

Matching

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Linear Methods in Causal Inference

POLI784

Review

- ▶ We discussed the difference between experiments and observational studies.
- ▶ Both require (conditional) randomization of the treatment for causal identification.
- ▶ The difference is that we do not know the probability of being treated in the latter.
- ▶ We have to estimate nuisance parameters under imposed structural restrictions.
- ▶ We can estimate either propensity scores or response surfaces.

Blocking

- ▶ Suppose our data are generated by block randomization.
- ▶ We know covariates that are used to form blocks but not the probability of being treated within each block.
- ▶ It is a natural idea to recover the blocks first—units with the same covariates values will be allocated into the same group.
- ▶ Next, we estimate the CATE in each group and aggregate them to estimate the SATE.
- ▶ This method is known as blocking in the literature.
- ▶ It does not work when there are many confounders or some confounders are continuous.

Matching

- ▶ Instead, we can create a block for each unit using similar units (just like kernel regression).
- ▶ For any treated (untreated) unit i , we find M units from the control (treatment) group that are similar to it in covariates (nearest-neighbor matching or NN matching).
- ▶ Or, we find M units from the control (treatment) group that are similar to it in the propensity score (propensity score matching or PS matching).
- ▶ We need to decide the number of neighbors (M) and whether replacement is allowed.
- ▶ If not, each unit from the control (treatment) group can only be matched to one treated (untreated) unit.
- ▶ Not all the units from the control (treatment) group will be matched to a treated (untreated) unit.
- ▶ The existence of such units usually suggests the violation of positivity.

Matching

- ▶ We also need a distance metric to measure how similar two units are.
- ▶ A natural choice is the Euclidean distance; but it is sensitive to the units of the variables.
- ▶ An alternative is the Mahalanobis distance:

$$d(\mathbf{X}_i, \mathbf{X}_j) = \sqrt{(\mathbf{X}_i - \bar{\mathbf{X}})' \mathbf{S}^{-1} (\mathbf{X}_j - \bar{\mathbf{X}})},$$

where \mathbf{S} is a positive-definite matrix such as the variance-covariance matrix of the variables.

- ▶ This metric standardizes all the variables such that units no longer matter.

Matching

- ▶ The basic steps are as follows
 1. Decide your estimand (ATE or ATT),
 2. Choose the matching method (what covariates to be matched on, NN or PS matching, number of neighbors, with or without replacement, etc.),
 3. Choose a proper distance metric,
 4. Find matches on your set of covariates/propensity scores, and get rid of non-matches,
 5. Check balance in your matched data set,
 6. Repeat these steps until your set exhibits acceptable balance,
 7. Calculate the estimate on your matched dataset,
 8. Derive standard errors and construct confidence intervals.

Nearest-neighbor matching

- ▶ Nearest-neighbor matching is similar to blocking if all the covariates only take discrete values (exact matching).
- ▶ But in practice, there may be many covariates, some of which are continuous.
- ▶ We can only match each treated/untreated observation with M untreated/treated neighbors who are the nearest.
- ▶ \mathbf{X}_i is never identical to the average covariates of i 's nearest neighbors even in large samples.
- ▶ This inaccuracy creates severe problems for statistical inference.
- ▶ Abadie and Imbens (2006) first derive the asymptotic distribution of the nearest-neighbor matching estimator.
- ▶ It equals to a normal distribution plus an exponential distribution (the bias).

Nearest-neighbor matching: algorithm

- ▶ Match with M nearest neighbors; replacement is allowed; covariates can be continuous.
- ▶ We impute the counterfactual of each unit with the average of the matched units.
- ▶ For each treated observation i ,

$$\hat{Y}_i(1) = \begin{cases} Y_i & D_i = 1 \\ \frac{1}{M} \sum_{j \in \mathcal{J}_M(i)} Y_j & D_i = 0, \end{cases}$$
$$\hat{Y}_i(0) = \begin{cases} \frac{1}{M} \sum_{j \in \mathcal{J}_M(i)} Y_j & D_i = 1 \\ Y_i & D_i = 0, \end{cases}$$

where $\mathcal{J}_M(i)$ is the set of units matched to i .

