.000	1.029
4	0.671	1.000
5	0.000	0.529
6	0.171	1.000
7	1.000	0.886
8	0.529	0.000
9	0.000	0.671
10	0.529	1.000

```
> mean(df$yhat_1 - df$yhat_0)
```

```
[1] 0.3571429
```

Directed Acyclic Graphs

- DAGs: what problem are we solving?
- We keep writing assumptions like:

$$Y_i(d) \perp\!\!\!\perp D_i \mid X_i \quad \text{or} \quad Y_i \perp\!\!\!\perp R_i \mid X_i.$$

- A DAG is a compact way to encode *which conditional independences are plausible* based on the data-generating process.
- Main use today: selecting (and *not* selecting) adjustment variables.

Greenland et al. (1999)

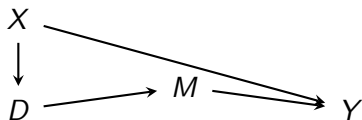
Association vs causation: $\Pr[Y \mid D]$ vs $\Pr[Y \mid do(D)]$

- $\Pr[Y = y \mid D = d]$: observational association.
- $\Pr[Y = y \mid do(D = d)]$: distribution of Y *under intervention* setting $D := d$.
- **Graph surgery:** $do(D = d)$ deletes all arrows *into* D (intervention breaks causes of D).
- Conditioning does *not* change the graph; it filters/stratifies the observed data.

Pearl et al. (2016)

DAG primitives: nodes, arrows, paths, ancestors

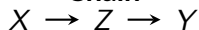
- Node = variable.
- Arrow $A \rightarrow B$ means A is a direct cause of B .
- A *path* is any sequence of adjacent arrows (ignore direction).
- A *directed path* is a causal pathway (all arrows forward).
- A is an *ancestor* of B if there is a directed path $A \rightarrow \dots \rightarrow B$.
(ancestor/descendant : parent/child)



$D \rightarrow M \rightarrow Y$ is a directed path;
 $D \leftarrow X \rightarrow Y$ is a backdoor path.

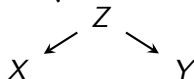
Chain, fork, collider

Chain



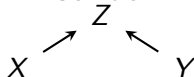
Conditioning on Z blocks the path.

Fork (confounder)



Conditioning on Z blocks the backdoor.

Collider

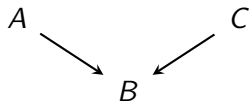


Path blocked unless you condition on Z (or a descendant).

d-separation: the blocking definition

- “Blocking a path” means: given a conditioning set Z , that path cannot transmit statistical association between its endpoints under the graphical rules of d-separation.
- A path is **blocked** by a conditioning set Z if *there exists at least one node* on the path such that:
 - the path contains a **chain** or **fork** $A \rightarrow B \rightarrow C$ or $A \leftarrow B \rightarrow C$ with the middle node $B \in Z$; or
 - the path contains a **collider** $A \rightarrow B \leftarrow C$ with $B \notin Z$ and no descendant of B in Z .
- If every path between X and Y is blocked by Z , then X and Y are **d-separated** by Z .
- Pearl et al. convention: d-separated \Rightarrow *guaranteed* conditional independence (given the model); d-connected \Rightarrow dependence is *typical* (except cancellations).

Collider intuition: “selection” creates dependence



$A \rightarrow B \leftarrow C$ (collider at B)

- Think of:
 - A = ability, C = effort,
 B = admission to a selective program.

- In the full population, ability and effort can be independent:

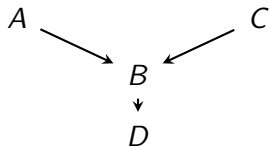
$$A \perp\!\!\!\perp C \iff \Pr[C | A] = \Pr[C].$$

- The collider B blocks the path between A and C *unless we condition on B .*

Conditioning on admission opens the collider path

- Now restrict attention to admitted students: condition on $B = 1$.
- Intuition: admission depends on *either* high ability or high effort (or both).
 - If A is low but $B = 1$, then C must be high to “compensate.”
 - If A is high and $B = 1$, then C can be lower and admission still occurs.
- Result: within the selected group $B = 1$, A and C become dependent:
$$\Pr[C \mid A, B = 1] \neq \Pr[C \mid B = 1].$$
- DAG language: conditioning on a collider **opens** the path $A \rightarrow B \leftarrow C$.

