Quant II

Conditioning: Matching, Weighing, and Sensitivity Analysis

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Outline

- Blocking and rerandomization
- Matching
 - Why matching?
 - Various algorithms
 - Asymptotics of matching
- ► IPW
 - ▶ Why do we love/hate it?
 - Covariate balancing
- ▶ What if confounders are unobservable?
 - Placebo
 - Sensitivity

Blocking

- ▶ Blocking: covariates adjustment before assignment
- Usually results in more efficient estimates
- ► Easier to get balance in covariates
- What is the optimal blocking algorithm?

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Rerandomization

- What if your first draw leads to imbalance in covariates?
- Rubin: draw the assignment again and do not tell anybody!
- But what is the distribution of the ATE estimates?
- ▶ Ding, Li and Rubin (2017): A truncated Gaussian distribution
- Rerandomization can be combined with regression adjustment

- ► To approximiate a blocking experiment
- ▶ To get rid of model dependence Matching is completely nonparametric: $\hat{\tau}_i = Y_i \sum_{\mathcal{M}_i} Y_{i \in \mathcal{M}_i}$.

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- To guarantee common support (positivity)
 Suppose we estimate τ using Lin's approach, then,

$$\hat{\tau} = \bar{Y}_1 - \bar{Y}_0 - (\frac{N_0}{N_0 + N_1} * \hat{\beta}_1 + \frac{N_1}{N_0 + N_1} * \hat{\beta}_0)'(\bar{X}_1 - \bar{X}_0)$$

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Matching cannnot help you get unconfoundedness.

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- 5. Calulate the ATT/ATE on your matched dataset

An example

- ▶ Boyd et al. (2010)
- The effect of gender on decision making
- Unit of analysis: the appellate court case
- ► Treatment: whether there is at least one female in the three judge panel
- ► Covariates: median ideology, median age, one racial minority, indicator for ideological direction of lower court's decision, indicator for whether a majority of the judges were nominated by Republicans, indicator for whether a majority of the judges on the panel had judicial experience prior to their nomination

View Initial Balance

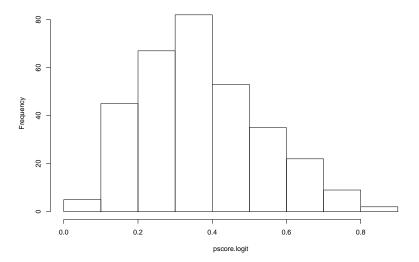
```
initial.balance <- round(t(rbind(means,t.p,ks.p)),digits=3)[c(2:8),] initial.balance
```

##		Treated	Control	t.p	ks.p
##	median.ideo	0.900	0.802	0.008	0.006
##	repub.majority	0.752	0.585	0.002	0.030
##	has.minority	0.233	0.212	0.666	1.000
##	maj.experienced	0.446	0.373	0.202	0.826
##	median.age	63.416	60.483	0.000	0.001
##	${\tt liberal.lower.direction}$	0.208	0.161	0.292	0.997
##	liberalOutcome	0.366	0.424	0.314	0.967

Propensity score matching

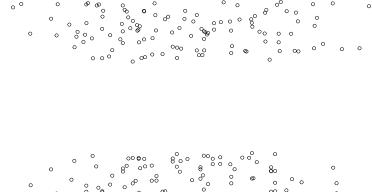
- ▶ Pros: reduce the number of dimensions
- ► Cons: may not use information in the most efficient way

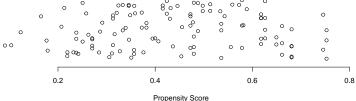
 Histogram of pscore.logit



Propensity score matching

Treatment and Control





Nearest Neighbor Matching

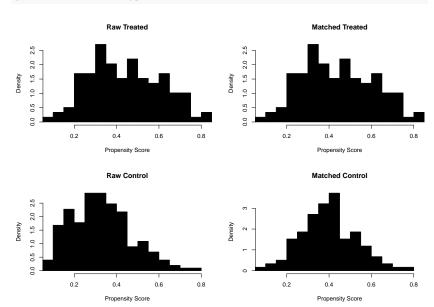
- Approximate a blocking experiment
- ▶ You can also use MatchIt

Nearest Neighbor Matching

##		Means.Treated	Means.Control	t.NN
##	median.ideo	0.8024492	0.8995520	0.2161134
##	median.age	60.4830508	63.4158416	0.4253905
##	repub.majority	0.5847458	0.7524752	1.0000000
##	has.minority	0.2118644	0.2326733	0.5952787
##	maj.experienced	0.3728814	0.4455446	0.2003073
##	liberal.lower.direction	0.1610169	0.2079208	0.8586550

Nearest Neighbor Matching

plot(matched.NN, type="hist", col = "black", breaks = 20)



Genetic Matching

 Set an objective function and update the distance metric iteratively

$$\sqrt{(X_i-X_j)'(S^{-1/2})'WS^{-1/2}(X_i-X_j)}$$

- Based upon evolutionary algorithm
- It is very slow (especially if you choose a reasonable pop.size)
- ▶ Can also do it with MatchIt or GenMatch

Genetic Matching

```
## Control Treat t.p
## median.ideo 0.826 0.802 0.449
## repub.majority 0.585 0.585 0.552
## has.minority 0.212 0.212 0.265
## maj.experienced 0.373 0.373 0.849
## median.age 60.839 60.483 0.626
## liberal.lower.direction 0.136 0.161 0.391
```

And then you can calculate the effect of interest

CEM

- CEM creates bins along each covariate dimension (either pre-specified or automatic)
- Units lying in the same strata are then matched together
- Curse of dimensionality means that with lots of covariates, we'll only rarely have units in the same strata.