- ▶ The ATE estimate using matching is

$$\hat{\tau}_M = \frac{1}{N} \sum_{i=1}^N (\hat{Y}_i(1) - \hat{Y}_i(0)).$$

Nearest-neighbor matching: bias (*)

- ▶ Denote $E[Y_i(D_i)|\mathbf{X}_i]$ as $m_{D_i}(\mathbf{X}_i)$ and $\varepsilon_i = Y_i - m_{D_i}(\mathbf{X}_i)$.
- ▶ Each unit i might be matched to multiple other units and we denote the number as $K_M(i)$.
- ▶ The bias from matching can be decomposed into three parts:

$$\hat{\tau}_M - \tau = \overline{\tau(\mathbf{X})} - \tau + E_M + B_M$$

where

$$\overline{\tau(\mathbf{X})} = \frac{1}{N} \sum_{i=1}^N (m_1(\mathbf{X}_i) - m_0(\mathbf{X}_i))$$

and

$$E_M = \frac{1}{N} \sum_{i=1}^N (2D_i - 1) \left(1 + \frac{K_M(i)}{M}\right) \varepsilon_i$$

Nearest-neighbor matching: bias (*)

- ▶ Abadie and Imbens (2006) show that both $\overline{\tau(\mathbf{X})} - \tau$ (difference in conditional expectations) and E_M (sum of residuals) are asymptotically small.
- ▶ However,

$$B_M = \frac{1}{N} \sum_{i=1}^N (2D_i - 1) \left[\frac{1}{M} \sum_{m=1}^M (m_{1-D_i}(\mathbf{X}_i) - m_{1-D_i}(\mathbf{X}_{j_m(i)})) \right]$$

is not.

- ▶ The bias is caused by “mismatch” between \mathbf{X}_i and $\mathbf{X}_{j_m(i)}$.
- ▶ It can decline to zero very slowly and the convergence rate decreases with the number of continuous covariates ($O_P(N^{1/\kappa})$).

Nearest-neighbor matching: bias (*)

- ▶ B_M actually converges to an exponential distribution.
- ▶ Consider a single covariate, $M = 5$, one treated unit i and 100 untreated ones.
- ▶ Suppose $j_5(i)$ is the fifth closest neighbor to i , then the probability for any unit l to be a closer neighbor is $P = P[\|X_l - X_i\| \leq \|X_{j_5(i)} - X_i\|]$.
- ▶ There are 4 closer neighbors and 95 more distant neighbors.
- ▶ The probability for this event to happen is

$$\binom{99}{4} P^4 (1 - P)^{95}$$

- ▶ It obeys the binomial distribution and converges to an exponential distribution.

Nearest-neighbor matching: bias

- ▶ The bias term is undesirable and makes matching inefficient.
- ▶ There is no need to worry about the bias if there is at most one continuous covariate used for matching.
- ▶ Or if the following conditions hold:
 1. we are only interested in the ATT,
 2. matching is conducted without replacement, and
 3. the number of untreated units is much larger than that of the treated ones (Abadie and Imbens 2012).

Nearest-neighbor matching: inference (*)

- ▶ Abadie and Imbens (2006) prove that

$$\sqrt{N}(\hat{\tau}_M - \tau - B_M) \rightarrow \mathcal{N}(0, V)$$

- ▶ We can estimate B_M directly using nonparametric regression and subtract it from $\hat{\tau}_M$.
- ▶ This is known as the bias correction estimator for NN matching.
- ▶ They also provide an estimator for the variance based on jackknife.
- ▶ Lin, Ding, and Han (2023) showed that if we allow M to grow with N , the bias correction estimator is consistent and efficient.
- ▶ Because of the bias, bootstrap cannot be used to approximate the estimate's distribution (Abadie and Imbens 2008).

Propensity score matching: asymptotics

- ▶ Note that the propensity score is a unidimensional continuous variable.
- ▶ Matching on the propensity score does not induce the bias term.
- ▶ Abadie and Imbens (2016) show that

$$\sqrt{N}(\hat{\tau}_M - \tau) \rightarrow \mathcal{N}(0, V)$$

- ▶ Since the propensity score is an estimate rather an variable, the asymptotic variance is affected by its estimation.
- ▶ We must account for this extra uncertainty in variance estimation.
- ▶ PS matching requires extra structural restrictions hence is less agnostic (Ho et al. 2007).
- ▶ But it does approximate a block randomization.

