# Module 7: Matching and Weighting Estimators

Fall 2021

Matthew Blackwell

Gov 2003 (Harvard)

# 1/ Matching estimators

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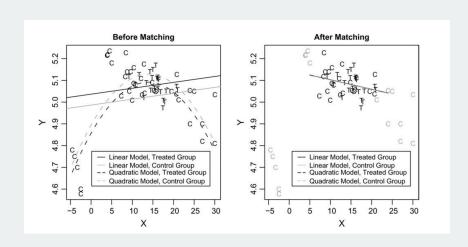
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# Model dependence



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- What matching isn't: a solution for selection on unobservables.
  - Matching is an estimation technique, not an identification strategy.

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  - Have to drop treated units in bins with no controls → changes estimand.
  - Allows you to control bias/variance tradeoff through coarsening.

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• Some use the linear predictor:  $D(\mathbf{X}_i, \mathbf{X}_i) = |\operatorname{logit}(\widehat{\pi}(\mathbf{X}_i)) - \operatorname{logit}(\widehat{\pi}(\mathbf{X}_i))|$ 

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• Implies we only need to match/balance on  $\pi(x)$ :

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- → "propensity score tautology"

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• Abadie and Imbens (2006) provides matching-based variance estimators.

# 2/ Weighting estimators

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- Weighting estimators choose the weights directly to reduce imbalance.

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· Key idea: reweight sample to be representative of population.

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- $\cdot$  Logic: upweight units with "rare" treatment values for their values of  $\mathbf{X}_i$ 
  - A kind of "continuous" version of matching with replacement.

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Practically, weighted least squares gives automatic normalization:

$$(\hat{\alpha}_{\text{wls}}, \widehat{\tau}_{\text{wls}}) = \operatorname*{arg\,min}_{\alpha,\tau} \sum_{i=1}^{n} \left( \frac{D_{i}}{\widehat{\pi}(\mathbf{X}_{i})} + \frac{1-D_{i}}{1-\widehat{\pi}(\mathbf{X}_{i})} \right) \left( Y_{i} - \alpha - \tau D_{i} \right)^{2}$$

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· Moment conditions for weighting estimators:

$$\begin{split} & \text{HT: } \mathbb{E}\left[\frac{D_iY_i}{\pi_{\theta}(\mathbf{X}_i)} - \mathbb{E}[Y_i(1)]\right] = \mathbb{E}\left[\frac{(1-D_i)Y_i}{1-\pi_{\theta}(\mathbf{X}_i)} - \mathbb{E}[Y_i(0)]\right] = 0 \\ & \text{Hajek: } \mathbb{E}\left[\frac{D_i(Y_i - \mathbb{E}[Y_i(1)])}{\pi_{\theta}(\mathbf{X}_i)}\right] = \mathbb{E}\left[\frac{(1-D_i)(Y_i - \mathbb{E}[Y_i(0)])}{1-\pi_{\theta}(\mathbf{X}_i)}\right] = 0 \end{split}$$

- If  $\widehat{\pi}(\mathbf{X}_i)$  is estimated, how to estimate  $\mathbb{V}[\widehat{\tau}_{\mathsf{ipw}}]$  or  $\mathbb{V}[\widehat{\tau}_h]$ ?
- First option: bootstrap (possibly with clustering if needed)
- · Second option: method of moments (Newey and McFadden, 1994)
  - Treat this a joint estimation problem and use the delta method.
  - Moment conditions for the propensity score model with parameters  $\theta$ :

$$\mathbb{E}\left[\underbrace{\left(\frac{D_i}{\pi_{\theta}(\mathbf{X}_i)} - \frac{1 - D_i}{1 - \pi_{\theta}(\mathbf{X}_i)}\right) \frac{\partial \pi_{\theta}(\mathbf{X}_i)}{\partial \theta}}_{\text{score for treatment model}}\right] = 0$$

