Matching Algorithms for Causal Inference with Multiple Treatments

Anthony D. Scotina

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BROWN
School of Public Health

Motivation

- Estimating causal effects of multiple treatments/interventions
- Common in many studies. For example:
  1. Estimating the effects of nutrition label use on body mass index
  2. Evaluating treatment programs for adolescent substance abuse
  3. Evaluating the cardiovascular safety of multiple drug classes for type 2 diabetes

Randomized Design

- Ideal for estimating causal effects:
  - Treatment groups are guaranteed to be similar in terms of covariates, $\mathbf{X}$.
- But...
  - Expensive
  - Unethical
  - Restricted population used in the experiments
- Sometimes, we need to rely on observational data!

The Assignment Mechanism

$$P(W = w \mid Y(1), \ldots, Y(Z), \mathbf{X})$$

1. Individualistic: Treatment assignment for one unit does not depend on covariates or potential outcomes of other units

2. Unconfoundedness:
   $P(W = w \mid Y(1), \ldots, Y(Z), \mathbf{X}) = P(W = w \mid \mathbf{X})$

3. Positivity: $0 < P(W = w \mid \mathbf{X}) < 1$ for all $w \in \mathcal{W}$

Steps in Implementing Matching Methods

Stuart (2010) –

1. Defining "closeness": Use a **distance measure** in order to determine whether an individual is a good match for another.

2. Given the distance measure, implement a **matching method**.

3. Assessing the **quality** of the matched cohort.

4. Analysis of the **outcome** and estimation of the treatment effect.

1. Defining Closeness

- Multiple treatments: Match on the **generalized propensity score** (GPS) vector,

$$\begin{aligned} R(\mathbf{X}_i) &= \{P(W_i = 1 \mid \mathbf{X}_i), \ldots, P(W_i = Z \mid \mathbf{X}_i)\} \\ &= \{r(1, \mathbf{X}_i), \ldots, r(Z, \mathbf{X}_i)\}. \end{aligned}$$

  - Some possible distance measures:

    (i) Exact (usually on $\mathbf{X}$)

    (ii) Mahalanobis distance (of $R(\mathbf{X})$, or $\mathbf{X}$)

    (iii) Linear GPS: For reference treatment t,

$$|\text{logit}[r(t, \mathbf{X}_i)] - \text{logit}[r(t, \mathbf{X}_j)]|$$

2. Implementing a Matching Method

Matching for ATT: $\mathrm{E}[Y(j) - Y(k) \mid W = t]$, $(j, k) \in \mathcal{W}^2$, $j \neq k$

- 1:1:1 nearest-neighbor matching (ex: for $Z = 3$ treatments)
  - Set a reference treatment, say, treatment 1.
  - For subject i receiving reference treatment 1, select a subject from each of treatments 2 and 3 with the smallest distance from subject i.
  - Extract the matched triplet *only if* subject i has a match in each of treatment groups 2 and 3.

- Some considerations:
  - Selecting the number of matches per subject
  - With or without replacement

2. Implementing a Matching Method – Vector Matching

- Lopez & Gutman (2017) – Match on a vector of generalized propensity scores (GPS)

- Stratify on $R(\mathbf{X}) = \{r(1, \mathbf{X}), \ldots, r(Z, \mathbf{X})\}$ using k-means clustering, match within strata.
  - Some possible matches may not be considered by VM because they are on the boundaries of clusters.

- Use the linear GPS, $|\text{logit}[r(t, \mathbf{X}_i)] - \text{logit}[r(t, \mathbf{X}_j)]|$ as the distance measure, where t is the reference treatment.

- Vector matching (VM) has been shown to produce matched sets with low covariate bias for $Z = 3$ treatments.

2. Implementing a Matching Method – Proposed Matching

- **Fuzzy Matching (FM)**: Matching within *fuzzy clusters*, using the Mahalanobis distance of pairs of GPS vector components as the distance measure
  - Fuzzy clustering allows for subjects to belong to multiple clusters
  - Ex: A subject belonging to two clusters can be matched to a subject appearing in *either* of the two clusters.
  - Matching on pairs of components of $R(\mathbf{X})$ may be useful when the total number of components is large (i.e., large Z)
- **GPS Matching (GPS)**: Matching on the Mahalanobis distance of the GPS vector, $R(\mathbf{X})$
- **Covariate Matching (COV)**: Matching on the Mahalanobis distance of the covariates, $\mathbf{X}$

3. Assessing Quality of Matching

- How well does a matching method improve covariate balance between treatment groups?

