PLSC 30600

Week 5: More estimation. Overlap and positivity.

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Science table: strong ignorability and the propensity score

i	$X_{[1]i}$	$X_{[2]i}$	$p_D(\boldsymbol{X}_i)$	$Y_i(0)$	$Y_i(1)$	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

Code: science table data

```
> 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)
> # propensity model (same as week 4)
> X <- model.matrix(~ X_1 + X_2, data = df)
> D <- df$D
> neg_loglik <- function(beta, X, D) {
+   eta <- as.vector(X %*% beta)
+   p <- pnorm(eta)
+   -sum(D * log(p) + (1 - D) * log(1 - p))
+ }
> fit <- optim(par = rep(0, ncol(X)),
+              fn = neg_loglik,
+              X = X,
+              D = D)
> df$p_hat <- pnorm(as.vector(X %*% fit$par))
```

IPW vs. stabilized IPW

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$$\widehat{\mathrm{E}}_{IPW}[\tau_i] = \frac{1}{n}\sum_{i=1}^{n}\left(\frac{Y_i D_i}{\hat{p}_D(\boldsymbol{X}_i)} - \frac{Y_i(1-D_i)}{1-\hat{p}_D(\boldsymbol{X}_i)}\right).$$

- Stabilized IPW (Hájek / ratio estimator):

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- Stabilized IPW (Hájek / ratio estimator):

$$\widehat{\mathrm{E}}_{SIPW}[\tau_i] = \frac{\frac{1}{n}\sum_{i=1}^{n}\frac{Y_i D_i}{\hat{p}_D(\boldsymbol{X}_i)}}{\frac{1}{n}\sum_{i=1}^{n}\frac{D_i}{\hat{p}_D(\boldsymbol{X}_i)}} - \frac{\frac{1}{n}\sum_{i=1}^{n}\frac{Y_i(1-D_i)}{1-\hat{p}_D(\boldsymbol{X}_i)}}{\frac{1}{n}\sum_{i=1}^{n}\frac{1-D_i}{1-\hat{p}_D(\boldsymbol{X}_i)}}.$$

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- With the true propensity score,

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  so stabilization targets the same estimand.
- In practice, stabilized IPW reduces variance relative to raw IPW.

Code: stabilized IPW

```
> # IPW and stabilized IPW using the science table data frame df
> w_t <- df$D / df$p_hat
> w_c <- (1 - df$D) / (1 - df$p_hat)
> ipw_ate <- mean(w_t * df$Y - w_c * df$Y)
> sipw_ate <- (sum(w_t * df$Y) / sum(w_t)) -
+   (sum(w_c * df$Y) / sum(w_c))
> c(ipw_ate = ipw_ate, sipw_ate = sipw_ate)

  ipw_ate  sipw_ate
0.3499516 0.3499739
```

Doubly robust theorem (Thm. 7.2.8)

- Let $\tilde{m}_d(x)$ approximate $\mathrm{E}[Y_i \mid D_i = d, \boldsymbol{X}_i = x]$ and let $\tilde{p}_D(x)$ approximate $p_D(x) = \Pr[D_i = 1 \mid \boldsymbol{X}_i = x]$.

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- Under strong ignorability, if either:
  - $\tilde{m}_d(x)$ is correct for $d \in \{0, 1\}$ and $0 < \tilde{p}_D(x) < 1$, or
  - $\tilde{p}_D(x) = p_D(x)$ for all x,

  then

$$\mathrm{E}\left[\tau_i\right] = \mathrm{E}\left[\tilde{m}_1(\boldsymbol{X}_i) - \tilde{m}_0(\boldsymbol{X}_i) \; + \; \frac{D_i\{Y_i - \tilde{m}_1(\boldsymbol{X}_i)\}}{\tilde{p}_D(\boldsymbol{X}_i)} - \frac{(1 - D_i)\{Y_i - \tilde{m}_0(\boldsymbol{X}_i)\}}{1 - \tilde{p}_D(\boldsymbol{X}_i)}\right].$$

