Section 8

Matching and Weighting Estimators

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Overview

- Logistics:
  - **Pset 7 released!** Due at 11:59 pm (ET) on Nov 10

- Today's topics:
  1. Matching estimators
  2. Weighting estimators

[Review] Observational studies

- **Identification**
  - Most common observational assumptions:
    - No unmeasured confounders: $D_i \perp\!\!\!\perp \big(Y_i(0), Y_i(1)\big) \mid \mathbf{X}_i$ $E[Y_i \mid D_i = 0, X_i]$
    - Overlap/positivity: $0 < \mathbb{P}(D_i = 1 \mid \mathbf{X}_i = x) < 1$ $\parallel$
  - Estimand: $\mu_0(X_i)$
    - ATE $= \mathbb{E}[\, Y_i(1) - Y_i(0)]$ (We identified this in Module 5) $\mu_1(X_i)$
    - ATT $= \mathbb{E}[\, Y_i(1) - Y_i(0) \mid D_i = 1]$
    - ATC $= \mathbb{E}[\, Y_i(1) - Y_i(0) \mid D_i = 0]$

[Review] Observational studies

- **Identification**
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  - Estimand:
    - ATE $= \mathbb{E}[Y_i(1) - Y_i(0)]$ (We identified this in Module 5)
    - ATT $= \mathbb{E}[Y_i(1) - \underline{Y_i(0) \mid D_i = 1}]$
    - ATC $= \mathbb{E}[Y_i(1) - Y_i(0) \mid D_i = 0]$

DAG

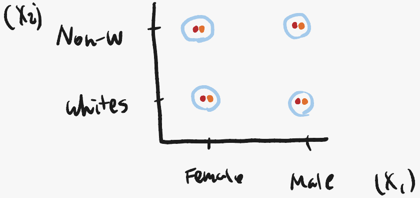
- **Estimation**
  - Regression estimators: $\widehat{\mu}_1(\mathbf{x})$ and $\widehat{\mu}_0(\mathbf{x})$ (Module 5)
  - Matching estimator (for ATT):

$$\widehat{\tau}_m = \frac{1}{n_1} \sum_{i=1}^{n} D_i \left(Y_i - \frac{1}{M} \sum_{j \in \mathcal{J}_M(i)} Y_j \right)$$

  - Weighting estimators:
    - Horvitz-Thompson estimator (= IPW estimator)
    - Hajek estimator (normalized weights)

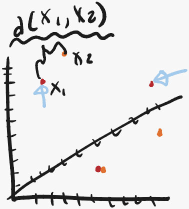
Types of matching

- Exact matching: choose matches that have the same value of $\mathbf{X}_i$
    - Cf: Coarsened Exact Matching (CEM)



● Treat

● Control



Exact match

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- Propensity score matching:

← Pset 7

$$\big(Y_i(0), Y_i(1)\big) \perp\!\!\!\perp D_i \mid \mathbf{X}_i \Rightarrow \big(Y_i(0), Y_i(1)\big) \perp\!\!\!\perp D_i \mid \pi(\mathbf{X}_i)$$

  - This holds under **true** propensity score $\pi(\mathbf{X}_i)$.
  - We need to estimate it ($\widehat{\pi}(\mathbf{X}_i)$): e.g., using logistic regression (can add interactions) or machine learning.
  - Have to check if $\mathbf{X}_i$ is actually balanced.

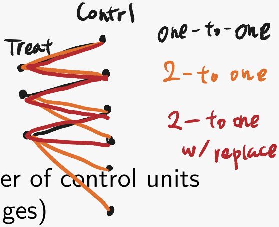
ps_mod ← glm(D ~ X , family = binomial)

ps_scores ← ps_mod $ fitted_values

$\hat{\pi}(X_i)$

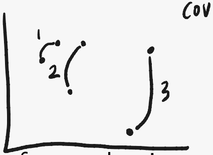
King, Nielsen (2019)

Types of matching



- Other choices
    - Matching ratio: *m*-to-one matching
    - w/ or w/o replacement: consider the number of control units
    - Caliper: drop poor matches (estimand changes)