CEM

```
## G0 G1
## All 202 118
## Matched 15 18
## Unmatched 187 100
```

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- ▶ What is the real standard error of $\hat{\tau}$?
- ► Roadmap:
 - ► Abadie and Imbens (2006): asymptotic distribution for NN matching (with replacement)
 - ▶ Abadie and Imbens (2011): debiased matching estimator
 - ► Abadie and Imbens (2008): boostrap doesn't work for matching
 - ► Abadie and Imbens (2012): matching as a martingale (NN without replacement)
 - Abadie and Imbens (2016): asymptotic distribution for PS matching
 - ▶ Otsu and Rai (2017): wild bootstrap for NN matching
 - ▶ Bodory et al. (2018): wild bootstrap for PS matching

- ▶ Denote $E[Y_i(D_i)|X_i]$ as $\mu_{D_i}(X_i)$, then $Y_i = \mu_{D_i}(X_i) + \epsilon_i$
- ► Match with K nearest neighbors; replacement is allowed; covariates can be continuous

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$$\hat{\tau}_{M} = \frac{1}{N} \sum_{i=1}^{N} (\widehat{Y}_{i}(1) - \widehat{Y}_{i}(0))$$

► The bias from NN matching can be decomposed into three parts:

$$\hat{\tau}_{M} - \tau = \overline{\tau(X)} - \tau + E_{M} + B_{M}$$

where

$$\overline{\tau(X)} = \frac{1}{N} \sum_{i=1}^{N} (\mu_1(X_i) - \mu_0(X_i))$$

and

$$E_M = rac{1}{N} \sum_{i=1}^N (2D_i - 1)(1 + rac{\mathcal{K}_M(i)}{M})\epsilon_i$$

- Abadie and Imbens (2006) show that both $\tau(X)$ (difference in conditional expectations) and E_M (sum of residuals) are asymptotically unbiased.
- However,

$$B_{M} = \frac{1}{N} \sum_{i=1}^{N} (2D_{i} - 1) \left[\frac{1}{M} \sum_{m=1}^{M} (\mu_{1-D_{i}}(X_{i}) - \mu_{1-D_{i}}(X_{j_{m}(i)})) \right]$$

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is not.

- ▶ The bias caused by "mismatch"; it declines very slowly.
- The speed depends on the number of continuous covariates.
- \triangleright B_M actually converges to an exponential distribution.
- ▶ We may estimate B_M directly using the serial estimator proposed by Newey (1995).
- ► Take-away: do not use bootstrap for NN matching!

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- ► The duality of IPW and propensity score matching suggests two basic ways of conducting causal inference:
 - ► Adjust the response surface (matching, regression)
 - Adjust the assignment probability (weighting)
 - ▶ Either approach returns unbiased estimate
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 - ► Adjust the response surface (matching, regression)
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 - ▶ We can combine them to obtain doubly robustness
- IPW can be extended to panel data (dynamic treatment regime).

The benefits of IPW

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- ▶ Hirano et al. (2003): the variance of IPW estimators can reach the Cramer-Rao lower bound
- What if we use the real propensity score?
- ▶ The variance will be larger! (Hahn, 1998)
- Empirical propensity scores take into account all the actual imbalances in the sample

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- One solution is to stabilize it using the Hajek estimator
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- Changes the quantity of interest
- ► Ma and Wang (2019): asymptotic distribution for both trimed/untrimed IPW
- They also provide a bias correction method based on resampling

```
##
## median.ideo
                            0.8995520
                                       0.8024492
## repub.majority
                            0.7524752
                                       0.5847458
                                       0.2118644
## has.minority
                            0.2326733
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                            0.2079208
                                       0.1610169
                            0.0000000
## has.woman
                                       1.0000000
## liberalOut.come
                            0.3663366
                                       0.4237288
```

CBPS and covariates balancing

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- ▶ What can you do when the treatment is continuous?
- ► Imai and Ratkovic (2013); Fong, Hazlett and Imai (2018): Covariate Balancing Propensity Score
- ▶ Idea: find weights that are orthogonal to *X*, *D*, and their interaction

$$\sum_{i}^{N} w_{i}(X_{i}^{*}, D_{i}^{*}, X_{i}^{*} * D_{i}^{*}) = 0, \sum_{i}^{N} w_{i} = N$$

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- ► Hainmueller (2012); Hazlett (2015); Arbour and Dimmery (2019)
- Various forms of convex optimization

##

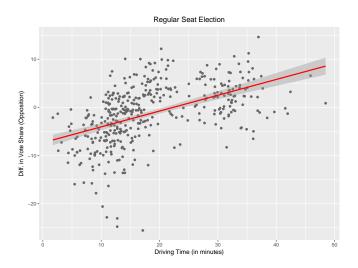
median.ideo 0.8995520 0.8024492

▶ Wang and Wong (2018)

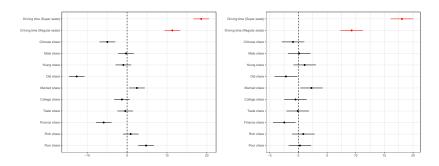
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Driven by protest exposure, or other features of the central city?