Why it works

$$\mathrm{E}\left[\tau_i\right] = \mathrm{E}\left[\tilde{m}_1(\boldsymbol{X}_i) - \tilde{m}_0(\boldsymbol{X}_i) \; + \; \frac{D_i\{Y_i - \tilde{m}_1(\boldsymbol{X}_i)\}}{\tilde{p}_D(\boldsymbol{X}_i)} - \frac{(1-D_i)\{Y_i - \tilde{m}_0(\boldsymbol{X}_i)\}}{1-\tilde{p}_D(\boldsymbol{X}_i)}\right.$$

- If the outcome model is correct, then

$$\mathrm{E}\left[Y_i - \tilde{m}_d(\boldsymbol{X}_i) \mid D_i = d, \boldsymbol{X}_i\right] = 0,$$

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- Intuition: with correct $p_D(\boldsymbol{X}_i)$, weighting makes the residuals average over the *target* X distribution, so

  $$\mathrm{E}\left[\frac{D_i}{p_D(\boldsymbol{X}_i)}(Y_i - \tilde{m}_1(\boldsymbol{X}_i))\right] = \mathrm{E}\left[\mathrm{E}\left[Y_i(1) - \tilde{m}_1(\boldsymbol{X}_i) \mid \boldsymbol{X}_i\right]\right],$$

  and the analogous control term offsets bias.

Why it works

$$\mathrm{E}\left[\tau_i\right] = \mathrm{E}\left[\tilde{m}_1(\boldsymbol{X}_i) - \tilde{m}_0(\boldsymbol{X}_i) \; + \; \frac{D_i\{Y_i - \tilde{m}_1(\boldsymbol{X}_i)\}}{\tilde{p}_D(\boldsymbol{X}_i)} - \frac{(1-D_i)\{Y_i - \tilde{m}_0(\boldsymbol{X}_i)\}}{1-\tilde{p}_D(\boldsymbol{X}_i)}\right.$$

- If the outcome model is correct, then

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  and the analogous control term offsets bias.

- Thus the expression for $\mathrm{E}\left[\tau_i\right]$ holds if *either* model is correct.

Doubly robust estimator

$$\widehat{\mathrm{E}}_{DR}[\tau_i] = \frac{1}{n}\sum_{i=1}^{n} \underbrace{\hat{m}_1(\boldsymbol{X}_i) - \hat{m}_0(\boldsymbol{X}_i)}_{\text{outcome model}} + \underbrace{\frac{1}{n}\sum_{i=1}^{n} \frac{D_i\,(Y_i - \hat{m}_1(\boldsymbol{X}_i))}{\hat{p}_D(\boldsymbol{X}_i)} - \frac{(1-D_i)\,(Y_i - \hat{m}_0(\boldsymbol{X}_i))}{1-\hat{p}_D(\boldsymbol{X}_i)}}_{\text{residual correction}}$$

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- The outcome model can be estimated by regression or ML.

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- The propensity model can be estimated by logit, probit, or ML.

Code: doubly robust estimator

```
> # Outcome models
> fit_dr <- lm(Y ~ D + X_1 + X_2, data = df)
> df$m1_hat <- predict(fit_dr, newdata = transform(df, D = 1))
> df$m0_hat <- predict(fit_dr, newdata = transform(df, D = 0))
> # DR estimator (uses p_hat from propensity model)
> dr_ate <- mean(
+   df$m1_hat - df$m0_hat +
+     df$D * (df$Y - df$m1_hat) / df$p_hat -
+     (1 - df$D) * (df$Y - df$m0_hat) / (1 - df$p_hat)
+ )
> dr_ate
[1] 0.3499874
```

Overlap and positivity: definitions

- **Positivity (overlap in treatment probabilities):** There exists $\varepsilon > 0$ such that for all $x \in \operatorname{Supp}[\boldsymbol{X}_i]$,

$$\varepsilon < p_D(x) < 1 - \varepsilon.$$

- Interpretation: every covariate profile has nonzero probability of both treatment and control.

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- **Complete population overlap:** the supports of $\boldsymbol{X}_i$ in treated and control groups overlap.