Types of matching



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    - Matching ratio: m-to-one matching
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    - Caliper: drop poor matches (estimand changes)
- Algorithm:
    - Greedy algorithm: pair two units with the shortest distance, set them aside, and repeat ⇝ depends on order and thus may not be optimal
    - Optimal matching:
        - **D**: $n \times n$ matrix of pairwise distance or a cost matrix
        - Select n elements of **D** such that there is only one element in each row and one element in each column and the sum of pairwise distances is minimized ⇝ linear sum assingment problem

$d(x_1, x_2)$

$$D = \begin{array}{c|ccccc} & 1 & 2 & 3 & \cdots & n \\ \hline 1 & 0 & \cdot & & & \\ 2 & & \ddots & & & \\ \vdots & & & \ddots & & \\ n & & & & & 0 \end{array}$$

Types of matching

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- Assessing balance
  - standardized mean differences
  - Kolmogorov–Smirnov statistic (comparing distributions)

mean of age among treated

− matched control

QQ plot

Matching estimators

- Workflow (in general):
  1. Check the balance before the matching
  2. Choose matching type (compute/estimate the distance/balancing score if necessary)
  3. Conduct matching (check the matched dataset)
  4. Check the balance after the matching
  5. Estimate ATT using matching estimator ($\widehat{\tau}_m$)
  6. Estimate the standard error
  - w/o replacement: cluster bootstrap
  - w/ replacement: use Abadie and Imbens (2006) estimator

Matching estimators

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- Useful packages:

  table - balance

  - `cobalt`: for balance check (`bal.tab()` and `love.plot()`)
  - `MatchIt`: for matching
  - `Matching`: for matching + estimating
  - Machine learning packages for estimating $\widehat{\pi}(\mathbf{X}_i)$: e.g., `randomForest`
  - Optimal matching: `clue::solve_LSAP()`

Example: LaLonde dataset

- The effectiveness of a job trainining program (National Supported Work Demonstration; NSW) on wage increases.
- The federal government instituted a randomized evaluation of this program
- How well the result may be recovered when the experimental controls are replaced with a set of observational controls (Population Survey of Income Dynamics; PSID)?
- **Problem**: Imbalances between the experimental and observational data $\rightsquigarrow$ use matching

Example: LaLonde dataset

- Data:
  - Treated: 185 units from NSW
  - Control: 2490 units from PSID
  - Treatment: Participation in the job training program (`nsw`)
  - Outcome: 1978 earnings (in dollars; `re78`)
  - Pre-treatment covariates: age, race, marriage, past earnings, past employment

Example: Balance before matching

```r
library(cobalt)
bal.tab(x = dat[,pretreat_covariates],
        treat = dat$nsw, continuous = "std", binary = "std")
```

Example: Balance before matching

```
## Balance Measures
##             Type Diff.Un
## age      Contin. -1.0094
## educ     Contin. -0.6805
## black     Binary  1.4816
## hisp      Binary  0.1288
## married   Binary -1.8453
## re74     Contin. -1.7178
## re75     Contin. -1.7744
## u74       Binary  1.6454
## u75       Binary  1.2309
##
## Sample sizes
##     Control Treated
## All    2490     185
```

Example: Propensity score matching

```
# Estimate propensity score using logistic regression
# Propensity score
```

treat

pre-treat cov.

```
pscores <- glm(nsw ~ age + I(age^2) + black + married + hisp + u74,
                   family = binomial(), data = dat)$fitted.values
# Conduct one-to-one nearest neighbor propensity score matching
library(Matching)
match_ps <- Match(Y=dat$re78, Tr=dat$nsw,
                   X=pscores, M=1, replace = TRUE, ties = FALSE)
summary(match_ps)
```

