MATCHING METHODS FOR CATEGORICAL AND CONTINUOUS TREATMENTS

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Let \mathcal{Z} be the sample space for the treatment assignment Z.

• Most of our course has only considered binary treatments.

 $Z \in \mathcal{Z} = \{0, 1\}$

Causal estimands are comparisons of counterfactual outcomes $Y_i(Z_i = 1)$ vs $Y_i(Z_i = 0)$

- Now we consider nonbinary treatments
 - Categorical (possibly ordinal): Z = {1, 2, ..., k}, e.g. multiple treatment arms
 - **Continuous**: $\mathcal{Z} \subseteq \mathbb{R}$, e.g. drug dose

Causal estimands in the Rubin Causal Model

Categorical treatment with *k* categories:

• There are $\binom{k}{2}$ pairwise comparisons of treatment assignment

$$Y_i(Z_i = j)$$
 vs. $Y_i(Z_i = j')$ for $j, j' \in \{1, 2, ..., k\}$

Continuous treatment:

• Finite difference comparison

$$Y_i(Z_i = z)$$
 vs. $Y_i(Z_i = z')$ for $z \neq z'$

Average dose-response function

 $\mu(z) = \mathbb{E}[Y_i(z)]$

Generalized propensity score

Let *X* be the vector of observed covariates.

Definition: Generalized propensity score^{*} (GPS)

Let r(z, x) be the conditional density (or mass function) of the treatment given the covariates:

 $r(z, x) = f_{Z|X}(z \mid x)$

The generalized propensity score is R = r(Z, X).

Note that *R* may be a vector, e.g. if *Z* is categorical.

^{*}Imbens (2000); Hirano and Imbens (2004)

Sävje et al. (2017) Wu et al. (2020)

Overlap

Assumption: Overlap

$$r(z, x) = f_{Z|X}(z \mid x) > 0 \quad \forall z \in \mathcal{Z}$$

Generalized propensity score

Assumption: Weak unconfoundedness

 $Y(z) \perp Z \mid X \text{ for all } z \in \mathbb{Z}$

Note: this does not require joint independence of all potential outcomes $\{Y(z)\}_{z \in \mathbb{Z}}$

Similar to Rosenbaum and Rubin (1983) for the case of binary Z, Imbens (2000) and Hirano and Imbens (2004) demonstrate:

Theorem: Weak unconfoundedness given the GPS

If weak unconfoundedness holds given X, then, for every z,

 $f_Z(z \mid r(z, X), Y(z)) = f_Z(z \mid r(z, X)).$

Existing methods mostly rely on GPS

- Imai and van Dyk (2004): Subclassify on GPS, then take average over subclasses
- Hirano and Imbens (2004): Parametric model for *Y* | *Z*, *R*, then marginalize over *R*
- Robins et al. (2000): IPTW estimator using GPS

Disadvantage: These methods rely on parametric assumptions

Work on matching for nonbinary treatments is relatively new

Outline

Presenting methodologies from three papers:

- (i) Nattino et al. (2020): Compare treatment effects across 3 treatment arms (*categorical*)
- (ii) Sävje et al. (2017): Generalized full matching for multiple treatment categories (*categorical*)
- (iii) Wu et al. (2020): Use matching to estimate average dose-response (*continuous*)

Nattino et al. (2020)

Nattino et al. (2020)

Goal: Compare effectiveness of trauma centers as measured by *emergency department mortality*, for three classes of trauma center,

- level 1 trauma center (TC I)
- level 2 trauma center (TC II)
- nontrauma center (NTC)

Counterfactual of interest: "... the key research question is whether TC II is a justified investment of limited trauma care resources. If trauma patients treated at TC II had, instead, been treated at TC I or NTC, would their outcomes have been different?" – p. 1

Assumptions

Let $Y_{\ell}^{(z)}$ for $z \in \{1, 2, 3\}$ denote the counterfactual outcome (1 for death, 0 for survival) for unit $\ell = 1, ..., N$.