· Moment conditions for weighting estimators:

$$\begin{split} & \text{HT: } \mathbb{E}\left[\frac{D_iY_i}{\pi_{\theta}(\mathbf{X}_i)} - \mathbb{E}[Y_i(1)]\right] = \mathbb{E}\left[\frac{(1-D_i)Y_i}{1-\pi_{\theta}(\mathbf{X}_i)} - \mathbb{E}[Y_i(0)]\right] = 0 \\ & \text{Hajek: } \mathbb{E}\left[\frac{D_i(Y_i - \mathbb{E}[Y_i(1)])}{\pi_{\theta}(\mathbf{X}_i)}\right] = \mathbb{E}\left[\frac{(1-D_i)(Y_i - \mathbb{E}[Y_i(0)])}{1-\pi_{\theta}(\mathbf{X}_i)}\right] = 0 \end{split}$$

 Replace with sample versions and use delta method to get asymptotic variance.

#### **Estimated versus known pscores**

```
ht.est <- function(y, d, w) {</pre>
  n <- length(v)</pre>
  (1/n) * sum((v * d * w) - (v * (1-d) * w))
n <- 200
x \leftarrow rbinom(n, size = 1, prob = 0.5)
dprobs <- 0.5*x + 0.4*(1-x)
d <- rbinom(n, size = 1, prob = dprobs)</pre>
y < -5 * d - 10 * x + rnorm(n, sd = 5)
true.w <- ifelse(d == 1, 1/dprobs, 1/(1-dprobs))</pre>
pprobs <- predict(glm(d ~ x))
est.w <- ifelse(d == 1, 1/pprobs, 1/(1 - pprobs))
ht.est(y, d, est.w)
```

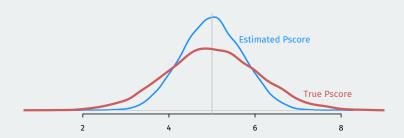
```
## [1] 5.22
ht.est(y, d, true.w)
```

```
## [1] 5.56
```

#### Sampling distribution of the HT estimators

```
sims <- 10000
true.holder <- rep(NA, sims)</pre>
est.holder <- rep(NA, sims)
for (i in 1:sims) {
  x \leftarrow rbinom(n, size = 1, prob = 0.5)
  dprobs <-0.5*x + 0.4*(1-x)
  d <- rbinom(n, size = 1, prob = dprobs)</pre>
  y < -5 * d - 10 * x + rnorm(n, sd = 5)
  true.w <- ifelse(d == 1, 1/dprobs, 1/(1-dprobs))
  pprobs <- predict(glm(d ~ x))</pre>
  est.w <- ifelse(d == 1, 1/pprobs, 1/(1 - pprobs))
  est.holder[i] <- ht.est(y, d, est.w)</pre>
  true.holder[i] <- ht.est(y, d, true.w)
```

# Sampling distribution of the HT estimators



## Sampling distribution of the HT estimators



#### var(est.holder)

## [1] 0.506

var(true.holder)

## [1] 1.15

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- · True PS only adjusts for the **expected** differences between samples.
- · Only true if propensity score model is correctly specified!!

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$$\begin{split} \widehat{\tau}_{\text{aipw}} &= \frac{1}{n} \sum_{i=1}^{n} \left\{ \frac{D_{i} Y_{i}}{\widehat{\pi}(\mathbf{X}_{i})} - \frac{(1 - D_{i}) Y_{i}}{1 - \widehat{\pi}(\mathbf{X}_{i})} \right. \\ & \left. - \left( \frac{D_{i} - \widehat{\pi}(\mathbf{X}_{i})}{\widehat{\pi}(\mathbf{X}_{i})} \widehat{\mu}_{1}(\mathbf{X}_{i}) - \frac{D_{i} - \widehat{\pi}(\mathbf{X}_{i})}{1 - \widehat{\pi}(\mathbf{X}_{i})} \widehat{\mu}_{0}(\mathbf{X}_{i}) \right) \right\} \end{split}$$

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