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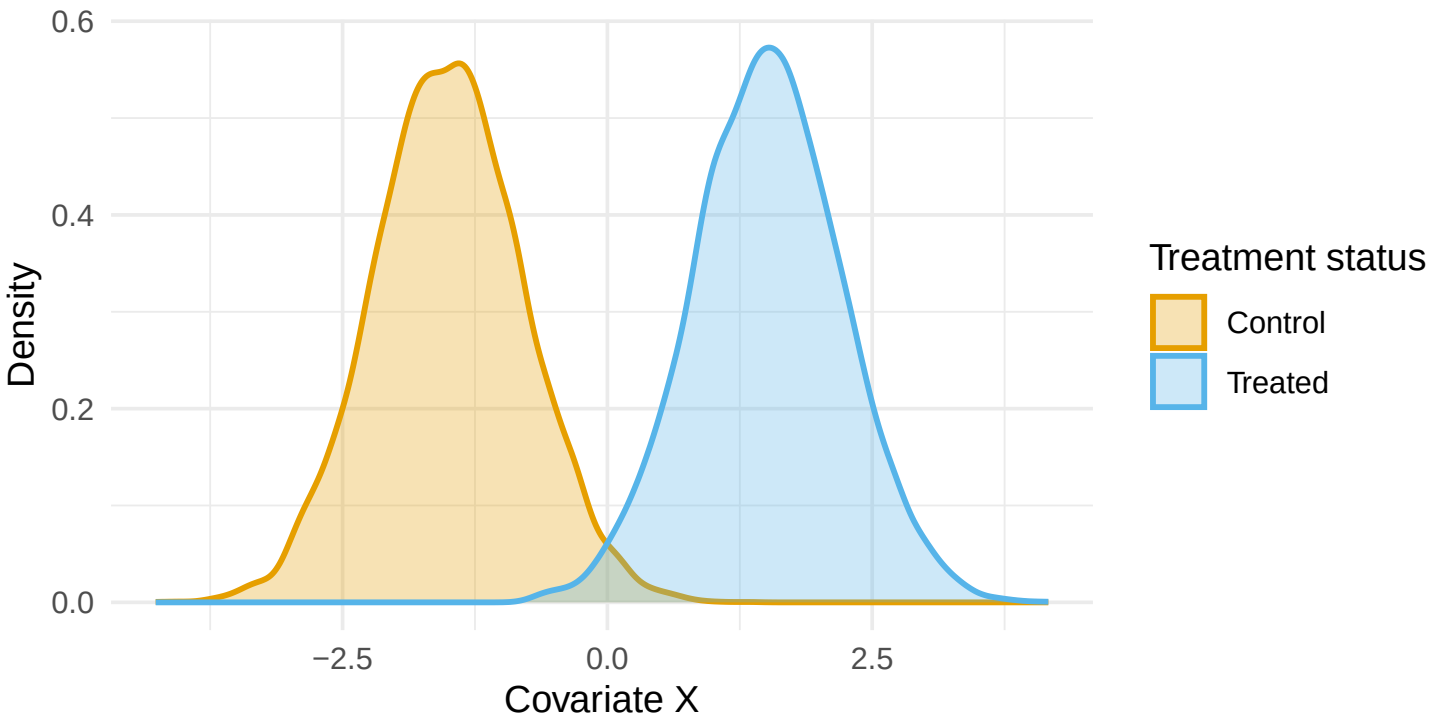
- Interpretation: every covariate profile has nonzero probability of both treatment and control.

- **Complete population overlap:** the supports of $\boldsymbol{X}_i$ in treated and control groups overlap.

- Failure of positivity $\Rightarrow$ incomplete overlap (regions of x with only treated or only control).

Example: failure of overlap



Little overlap in X implies $p_D(x)$ near 0 or 1 for some x.

