

Module 7b: Weighting Estimators

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Gov 2003 (Harvard)

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- $K_M(i)$ is the number of times i is used as a match.
- Weighting estimators choose the weights directly to reduce imbalance.

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

Horvitz-Thompson for treatment effects

- Applying HT potential outcomes: weight by inverse propensity score.

$$\widehat{ATE} = \widehat{\tau}_{ipw} = \frac{1}{n} \sum_{i=1}^n \left(\frac{D_i Y_i}{\widehat{\pi}(\mathbf{X}_i)} - \frac{(1 - D_i) Y_i}{1 - \widehat{\pi}(\mathbf{X}_i)} \right)$$

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 - A kind of “continuous” version of matching with replacement.

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- Practically, weighted least squares gives automatic normalization:

$$(\hat{\alpha}_{\text{wls}}, \hat{\tau}_{\text{wls}}) = \arg \min_{\alpha, \tau} \sum_{i=1}^n \left(\frac{D_i}{\hat{\pi}(\mathbf{X}_i)} + \frac{1 - D_i}{1 - \hat{\pi}(\mathbf{X}_i)} \right) (Y_i - \alpha - \tau D_i)^2$$

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 - Moment conditions for the propensity score model with parameters θ :

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

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

Estimated versus known pcores

```
ht.est <- function(y, d, w) {  
  n <- length(y)  
  (1/n) * sum((y * d * w) - (y * (1-d) * w))  
}  
n <- 200  
x <- rbinom(n, size = 1, prob = 0.5)  
dprobs <- 0.5*x + 0.4*(1-x)  
d <- rbinom(n, size = 1, prob = dprobs)  
y <- 5 * d - 10 * x + rnorm(n, sd = 5)  
  
true.w <- ifelse(d == 1, 1/dprobs, 1/(1-dprobs))  
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)
```

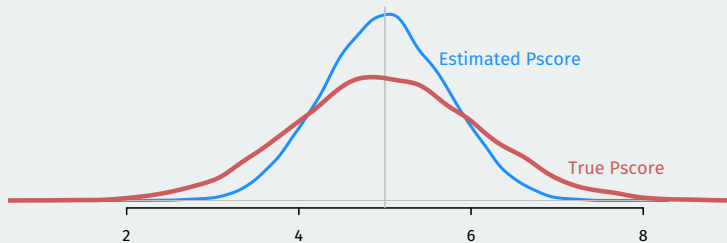
```
## [1] 5.56
```

Sampling distribution of the HT estimators

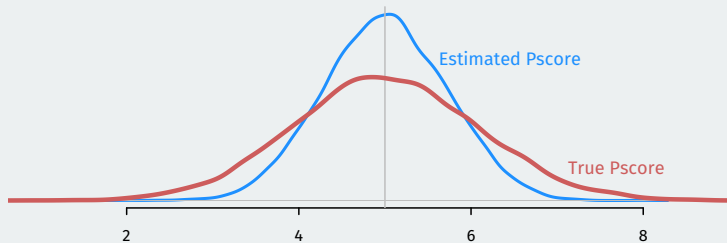
```
sims <- 10000
true.holder <- rep(NA, sims)
est.holder <- rep(NA, sims)
for (i in 1:sims) {
  x <- rbinom(n, size = 1, prob = 0.5)
  dprobs <- 0.5*x + 0.4*(1-x)
  d <- rbinom(n, size = 1, prob = dprobs)

  y <- 5 * d - 10 * x + rnorm(n, sd = 5)
  true.w <- ifelse(d == 1, 1/dprobs, 1/(1-dprobs))
  pprobs <- predict(glm(d ~ x))
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  est.holder[i] <- ht.est(y, d, est.w)
  true.holder[i] <- ht.est(y, d, true.w)
}
```

Sampling distribution of the HT estimators



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```
var(est.holder)
```

```
## [1] 0.506
```

```
var(true.holder)
```

```
## [1] 1.15
```

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- **Removing chance variations** using $\hat{\pi}(\mathbf{X}_i)$ adjusts for any small imbalances that arise because of a finite sample.
- True PS only adjusts for the **expected** differences between samples.
- Only true if propensity score model is **correctly specified!!**

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 - Can allow each model to be more flexible without hurting asymptotics.

Augmented IPW estimator

- **Augmented** IPW estimator combines regression and weighting:

$$\begin{aligned}\hat{\tau}_{\text{aipw}} &= \frac{1}{n} \sum_{i=1}^n \left\{ \frac{D_i Y_i}{\hat{\pi}(\mathbf{X}_i)} - \frac{(1 - D_i) Y_i}{1 - \hat{\pi}(\mathbf{X}_i)} \right. \\ &\quad \left. - \left(\frac{D_i - \hat{\pi}(\mathbf{X}_i)}{\hat{\pi}(\mathbf{X}_i)} \hat{\mu}_1(\mathbf{X}_i) - \frac{D_i - \hat{\pi}(\mathbf{X}_i)}{1 - \hat{\pi}(\mathbf{X}_i)} \hat{\mu}_0(\mathbf{X}_i) \right) \right\} \\ &= \frac{1}{n} \sum_{i=1}^n \left\{ \hat{\mu}_1(\mathbf{X}_i) - \hat{\mu}_0(\mathbf{X}_i) \right. \\ &\quad \left. + \left(\frac{D_i(Y_i - \hat{\mu}_1(\mathbf{X}_i))}{\hat{\pi}(\mathbf{X}_i)} - \frac{(1 - D_i)(Y_i - \hat{\mu}_0(\mathbf{X}_i))}{1 - \hat{\pi}(\mathbf{X}_i)} \right) \right\}\end{aligned}$$

- **Double robustness:** consistent if either $\hat{\pi}(\mathbf{X}_i)$ or $\hat{\mu}_d(\mathbf{X}_i)$ are consistent.
 - Can allow each model to be more flexible without hurting asymptotics.
- **Efficient:** lowest asymptotic variance among consistent estimators when PS model is correct.

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 - **Windsorizing**: trim weights beyond 5th and 9th percentile

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 - Find parameters that get closest to satisfying sample moment conditions

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 - Can include X_{ik}^2 etc to balance other parts of the distribution.