The observed value is $Y_{\ell} = Y_{\ell}^{\text{obs}} = \sum_{z=1}^{3} I(Z_{\ell} = z) Y_{\ell}^{(z)}$

 \mathbf{X}_ℓ is a vector of pre-treatment covariates

- SUTVA: no interference between units, no multiple versions of same treatment
- 2. Positivity

$$0 < \Pr(Z_{\ell} = z \mid Y_{\ell}^{(1)}, Y_{\ell}^{(2)}, Y_{\ell}^{(3)}, \mathbf{X}_{\ell}) < 1 \quad \forall z \in \{1, 2, 3\}$$

3. Strong ignorability

$$Z_{\ell} \perp Y_{\ell}^{(1)}, Y_{\ell}^{(2)}, Y_{\ell}^{(3)} \mid \mathbf{X}_{\ell}$$

Three-way matching

Idea: replicate conventional block randomization design, using triplets of units containing all treatment assignments z = 1, 2, 3

Let I, \mathcal{J} , and \mathcal{K} denote the sets of indices of subjects in subject. We will create $S = \min\{n_1, n_2, n_3\}$ matched triplets. Will match on variables **V** (either covariates **X** or the GPS).

• Define a distance metric $d^3(i, j, k), i \in I, j \in \mathcal{J}, k \in \mathcal{K}$ as a function of $\mathbf{V}_i, \mathbf{V}_j$ and \mathbf{V}_k , with additivity property

$$d^{3}(i, j, k) = d^{2}(i, j) + d^{2}(i, k) + d^{2}(j, k)$$

- Denote set of possible matches as M = {i, j_i, k_i}_{i∈I}, where the units j_i and k_i are matched to units i
- Goal is to find \mathcal{M} to minimize $D(\mathcal{M}) = \sum_{i \in \mathcal{I}} d^3(i, j_i, k_i)$

Triplet matching algorithm

Rough outline:

- (i) Select two treatment groups arbitrarily, and optimally match them into pairs
- (ii) Optimally match units in the third treatment group to each of the pairs from step (i) (keeping previous pairs fixed)
- (iii) Switch the two fixed treatment groups, and then optimally match units from the third treatment group
- (iv) Iterate through step (iii) until total distance cannot be decreased further

This method produces sets of matched triplets, but each step only requires two-way matching

Inference on mortality differences

Denote treatment and outcome vectors for triplet s = 1, ..., S as $\mathbf{Z}_s = \{Z_{s1}, Z_{s2}, Z_{s3}\}$ and $\mathbf{Y}_s = \{Y_{s1}, Y_{s2}, Y_{s3}\}$

- Fisher's sharp null hypothesis of no effect at all: $H_0 = Y_{sr}^{(1)} = Y_{sr}^{(2)} = Y_{sr}^{(3)}$ for subject r = 1, 2, 3.
- Consider two comparisons:

(1) NTC vs TC overall (z = 1 vs z = 1, 2 combined)

(2) TC II vs TC I (z = 2 vs z = 3)

Use Fisher randomization based inference

Comparing NTC vs TC overall

• Mantel-Haenszel test statistic is no. of events in NTC

$$\sum_{s=1}^{S} \sum_{r=1}^{3} I(Z_{sr} = 1) Y_{sr}$$

• Under null hypothesis, each subject is equally likely to be the patient assigned to NTC within each triplet. Conditioning on $m_s = \sum_{r=1}^{3} Y_{sr}$, define p_s as

$$p_s = \Pr(\sum_{r=1}^{3} I(Z_{sr} = 1)Y_{sr} = 1 \mid \sum_{r=1}^{3} = m_s).$$

$$p_s = 0, 1/3, 2/3, 1 \text{ for } m_s = 0, 1, 2, 3$$

• The standardized statistic is

$$T_{\mathsf{MH}} = \frac{\sum_{s=1}^{S} \sum_{r=1}^{3} I(Z_{sr} = 1)Y_{sr} - \sum_{s=1}^{S} p_s}{\sqrt{\sum_{s=1}^{S} p_s(1 - p_s)}}$$