Code: Lalonde propensity score overlap

```
> library(ggplot2)
> lalonde_url <-
+   "https://raw.githubusercontent.com/xuyiqing/lalonde/master/data/lalonde.RData"
> load(url(lalonde_url))
> covar <- c("age", "education", "black", "hispanic", "married", "nodegree",
+            "re74", "re75", "u74", "u75")
> ps_fit <- glm(treat ~ age + education + black + hispanic + married + nodegree +
+                 re74 + re75 + u74 + u75,
+               data = ldw, family = binomial())
> ldw$ps <- predict(ps_fit, type = "response")
> ldw$group <- factor(ifelse(ldw$treat == 1, "Treated", "Control"),
+                     levels = c("Control", "Treated"))
> ggplot(ldw, aes(x = ps, fill = group)) +
+   geom_histogram(aes(y = after_stat(density)),
+                  position = "identity", alpha = 0.5, bins = 30) +
+   scale_fill_manual(values = c("#E69F00", "#56B4E9")) +
+   labs(x = "Propensity score", y = "Density", fill = "Group") +
+   theme_minimal()
```

Figure: Lalonde propensity score overlap

- Treated vs. control propensity score overlap in the LDW data. (Xu et al. tutorial; see References)

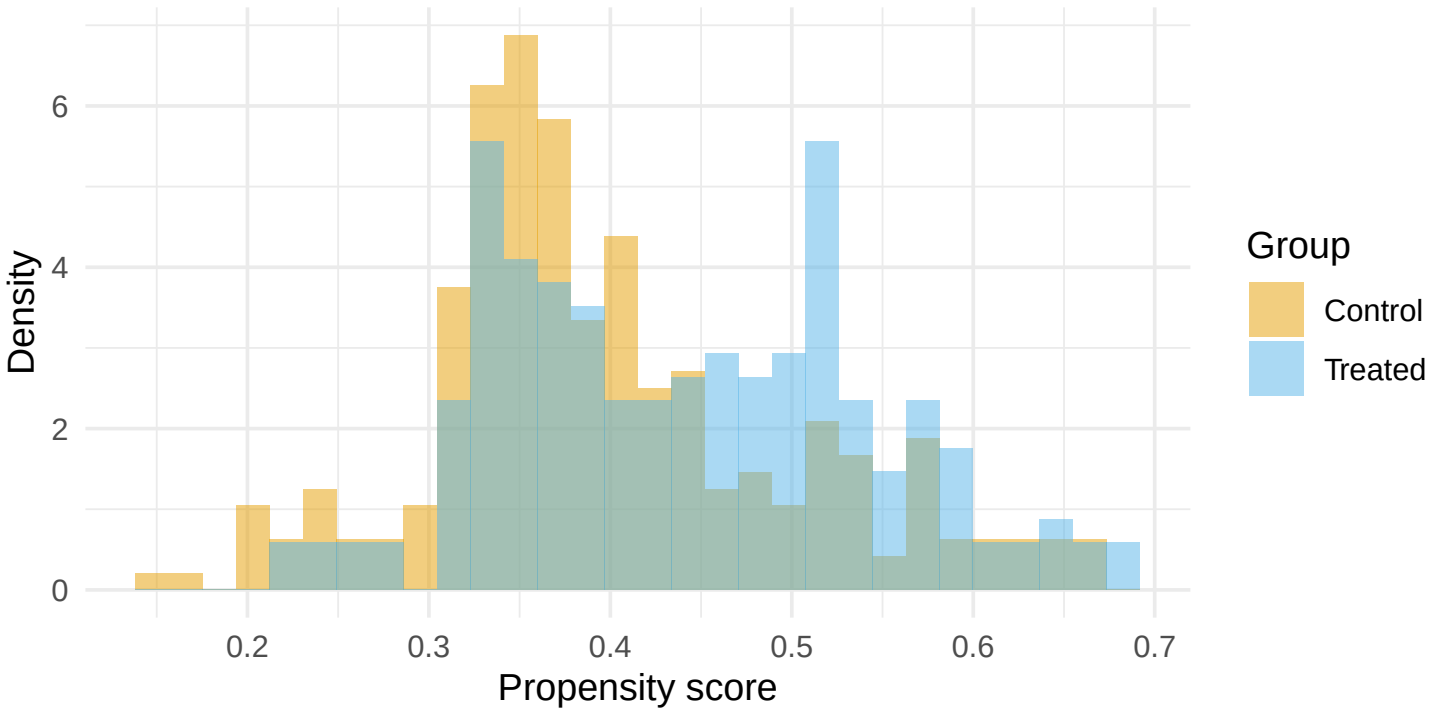
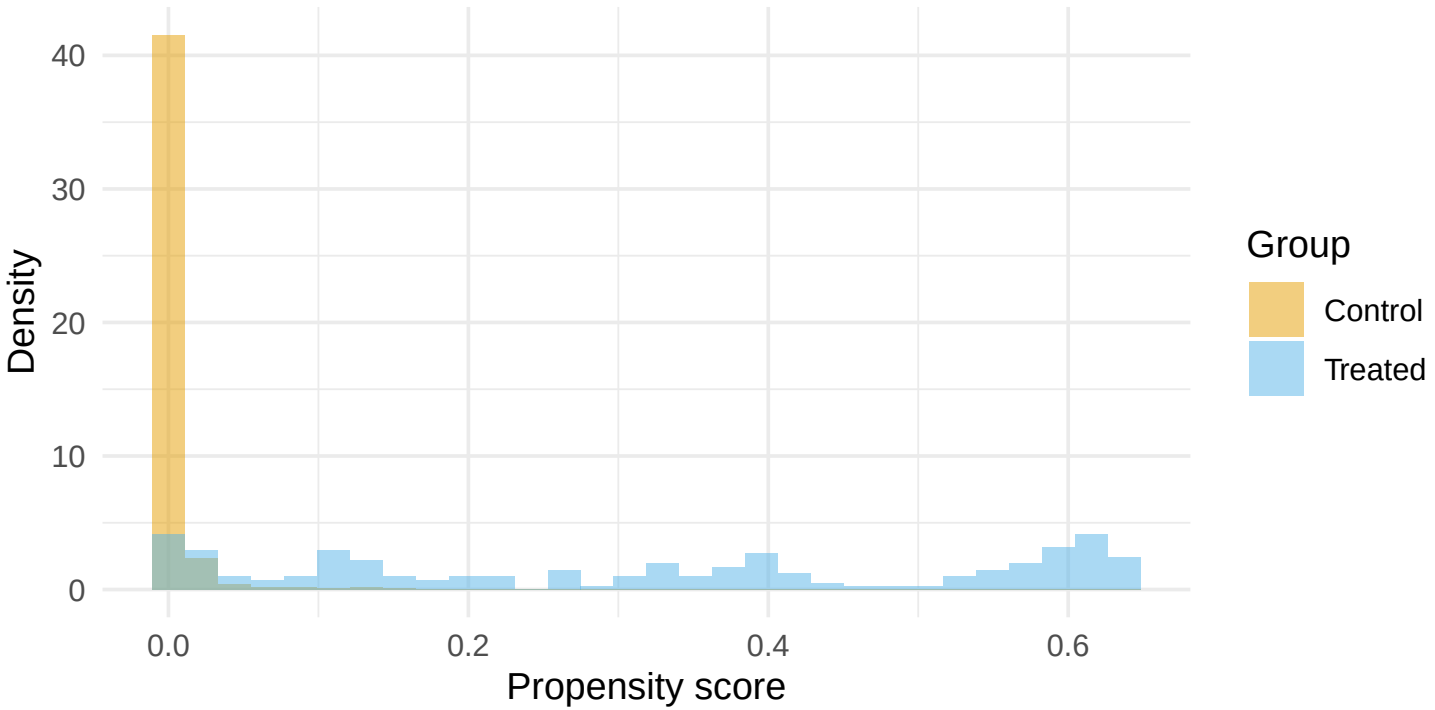


Figure: CPS1 overlap (observational controls)

- Treated LDW units + CPS controls. (Xu et al. tutorial; see References)



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- If $p_D(x)$ is near 0 or 1, weights explode and estimates become unstable.
- IPW: extreme weights $\Rightarrow$ high variance.
- Matching: few/no close matches $\Rightarrow$ bias or large variance.
- Regression: extrapolation where data are missing.

