Quant 2, Lab 5

Matching and Weighting

Sylvan Zheng

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- Matching is an approach that addresses these weaknesses
  - Nonparametric
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  - **Estimation** technique, not an identification strategy. Alternative to, eg DoubleML
  - Doesn't solve issues with bad/good controls, selection on unobservables, etc.

Matching overview

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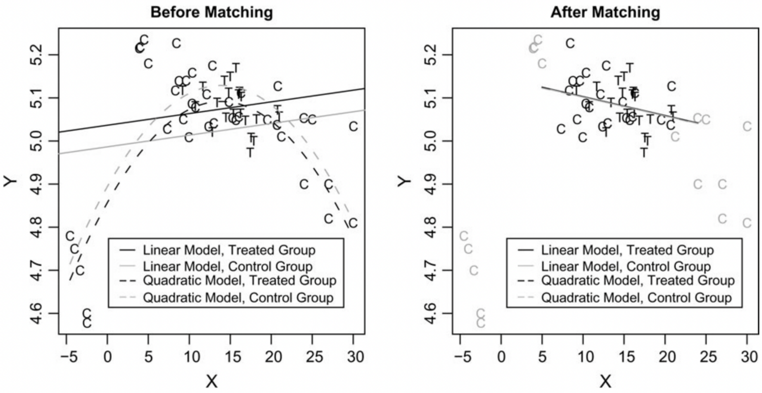
  - $\mathcal{J}(i)$ are the set of M closest control units to i in terms of X_i.

Example

Ho et al 2007



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  - Intuitively, you have to have observations to match on. This is an empirical question

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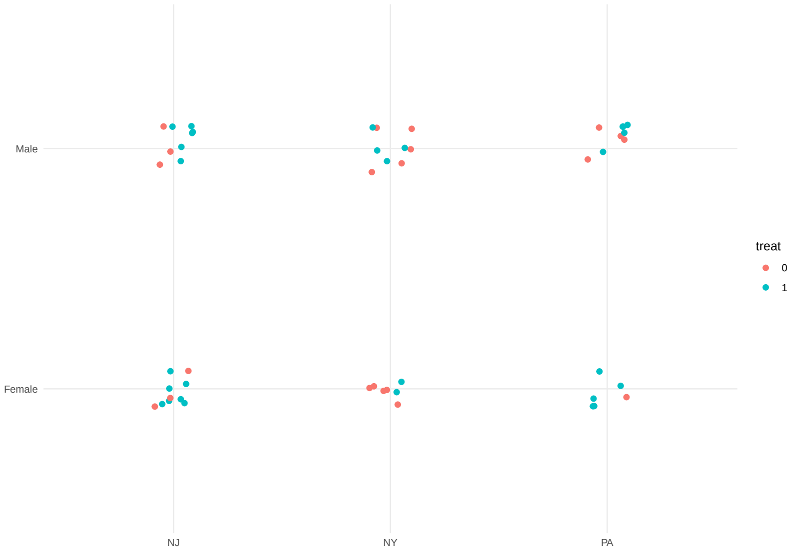
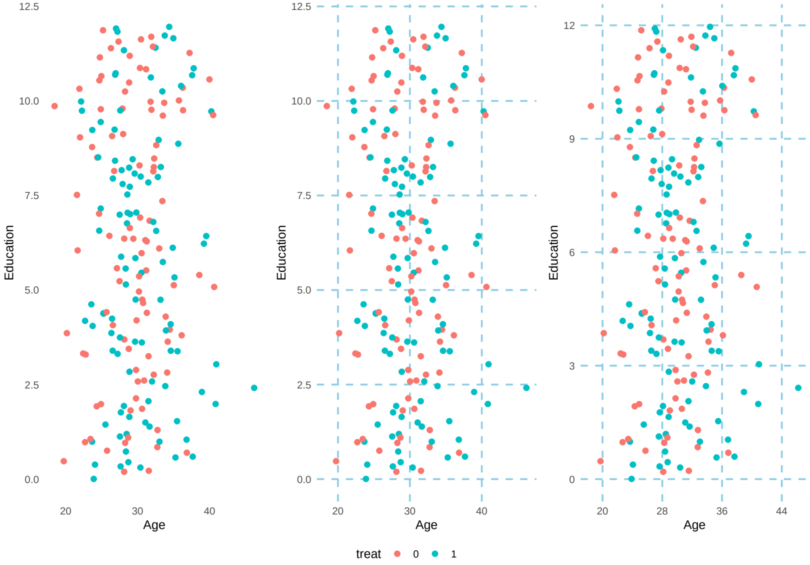
  - Divide continuous covariates into bins, then exact match
  - Problem: Sensitive to bin size
  - Problem: Still might be bins with no control units (more likely with many covariates)

Exact Matching: Example



CEM Example



12.5
10.0
7.5
5.0
2.5
0.0
Education
20
30
40
Age
12.5
10.0
7.5
5.0
2.5
0.0
Education
20
30
40
Age
12
9
6
3
0
Education
20
28
36
44
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treat
0
1

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  - Should we drop matches where the distance is too far (caliper)?