Why descendants of a collider matter (conditioning “leaks” information)



D is a descendant of the collider B

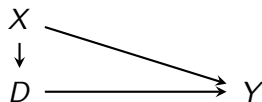
- Let D = program completion, where $B \rightarrow D$.
- Conditioning on $D = 1$ gives (partial) information about B .
- This can also induce dependence between A and C :
$$\Pr[C \mid A, D = 1] \neq \Pr[C \mid D = 1].$$
- Rule: a collider blocks a path *only if* we do not condition on the collider *and* do not condition on any of its descendants.

Adjustment for causal effects: backdoor criterion

- A **backdoor path** from D to Y is any path that begins with an arrow *into* D .
- A set Z satisfies the **backdoor criterion** for (D, Y) if:
 - no element of Z is a descendant of D , and
 - Z blocks every backdoor path from D to Y .
- If the backdoor criterion holds, then the causal effect is identified by:

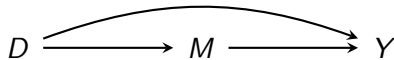
$$\Pr[Y = y \mid do(D = d)] = \sum_z \Pr[Y = y \mid D = d, Z = z] \Pr[Z = z].$$

Example: confounding and a valid adjustment set



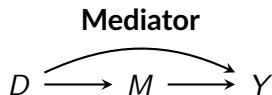
- Backdoor: $D \leftarrow X \rightarrow Y$.
- $Z = \{X\}$ blocks the backdoor and has no descendants of D .
- Graphically: $Y(d) \perp\!\!\!\perp D \mid X$ is plausible if this DAG is correct.

Post-treatment adjustment changes the estimand (and can bias)

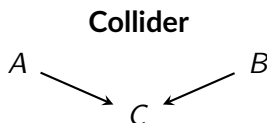


- M is a mediator: conditioning on M blocks part of the causal effect, and gives us a conditional association, not a causal effect.
- If you want the **total effect** ($\Pr[Y|do(D = d)]$), M is not in a backdoor adjustment set.
- More generally: descendants of D are excluded by the backdoor criterion.

Mediator vs collider: why the rule differs



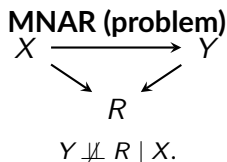
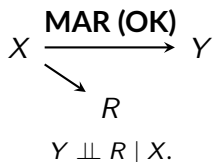
Conditioning on M changes the estimand (direct vs total effect).



Conditioning on C creates bias by opening a path.

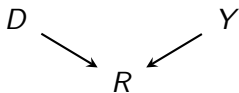
- Mediators: conditioning changes *which effect* you estimate.
- Colliders: conditioning breaks identification entirely.

Missing data as a DAG: MAR vs MNAR



- R is the response/observation indicator (e.g., Y observed if $R = 1$).
- Under MAR, conditioning on X blocks all paths between Y and R .

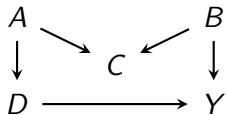
Complete-case analysis is conditioning on $R = 1$ (selection)



Conditioning on $R = 1$ opens the collider at R .

- Even if D and Y are independent marginally, restricting to the observed sample ($R = 1$) can induce D - Y association.
- This is the collider lesson applied to missingness/selection.
- Under MAR, we try to block the $Y \rightarrow R$ channel given *covariates* (previous slide).

Greenland et al. (1999): bad controls (conditioning can create confounding)



C is a collider on $A \rightarrow C \leftarrow B$.