Development of the matching method

▶ Roadmap:

- ▶ Abadie and Imbens (2006): asymptotic distribution for NN matching (with replacement)
- ▶ Abadie and Imbens (2008): bootstrap doesn't work for NN matching
- ▶ Abadie and Imbens (2011): bias correction matching estimator
- ▶ Abadie and Imbens (2012): matching as a martingale (NN matching without replacement)
- ▶ Diamond and Sekhon (2013): finding the optimal distance metric using evolutionary algorithm
- ▶ Abadie and Imbens (2016): asymptotic distribution for PS matching
- ▶ Huber et al. (2016): wild bootstrap for PS matching
- ▶ Otsu and Rai (2017): wild bootstrap for NN matching
- ▶ Abadie and Spiess (2021): regression after matching is valid only under the correct specification.
- ▶ Armstrong and Kolesár (2021): NN matching is finite-sample optimal when the outcome is not smooth in covariates
- ▶ Lin, Ding, and Han (2023): theoretical results for diverging M

Misconceptions about matching

- ▶ Matching makes your data look like a product of block randomization.
- ▶ It does not guarantee the existence of such a randomization process.
- ▶ It is an estimator rather than an identification assumption.
- ▶ Strong ignorability is the pre-condition and cannot be made more plausible by using any estimator.
- ▶ Matching can be used just to ensure positivity by trimming units that cannot be matched (Imbens 2015).
- ▶ But extra steps are needed to account for confounders.

Matching: application

- ▶ Let's revisit LaLonde (1986).
- ▶ We rely on the R-package *Matching* developed by Jas Sekhon.

```
## The OLS estimate is 1794.343
```

```
## The SE of OLS estimate is 670.9967
```

```
## The Lin regression estimate is 1583.468
```

```
## The SE of Lin regression estimate is 678.0574
```

Matching: application

```
##  
## Estimate... 2050.5  
## AI SE..... 1727.8  
## T-stat..... 1.1868  
## p.val..... 0.23532  
##  
## Original number of observations..... 2675  
## Original number of treated obs..... 185  
## Matched number of observations..... 185  
## Matched number of observations (unweighted). 201
```

Matching: application

```
##  
## Estimate...    1468.7  
## AI SE.....   1385.5  
## T-stat.....   1.06  
## p.val.....    0.28914  
##  
## Original number of observations..... 2675  
## Original number of treated obs..... 185  
## Matched number of observations..... 185  
## Matched number of observations (unweighted). 932
```

Matching: application

##	mean.Tr	mean.Co	sdiff	T	pval
## age	25.816	34.851	-126.266	0.000	
## education	10.346	12.117	-88.077	0.000	
## black	0.843	0.251	162.564	0.000	
## hispanic	0.059	0.033	11.357	0.132	
## married	0.189	0.866	-172.406	0.000	
## nodegree	0.708	0.305	88.378	0.000	
## re74	2095.574	19428.746	-354.707	0.000	
## re75	1532.056	19063.338	-544.576	0.000	
## u74	0.708	0.086	136.391	0.000	
## u75	0.600	0.100	101.786	0.000	

Matching: application

##	mean.Tr	mean.Co	sdiff	T	pval
## age	25.816	26.288	-6.598	0.368	
## education	10.346	10.580	-11.650	0.037	
## black	0.843	0.822	5.931	0.102	
## hispanic	0.059	0.059	0.000	1.000	
## married	0.189	0.195	-1.376	0.564	
## nodegree	0.708	0.659	10.672	0.006	
## re74	2095.574	2429.660	-6.837	0.004	
## re75	1532.056	2251.461	-22.347	0.000	
## u74	0.708	0.708	0.000	1.000	
## u75	0.600	0.600	0.000	1.000	

Matching: application

```
## Warning: glm.fit: fitted probabilities numerically 0 or
##
## Estimate... 1687.9
## AI SE..... 1565.4
## T-stat..... 1.0783
## p.val..... 0.28091
##
## Original number of observations..... 2675
## Original number of treated obs..... 185
## Matched number of observations..... 185
## Matched number of observations (unweighted). 2739
```

Matching: application

##	mean.Tr	mean.Co	sdiff	T	pval
## age	25.816	24.676	15.940	0.092	
## education	10.346	10.709	-18.058	0.101	
## black	0.843	0.828	4.108	0.694	
## hispanic	0.059	0.067	-3.269	0.767	
## married	0.189	0.120	17.644	0.021	
## nodegree	0.708	0.660	10.585	0.306	
## re74	2095.574	2624.597	-10.826	0.233	
## re75	1532.056	1862.146	-10.254	0.170	
## u74	0.708	0.651	12.431	0.111	
## u75	0.600	0.523	15.583	0.084	

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