Diagnostics and responses

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- Stabilized IPW reduces variance but does not fix identification when overlap fails.

ATT as a pseudo-population

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- Define weights:

$$w_i^{ATT} = \begin{cases} 1, & D_i = 1 \\ \dfrac{\hat{p}_D(\boldsymbol{X}_i)}{1 - \hat{p}_D(\boldsymbol{X}_i)}, & D_i = 0 \end{cases}$$

- In the weighted pseudo-population, controls look like treated units in X.

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- In the weighted pseudo-population, controls look like treated units in X.

- Then ATT is a difference in weighted means:

$$\widehat{\mathrm{E}}_{ATT}[\tau_i] = \bar{Y}_{D=1} - \frac{\sum_{i:D_i=0} w_i^{ATT} Y_i}{\sum_{i:D_i=0} w_i^{ATT}}.$$

Science table: ATT weights

i	$X_{[1]i}$	$X_{[2]i}$	$\hat{p}_D(\boldsymbol{X}_i)$	D_i	Y_i	w_i^{ATT}
1	A	0	$\hat{p}_D(\boldsymbol{X}_i)$	0	0	$\frac{\hat{p}_D(\boldsymbol{X}_i)}{1-\hat{p}_D(\boldsymbol{X}_i)}$
2	A	0	$\hat{p}_D(\boldsymbol{X}_i)$	1	1	1
3	B	0	$\hat{p}_D(\boldsymbol{X}_i)$	0	1	$\frac{\hat{p}_D(\boldsymbol{X}_i)}{1-\hat{p}_D(\boldsymbol{X}_i)}$
4	B	0	$\hat{p}_D(\boldsymbol{X}_i)$	1	1	1
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10	B	1	$\hat{p}_D(\boldsymbol{X}_i)$	1	1	1

Code: ATT weights

```
> # ATT weights: treated = 1, control = p_hat / (1 - p_hat)
> w_att <- ifelse(df$D == 1, 1, df$p_hat / (1 - df$p_hat))
> att_ipw <- mean(df$Y[df$D == 1]) -
+   weighted.mean(df$Y[df$D == 0], w_att[df$D == 0])
> c(att_ipw = att_ipw)

 att_ipw
0.199926
```

ATT-specific IPW formulas

- Target estimand:

$$\mathrm{E}\left[\tau_i \mid D_i = 1\right] = \mathrm{E}\left[Y_i(1) - Y_i(0) \mid D_i = 1\right].$$

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- IPW ATT estimator (controls reweighted by p_D):

$$= \frac{1}{n_1} \sum_{i=1}^{n} Y_i D_i - \frac{1}{n_1} \sum_{i=1}^{n} Y_i (1 - D_i) \frac{\hat{p}_D(\boldsymbol{X}_i)}{1 - \hat{p}_D(\boldsymbol{X}_i)}, \quad n_1 = \sum_{i=1}^{n} D_i.$$

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- Stabilized (Hájek) ATT:

$$= \frac{\sum_{i=1}^{n} Y_i D_i}{\sum_{i=1}^{n} D_i} - \frac{\sum_{i=1}^{n} Y_i (1 - D_i) \frac{\hat{p}_D(\boldsymbol{X}_i)}{1 - \hat{p}_D(\boldsymbol{X}_i)}}{\sum_{i=1}^{n} (1 - D_i) \frac{\hat{p}_D(\boldsymbol{X}_i)}{1 - \hat{p}_D(\boldsymbol{X}_i)}}.$$

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$$= \frac{\sum_{i=1}^{n} Y_i D_i}{\sum_{i=1}^{n} D_i} - \frac{\sum_{i=1}^{n} Y_i(1-D_i)\frac{\hat{p}_D(\boldsymbol{X}_i)}{1-\hat{p}_D(\boldsymbol{X}_i)}}{\sum_{i=1}^{n}(1-D_i)\frac{\hat{p}_D(\boldsymbol{X}_i)}{1-\hat{p}_D(\boldsymbol{X}_i)}}.$$