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  - Reduces imbalance, but if you drop treated units, estimand changes.

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    - Why use $\hat{Y_{j0}}$ instead of observed Y_{j0}?

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Stabilized IPW

- The IPW approach works well, but in small samples can be high variance if you get big $\pi(X)$ values.

$$\hat{\tau}_{SIPW} = \frac{\frac{1}{n}\sum_i \frac{Y_i D_i}{\hat{\pi}(X_i)}}{\frac{1}{n}\sum_i \frac{D_i}{\hat{\pi}(X_i)}} - \frac{\frac{1}{n}\sum_i \frac{Y_i(1-D_i)}{1-\hat{\pi}(X_i)}}{\frac{1}{n}\sum_i \frac{(1-D_i)}{\hat{\pi}(X_i)}}$$

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- This estimator benefits by adjusting for unusually high or low values of $\pi(X)$

True vs. Estimated p-scores

- True propensity scores are only known sometimes (e.g., randomized experiments). In most non-experimental settings, the p-score is unknown and must be estimated
- When estimating, we have two cases:
  - If X is discrete, we know that $\hat{\pi}(X)$ can be an exact approximation (why?)
  - If X is not discrete (or high-dimensional), how should we approximate it?
- We need to estimate $\pi(X)$ in a way that is flexible and will converge to the truth in the limit – e.g., semi-parametric estimation of π.
  - Note a linear model of π will inherently be wrong b/c probabilities are bounded between 0 and 1
  - Practical implication: logit estimation of $\pi(X)$ is reasonable, allowing for flexible specification of X
  - As dimension of X grows, ML / lasso style models grow in value

True vs. Estimated p-scores

- Important result: even if you know the true function $\pi(X)$, better to use the estimated function than the truth (Imbens, Hirano and Ridder (2002))
  - Intuition: the deviations from the "true" propensity score $\hat{\pi}(X) - \pi(X)$ are informative for the estimation of the treatment effects (a la extra moment restrictions in GMM)
- Clear tension – as dimension of controls increases, the noisiness in π grows as well

True vs. Estimated p-scores

```r
set.seed(123)
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] 5.029735
```

```r
ht.est(y, d, true.w)
```

```
## [1] 5.740815
```

True vs. Estimated p-scores

```r
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))
  est.w <- ifelse(d == 1, 1 / pprobs, 1 / (1 - pprobs))
  est.holder[i] <- ht.est(y, d, est.w)
  true.holder[i] <- ht.est(y, d, true.w)
}
var(est.holder)
```

```
## [1] 0.5062535
```

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

```
## [1] 1.147964
```

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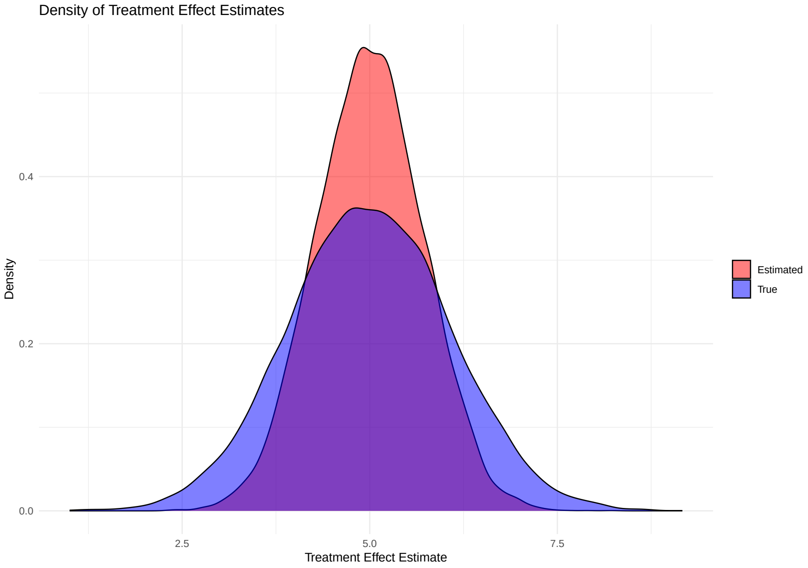

So??

- Why is the estimated propensity score more efficient than the true PS?
- Removing chance variations using $\hat{\pi}(X_i)$ 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!!