Under the null hypothesis, $T_{MH} \sim N(0, 1)$ as $S \rightarrow \infty$

Comparing TC I vs TC II overall

• McNemar test statistic is no. of events in TC II

$$\sum_{s=1}^{S} \sum_{r=1}^{3} I(Z_{sr} = 3) Y_{sr}$$

 Under null hypothesis, each subject is equally likely to be the patient assigned to NTC within each triplet. Conditioning on n_s = ∑_{r∈{2,3}} Y_{sr}, define q_s as
 q_s = Pr(∑³_{r=1} I(Z_{sr} = 3)Y_{sr} = 1 | ∑_{r∈{2,3}</sub> = n_s).

$$q_s = 0, 1/2, 1$$
 for $n_s = 0, 1, 2$

• The standardized statistic is

$$T_{\rm MH} = \frac{\sum_{s=1}^{S} \sum_{r=1}^{3} I(Z_{sr} = 1) Y_{sr} - \sum_{s=1}^{S} q_s}{\sqrt{\sum_{s=1}^{S} q_s (1 - q_s)}}$$

Under the null hypothesis, $T_{MN} \sim N(0, 1)$ as $S \rightarrow \infty$

Results on trauma center mortality data

- Estimate GPS using multinomial regression
- Match subjects on the basis of the linear predictor of GPS (log-odds)
- Results in 3158 matched triplets

Results: covariate balance after matching

Table 1. Absolute standardized differences after matching.

Variable	NTC vs. TC I	TC I vs. TC II	NTC vs. TC II	Maximum	Average
Age	1.05%	3.65%	2.60%	3.65%	2.43%
Sex (female)	3.75%	2.93%	0.87%	3.75%	2.52%
155	0.44%	0.09%	0.36%	0.44%	0.30%
Multiple injury	0.50%	0.65%	0.00%	0.65%	0.38%
Chronic conditions	10.43%	3.36%	13.62%	13.62%	9.14%
Median household income by patient zip code					
Q1 (0%-25%)	8.33%	12.13%	3.75%	12.13%	8.07%
Q2 (25%-50%)	6.10%	1.12%	4.82%	6.10%	4.01%
Q3 (50%-75%)	3.40%	3.50%	0.08%	3.50%	2.33%
Q4 (75%-100%)	9.17%	12.48%	3.42%	12.48%	8.36%
Primary expected payer					
Medicare	5.11%	0.00%	5.46%	5.46%	3.53%
Medicaid	2.89%	1.22%	1.68%	2.89%	1.93%
Private insurance	3.75%	10.17%	13.97%	13.97%	9.30%
Self-pay	4.41%	7.32%	11.39%	11.39%	7.71%
No charge	1.35%	0.97%	3.06%	3.06%	1.79%
Other	1.79%	1.18%	2.89%	2.89%	1.95%
Patient location					
Large central metropolitan area	5.40%	0.41%	6.50%	6.50%	4.10%
Large fringe metropolitan area	5.15%	13.10%	8.34%	13.10%	8.86%
Medium metropolitan area	5.93%	2.28%	7.88%	7.88%	5.36%
Small metropolitan area	2.77%	6.60%	8.72%	8.72%	6.03%
Micropolitan area	0.44%	4.36%	3.66%	4.36%	2.82%
Neither metropolitan nor micropolitan area	10.69%	9.74%	1.28%	10.69%	7.24%

Results: Comparisons between trauma centers

	E	efore matching	After matching		
	N	ED mortality $-N$ (%)	N	ED mortality — N (%)	
NTC	5314	760 (14.3%)	3158	319 (10.1%)	
TC I	13,383	503 (3.8%)	3158	134 (4.2%)	
TC II	3158	134 (4.2%)	3158	134 (4.2%)	

Table 2. Results of the outcome analysis.