- Doubly robust ATT (with outcome model $\hat{m}_d$ and propensity $\hat{p}_D$):

$$\begin{aligned} &\frac{1}{n_1}\sum_{i=1}^{n} D_i\left[\hat{m}_1(\boldsymbol{X}_i) - \hat{m}_0(\boldsymbol{X}_i)\right] \\ = &\quad + \frac{1}{n_1}\sum_{i=1}^{n} D_i\{Y_i - \hat{m}_1(\boldsymbol{X}_i)\} - \frac{1}{n_1}\sum_{i=1}^{n}(1-D_i)\frac{\hat{p}_D(\boldsymbol{X}_i)}{1-\hat{p}_D(\boldsymbol{X}_i)}\{Y_i - \hat{m}_0(\boldsymbol{X}_i)\}. \end{aligned}$$

DR estimator revisited

- Using plug-in models $\hat{m}_d(\boldsymbol{X}_i)$ and $\hat{p}_D(\boldsymbol{X}_i)$:

$$\widehat{\mathrm{E}}_{DR}[\tau_i] = \frac{1}{n}\sum_{i=1}^{n}\Big[\hat{m}_1(\boldsymbol{X}_i) - \hat{m}_0(\boldsymbol{X}_i) \; + \; \frac{D_i}{\hat{p}_D(\boldsymbol{X}_i)}\{Y_i - \hat{m}_1(\boldsymbol{X}_i)\} - \frac{1-D_i}{1-\hat{p}_D(\boldsymbol{X}_i)}\{Y_i - \hat{m}_0(\boldsymbol{X}_i)\}\Big].$$

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- Same estimator, grouped as treated-side minus control-side:

$$\widehat{\mathrm{E}}_{DR}[\tau_i] = \frac{1}{n}\sum_{i=1}^{n}\Big[\hat{m}_1(\boldsymbol{X}_i) + \frac{D_i}{\hat{p}_D(\boldsymbol{X}_i)}\{Y_i - \hat{m}_1(\boldsymbol{X}_i)\}\Big] - \frac{1}{n}\sum_{i=1}^{n}\Big[\hat{m}_0(\boldsymbol{X}_i) + \frac{1-D_i}{1-\hat{p}_D(\boldsymbol{X}_i)}\{Y_i - \hat{m}_0(\boldsymbol{X}_i)\}\Big].$$

DR scores: treated and control

- Define treated- and control-side scores:

$$\hat{\psi}_i^{(1)} = \hat{m}_1(\boldsymbol{X}_i) + \frac{D_i}{\hat{p}_D(\boldsymbol{X}_i)}\{Y_i - \hat{m}_1(\boldsymbol{X}_i)\}, \qquad \hat{\psi}_i^{(0)} = \hat{m}_0(\boldsymbol{X}_i) + \frac{1 - D_i}{1 - \hat{p}_D(\boldsymbol{X}_i)}\{Y_i - \hat{m}_0(\boldsymbol{X}_i)\}.$$

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- Then the DR estimator is the difference in average scores:

$$\widehat{\mathrm{E}}_{DR}[\tau_i] = \frac{1}{n}\sum_{i=1}^{n} \hat{\psi}_i^{(1)} - \frac{1}{n}\sum_{i=1}^{n} \hat{\psi}_i^{(0)}.$$

Science table: DR scores

i	$X_{[1]i}$	$X_{[2]i}$	$\hat{p}_D(\boldsymbol{X}_i)$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i	$\hat{\psi}_i^{(1)}$	$\hat{\psi}_i^{(0)}$	$\hat{\psi}_i^{(1)} - \hat{\psi}_i^{(0)}$
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	?	?	?