Placebo test

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- ► Find some variable/observation that should not be affected by the treatment
- Will the weight of your friends affect yours? How about height?
- More common in panel data analysis

Sensitivity analysis

► The basic idea: How influential unobservable confounders have to be to make the estimate insignificant/zero?

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- ► The basic idea: How influential unobservable confounders have to be to make the estimate insignificant/zero?
- Remember that confounders must be correlated with both D and Y
- Vary the two correlation coefficients and check how the estimate would change
- Compare the correlation coefficients against observable confounders
- Methods differ in their assumptions on the DGP

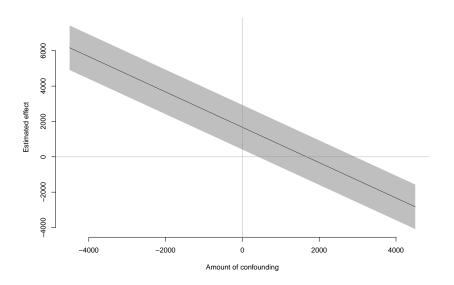
Sensitivity analysis

- ► First proposed by Rosenbaum and Rubin (1983)
- ▶ Imbens (2003): Full parametric model
- ▶ Blackwell (2013): Measure selection bias
- ▶ Dorie et al. (2016): Semi-parametric test using BART
- Cinelli and Hazlett (2020): Sensitivity from the OVB perspective

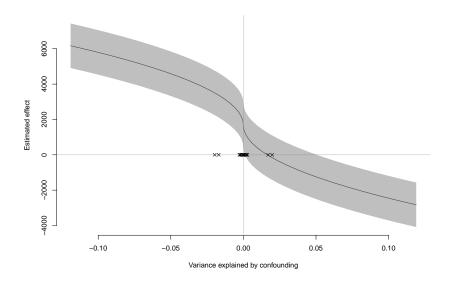
Blackwell (2013)

- Instead of imagining specific uni or multivariate omitted variable, imagine a function which defines the confounding.
- $q(d,x) = E[Y_i(d)|D_i = d, X_i = x] E[Y_i(d)|D_i = 1 d, X_i = x]$
- ▶ If q is positive units in group d have a higher mean potential outcome under d that those in group 1 d.
- ➤ So q encodes the selection bias of treatment assignment: it models violations of ignorability.
- After all, confounding means that potential outcomes vary by treatment status.
- Now, $Y_i^q = Y_i qPr(1 D_i|X_i)$ and we can redo the analysis.
- ▶ Package on CRAN: causalsens

Blackwell (2013)



Blackwell (2013)



- Sensitivity from the omitted variable bias perspective
- ▶ Suppose the correct model is $Y = \hat{\tau}D + \mathbf{X}\hat{\beta} + \hat{\gamma}Z + \hat{\varepsilon}_{full}$
- But Z is unobservable
- So the real model is $Y = \hat{\tau}_{res}D + \mathbf{X}\hat{\beta}_{res} + \hat{\varepsilon}_{res}$
- ▶ It is easy to see:

$$\begin{split} \hat{\tau}_{res} &= \frac{\textit{Cov}(D^{\perp \mathbf{X}}, Y^{\perp \mathbf{X}})}{\textit{Var}(D^{\perp \mathbf{X}})} \\ &= \frac{\textit{Cov}(D^{\perp \mathbf{X}}, \hat{\tau}D^{\perp \mathbf{X}} + \hat{\gamma}Z^{\perp \mathbf{X}})}{\textit{Var}(D^{\perp \mathbf{X}})} \\ &= \hat{\tau} + \hat{\gamma} \frac{\textit{Cov}(D^{\perp \mathbf{X}}, Z^{\perp \mathbf{X}})}{\textit{Var}(D^{\perp \mathbf{X}})} \\ &= \hat{\tau} + \hat{\gamma} \hat{\delta} \end{split}$$

- \blacktriangleright The difference between the correct estimate $\hat{\tau}$ and the real estimate $\hat{\tau}_{res}$ has two parts:
 - $\hat{\gamma}$: the impact of the unobservable $\hat{\delta}$: the imbalance of the unobservable
- Essentially, the estimate is robust to model misspecification when both Y and D can be largely explained by the observable covariates
- ▶ The idea could be extended to the nonlinear case where we use R^2 to measure the explanatory power of observable covariates
- ▶ Model misspecification is not dependent on the sample size