matching ratio

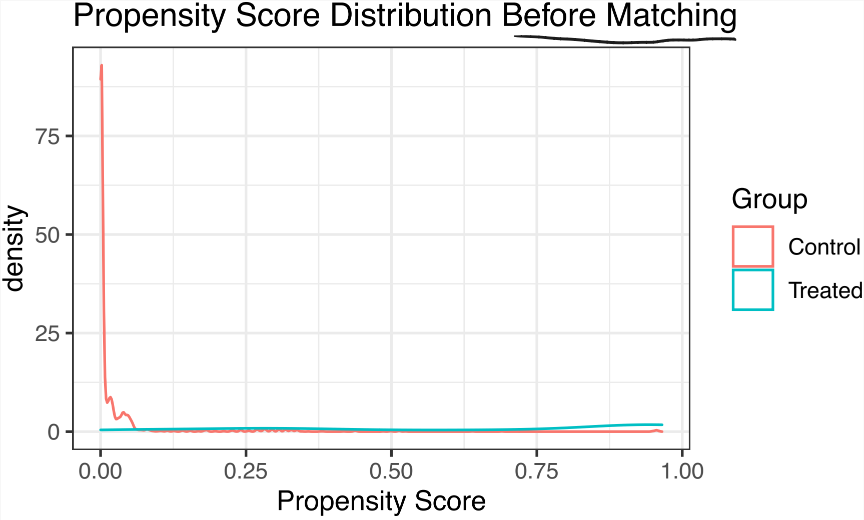
Example: Propensity score matching

```
##
## Estimate...  -941.15
## SE.........  903.91
## T-stat.....  -1.0412
## p.val......  0.29779
##
## Original number of observations..............  2675
## Original number of treated obs...............  185
## Matched number of observations...............  185
## Matched number of observations  (unweighted).  185
```

– ATT

– Abadie & Imbens

Example: Propensity score matching



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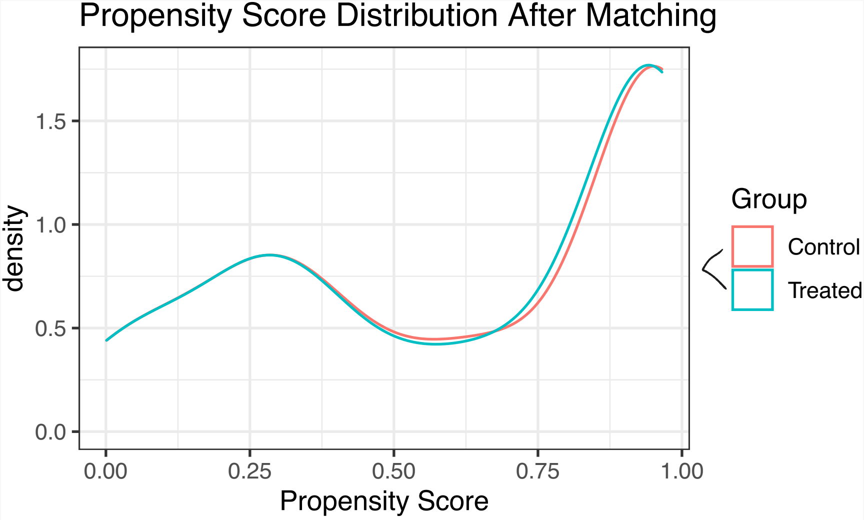
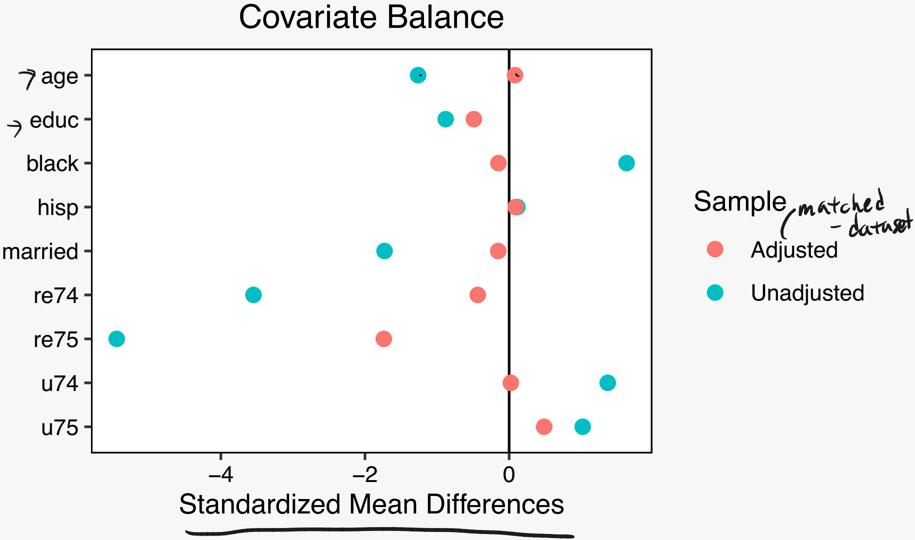