- NTC vs TC (TC I and TC II combined): $T_{\rm MH} = 11.45$, p < 0.001
- TC I vs TC II: $T_{MN} = 0, p = 0.500$
- Assess sensitivity to unobserved confounding (Rosenbaum, 1987) gives $\Gamma_{\text{MH}} = 2.34$.

Sävje et al. (2017)

Sävje et al (2017)

- **Hypothesis:** social norms influence citizens' propensity to vote (Gerber, Green, and Larimer, 2008).
- **Goal:** study effectiveness of a postcard intervention in increasing voter turnout. There are six total treatment conditions.
- Introduce *generalized full matching*, which extends full matching to the case of categorical treatment with *k* levels.

Gerber et al. prescreened voters to be included in the study, so the original results were not generalizeable to the entire population.

Full matching

This paper generalizes full matching[†]:

- Construct groups of units that are as homogeneous as possible
- Require that each group has at least one unit of each treatment condition
- So far, only developed for case of binary treatment

All units are matched to a subclass, hence the term "full"

[†]Rosenbaum (1991); Hansen (2004); Stuart and Green (2008)

Notation

- Denote the sample of *n* units by $\mathbf{U} = \{1, 2, \dots, n\}$
- Unit *i* is assigned to treatment condition $W_i \in \{1, 2, ..., k\}$
- The vectors w_x = {i : W_i = x} denote sets of units assigned to a given treatment condition
- Matched groups are denoted by m, and the union of matched groups is $M=\{w_1,w_2,\ldots\}$
- Define an objective function L : M → ℝ, where M is the set of possible matches

Match group constraints

Constrain the set of admissible matches \mathcal{M} as follows:

- Each match group **m** must contain c_x no. of units with treatment condition *x*
- Each match group must contain at least t ≥ ∑^k_{x=1} c_x no. of units overall
- Union of match groups must contain all units, $\mathbf{M}=\bigcup \mathbf{m}=\mathbf{U}$

. . .

Sävje et al. (2017)

Conclusion



Sävje et al. (2017)

Graphical example



Sävje et al. (2017)

Properties

Let \mathbf{M}_{alg} be the set of matches resulting from the algorithm

Theorem: Sävje et al. (2019)

$\mathit{L}(M_{\text{alg}}) \leq \min_{M \in \mathcal{M}} 4 \mathit{L}(M)$

Covariate balance

	U	nadjusted	Match	Matching adjustment		
	$\operatorname{Control}$	Non-experiment	Control	Non-experiment		
Birth year	1956.19	1957.96	1958.16	1957.87		
Female $(\%)$	49.89	53.32	53.29	53.15		
Voted Aug 2000 $(\%)$	25.19	14.65	15.19	15.19		
Voted Aug 2002 $(\%)$	38.94	22.59	23.42	23.43		
Voted Aug 2004 (%)	40.03	18.71	19.80	19.80		
Voted Nov 2000 (%)	84.34	52.49	54.11	54.11		
Voted Nov 2002 (%)	81.09	41.93	43.94	43.92		
Voted Nov 2004 (%)	100.00	67.57	100.00	68.76		

 Table 3: Covariate balance with and without matching adjustment.

Construct matched groups based on Mahalonobis distance

Results on voter turnout data (1)

Table 2: Unadjusted and matching adjusted average turnout in the 2006 primary election.

	$\operatorname{Control}$	Civic Duty	Haw the relation the second	Self	Neighbors	Non-experiment
Unadjusted turnout (%)	29.66	31.45	32.24	34.52	37.79	18.01
Adjusted turnout $(\%)$	21.43	23.73	23.01	25.16	26.88	18.60
Observations	$191,\!243$	38,204	38,218	38,201	38,218	$6,\!418,\!617$

The figures [in the second row] should be interpreted as estimates of turnout of the six conditions if scaled up to the whole population

Control and non-experiment groups should be more similar....