- Without conditioning on C , the collider blocks that path.
- Conditioning on C opens the collider and induces association between A and B .
- This opens a new backdoor from D to Y through A and B .
- Lesson: “control for C ” can *increase* bias.

Why this mistake is tempting: total vs direct effects

- In the DAG, C is *affected by* both A and B .
- Researchers often reason:
“ C is related to both treatment and outcome, so we should control for it.”
- But this mixes up two different causal questions:
 - **Total effect of D on Y :** effect through *all* causal paths.
 - **Direct effect of D on Y :** effect *not operating through intermediates*.
- Conditioning on C does *not* identify a direct effect here—it creates bias.

What conditioning on C actually does

- C is a **collider** on the path $D \leftarrow A \rightarrow C \leftarrow B \rightarrow Y$.
- Conditioning on C :
 - induces dependence between A and B ;
 - opens a backdoor path from D to Y ;
 - violates ignorability for the total effect.
- Formally, after conditioning on C :

$$\Pr[Y(d) \mid D, C] \neq \Pr[Y(d) \mid C].$$

- So the resulting estimand is neither:
 - the total effect of D on Y , nor
 - a well-defined direct effect.

Practical workflow for choosing controls

- Step 1: draw a DAG that reflects substantive knowledge.
- Step 2: decide the estimand (total effect? direct effect?).
- Step 3: find a backdoor adjustment set (blocks all arrows-into- D paths, avoids descendants of D).
- Step 4: check for **colliders** and **post-treatment variables** you might accidentally condition on.
- Step 5: translate to an estimator (regression / weighting / matching), then diagnose overlap and sensitivity later.

Science table: strong ignorability and the propensity score

i	$X_{[1]i}$	$X_{[2]i}$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i
1	A	0	0	?	0	0
2	A	0	?	1	1	1
3	B	0	1	?	0	1
4	B	0	?	1	1	1
5	A	1	0	?	0	0
6	A	1	?	1	1	1
7	B	1	1	?	0	1
8	B	1	?	0	1	0
9	A	0	1	?	0	0
10	B	1	?	1	1	1

Science table: add the (empirical) propensity score

i	$X_{[1]i}$	$X_{[2]i}$	$p_D(X_i)$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i
1	A	0	0.33	0	?	0	0
2	A	0	0.33	?	1	1	1
3	B	0	0.50	1	?	0	1
4	B	0	0.50	?	1	1	1
5	A	1	0.50	0	?	0	0
6	A	1	0.50	?	1	1	1
7	B	1	0.67	1	?	0	1
8	B	1	0.67	?	0	1	0
9	A	0	0.33	1	?	0	0
10	B	1	0.67	?	1	1	1

$X_{[1]}$	$X_{[2]}$	n	$p_D(X)$
A	0	3	0.33
A	1	2	0.50
B	0	2	0.50
B	1	3	0.67

Science table: hot deck imputation (propensity score)

i	$X_{[1]i}$	$X_{[2]i}$	$p_D(X_i)$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i
1	A	0	0.33	0	donor	0	0
2	A	0	0.33	donor	1	1	1
3	B	0	0.50	1	donor	0	1
4	B	0	0.50	donor	1	1	1
5	A	1	0.50	0	donor	0	0
6	A	1	0.50	donor	1	1	1
7	B	1	0.67	1	donor	0	1
8	B	1	0.67	donor	0	1	0
9	A	0	0.33	1	donor	0	0
10	B	1	0.67	donor	1	1	1

- For each missing potential outcome, choose a nearest-neighbor donor in $p_D(X)$ from the opposite treatment arm.
- Impute $\hat{Y}_i(0)$ or $\hat{Y}_i(1)$ with that donor's observed outcome.

References I

- Greenland, S., Pearl, J., and Robins, J. M. (1999). Causal diagrams for epidemiologic research. *Epidemiology*, 10(1):37–48.
- Pearl, J., Glymour, M., and Jewell, N. P. (2016). *Causal inference in statistics: A primer*. John Wiley & Sons.