Example: Propensity score matching

```r
library(cobalt)
love.plot(nsw ~ age+educ+black+hisp+married+re74+re75+u74+u75,
  data = dat,
  stats = "mean.diffs",
  weights = data.frame(Matched = get.w(match_ps)),
  method = c("matching"), binary = "std")
```

Example: Propensity score matching



Weighting estimators

- Matching is actually a special case of a weighting estimator
- Horvitz-Thompson estimator: weight by inverse propensity score.

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

D_i , X_i

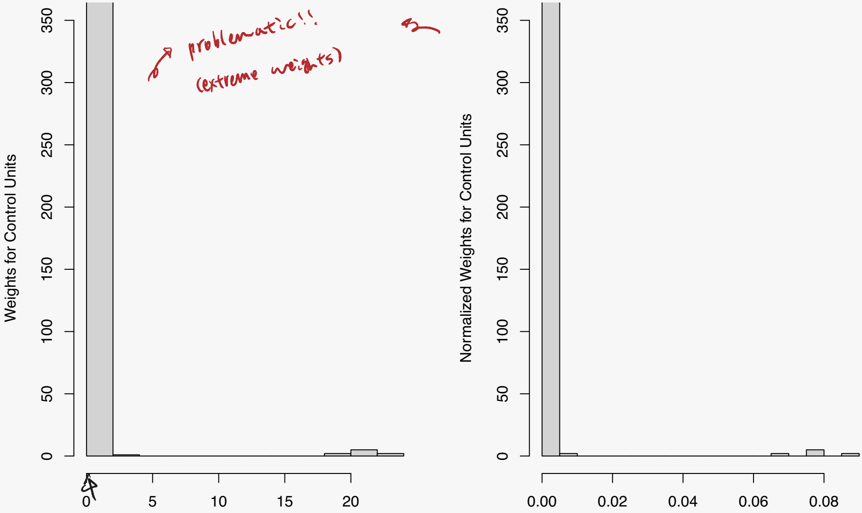
$Pr(D_i = 1 \mid X_i)$

  - Would be unbiased if we knew the true propensity scores, $\underline{\pi(\mathbf{X}_i)}$ (Pset 7 Q2 Bonus)
  - Under no unmeasured confounders, $\widehat{\tau}_{ipw} \overset{p}{\to} \tau$ (consistent)
  - Hajek estimator: normalizes the weights

- Potential of extreme weights due to lack of overlap: $\pi(\mathbf{X}_i)$ close to 0 or 1
  - Windsorizing: trim weights beyond 5th and 95th percentile

Example

```
# Generating propensity score weights for the ATT
W.out <- WeightIt::weightit(nsw ~ age + I(age^2) + black + married + hisp +
                  method = "ps", estimand = "ATT")
```



problematic!!

(extreme weights)

Estimating ATT with Weights

```r
## append estimated weights
dat <- dat %>% mutate(weights = W.out$weights)
## ATT
att_ipw <- function(dat, indices = NULL) {
  if (is.null(indices)) indices <- 1:nrow(dat)
  dat <- dat[indices,]

  weights   <- dat %>% filter(treat == 0) %>% pull(weights)
  reweights <- weights / sum(weights)
  Y1 <- dat %>% filter(treat == 1) %>% pull(re78)
  Y0 <- dat %>% filter(treat == 0) %>% pull(re78)
  att_ht  <- (sum(Y1) - sum(Y0 * weights)) / nobs
  att_hjk <- mean(Y1) - sum(reweights * Y0)
  return(c(att_ht, att_hjk))
}
## Use bootsrap for estimating SE
```

bootstrap data

→ $\hat{\pi}(X_i)$

→ ATT

} n times