Results on voter turnout data (2)

Now restrict to units that voted in 2004 election...

Table 4: Turnout in the 2006 primary election among voters in the 2004 partisan election.

	$\operatorname{Control}$	Civic Duty	Hawthorne	Self	Neighbors	Non-experiment
Unadjusted turnout $(\%)$	29.66	31.45	32.24	34.52	37.79	25.56
Adjusted turnout $(\%)$	26.59	28.86	27.95	30.87	32.90	25.89
Observations	$191,\!243$	38,204	38,218	$38,\!201$	38,218	4,337,193

Differences between Nattino et al. and Sävje et al.

- Nattio et al.
 - Attempt to mimic block randomization design
 - Adapts existing matched pair algorithm
 - Fisher randomization paradigm
 - Frequentist test and confidence intervals are standard
- Sävje et al.
 - Less conventional experimental design → more researcher degrees of freedom (how to set c_x?)
 - Novel algorithm which generalizes full matching
 - Direct comparison of average outcomes
 - Quantifying uncertainty appears difficult, and is not attempted by the authors

Wu et al. (2020)

Sävje et al. (2017)

Wu et al. (2020)

- Goal: Study effect of long-term PM_{2.5} exposure on mortality rates
- Estimand: E[Y(w)], where Y is mortality rate per 100 Medicare enrollees, and w is PM_{2.5} exposure in μg/m³

Local weak unconfoundedness

Treatment W_j and covariates \mathbf{C}_j

Assumption: Local weak unconfoundedness (Imbens, 2000)

 $W_j \perp Y_j(w) \mid \mathbb{C}_j \text{ for all } w \in \mathcal{W}$

Note: does not require joint independence of all potential outcomes $\{Y_j(w)\}_{w \in W}$

Define the indicator variable $I_j(\tilde{w}) = 1$ if $W_j = \tilde{w}$ and 0 otherwise.

Assumption: Local weak unconfoundedness (Wu et al.)

 $\{I_j(\tilde{w})\}_{\tilde{w}\in[w-\delta,w+\delta]} \perp Y_j(w) \mid \mathbb{C}_j \text{ for all } z \in \mathbb{Z}$

Note: this does not require joint independence of all potential outcomes $\{Y(z)\}_{z\in \mathbb{Z}}$

That is, the assignment is unconfounded within a neighborhood of w (not all $w \in W$)

Here δ is called the *caliper*.

Matching with continuous treatments

- Define a grid of values for w
- Idea: Match on both *w* and the estimated GPS *e*, i.e. the objective function for matching is

 $m(e_j, w) = \arg \min_{k: w_k \in [w-\delta, w+\delta]} \|\lambda \cdot [e^{\star}(w_k, \mathbf{c}_k) - e_j^{\star}] + (1-\lambda) \cdot [w_k^{\star} - w_j^{\star}]\|$

- The counterfactual outcome for unit *j* at level treatment level *w* is imputed as $\hat{Y}_j(w) = Y_{m(e(w, \mathbf{c}_j), w)}^{\text{obs}}$, i.e., impute it from the unit close to *w* (not *w*_j) and close in propensity score for unit *j*, *e*_j
- Must select tuning parameters λ and δ
- Take average within each level of *w*, then use a kernel smoother to estimate the dose-response curve

Results on PM_{2.5} mortality data



Sävje et al. (2017)

Results on PM_{2.5} mortality data



Causal Exposure-response Curves: PM2.5 v.s. Mortality

Confidence bands

Open questions from Wu et al.

- Is the bootstrap a valid way to represent uncertainty?
- This method cannot estimate heterogeneous effects (e.g., subgroups of the population)

Sävje et al. (2017)

Conclusion

Conclusion

Slides at spencerwoody.github.io/talks

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