Science table: DR scores

i	$X_{[1]i}$	$X_{[2]i}$	$\hat{p}_D(\boldsymbol{X}_i)$	$Y_i(0)$	$Y_i(1)$	D_i	Y_i	$\hat{\psi}_i^{(1)}$	$\hat{\psi}_i^{(0)}$	$\hat{\psi}_i^{(1)} - \hat{\psi}_i^{(0)}$
1	A	0	0.33	0	?	0	0	0.67	-0.16	0.83
2	A	0	0.33	?	1	1	1	1.66	0.31	1.35
3	B	0	0.50	1	?	0	1	1.03	1.33	-0.30
4	B	0	0.50	?	1	1	1	0.97	0.67	0.30
5	A	1	0.50	0	?	0	0	0.53	-0.17	0.70
6	A	1	0.50	?	1	1	1	1.47	0.17	1.30
7	B	1	0.67	1	?	0	1	0.89	1.94	-1.05
8	B	1	0.67	?	0	1	0	-0.44	0.53	-0.97
9	A	0	0.33	1	?	0	0	0.67	-0.16	0.83
10	B	1	0.67	?	1	1	1	1.06	0.53	0.53

$$\widehat{\mathrm{E}}_{DR}[\tau_i] = \frac{1}{n}\sum_{i=1}^{n}\left(\hat{\psi}_i^{(1)} - \hat{\psi}_i^{(0)}\right) = 0.35.$$

DR scores in matrix notation

$$\hat{\mathrm{m}}_1 = \begin{bmatrix} \hat{m}_1(\boldsymbol{X}_1) \\ \vdots \\ \hat{m}_1(\boldsymbol{X}_n) \end{bmatrix}, \quad \hat{\mathrm{m}}_0 = \begin{bmatrix} \hat{m}_0(\boldsymbol{X}_1) \\ \vdots \\ \hat{m}_0(\boldsymbol{X}_n) \end{bmatrix}, \quad \hat{\boldsymbol{p}} = \begin{bmatrix} \hat{p}_D(\boldsymbol{X}_1) \\ \vdots \\ \hat{p}_D(\boldsymbol{X}_n) \end{bmatrix}.$$

Let $\odot$ be elementwise multiplication and $\oslash$ elementwise division.

$$\hat{\boldsymbol{\psi}}^{(1)} = \hat{\mathrm{m}}_1 + \big(\boldsymbol{D} \oslash \hat{\boldsymbol{p}}\big) \odot (\boldsymbol{Y} - \hat{\mathrm{m}}_1), \qquad \hat{\boldsymbol{\psi}}^{(0)} = \hat{\mathrm{m}}_0 + \big((\boldsymbol{1} - \boldsymbol{D}) \oslash (\boldsymbol{1} - \hat{\boldsymbol{p}})\big) \odot (\boldsymbol{Y} - \hat{\mathrm{m}}_0).$$

$$\widehat{\mathrm{E}}_{DR}[\tau_i] = \frac{1}{n} \boldsymbol{1}^\top \big(\hat{\boldsymbol{\psi}}^{(1)} - \hat{\boldsymbol{\psi}}^{(0)}\big).$$

Compare to:

$$\hat{\psi}_i^{(1)} = \hat{m}_1(\boldsymbol{X}_i) + \frac{D_i}{\hat{p}_D(\boldsymbol{X}_i)} \{Y_i - \hat{m}_1(\boldsymbol{X}_i)\}, \quad \hat{\psi}_i^{(0)} = \hat{m}_0(\boldsymbol{X}_i) + \frac{1 - D_i}{1 - \hat{p}_D(\boldsymbol{X}_i)} \{Y_i - \hat{m}_0(\boldsymbol{X}_i)\}.$$

Placebo testing

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- If treated and control units differ on placebo outcomes after adjustment, that is evidence against the identifying assumptions.

- Placebo tests are *not* the same as balance tests: balance checks whether the reweighting/matching worked, placebo tests probe the causal identification.

Placebo outcomes (implementation)

- Choose an outcome measured *before* treatment (or otherwise unaffected by treatment).

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- Large or significant placebo effects suggest lack of overlap or residual confounding.

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Tutorial: https://yiqingxu.org/tutorials/lalonde/