- Calculate the **standardized bias** at each covariate p for each pair of treatments j and k,

$$SB_{pjk} = \frac{\overline{X}_{pj} - \overline{X}_{pk}}{\delta_{pt}},$$

  where δ_{pt} is the standard deviation of $\mathbf{X}_p$ among subjects receiving reference treatment t.

- Extract the maximum standardized bias at each covariate,

$$Max2SB_p = \max(|SB_{p12}|, |SB_{p13}|, |SB_{p23}|, \dots).$$

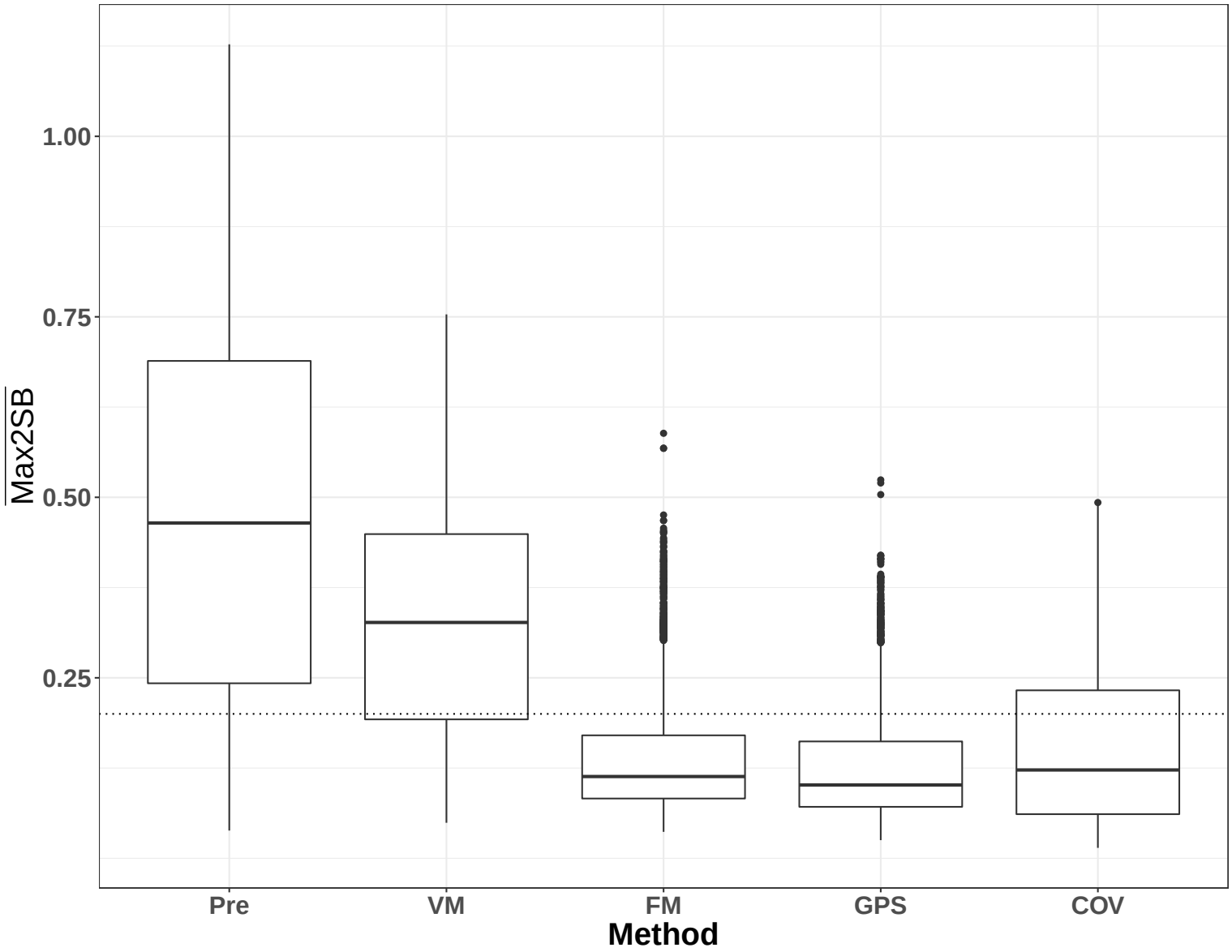
Simulations

- Performance of VM, FM, GPS, COV
  - Looked at $Z = 5$ and $Z = 10$
  - Number of covariates $P \in \{5, 10, 20\}$
- Simulation factors: covariate distributions, number of covariates, treatment group sample size, and others
- We summarized $Max2SB_p$ by averaging over p:

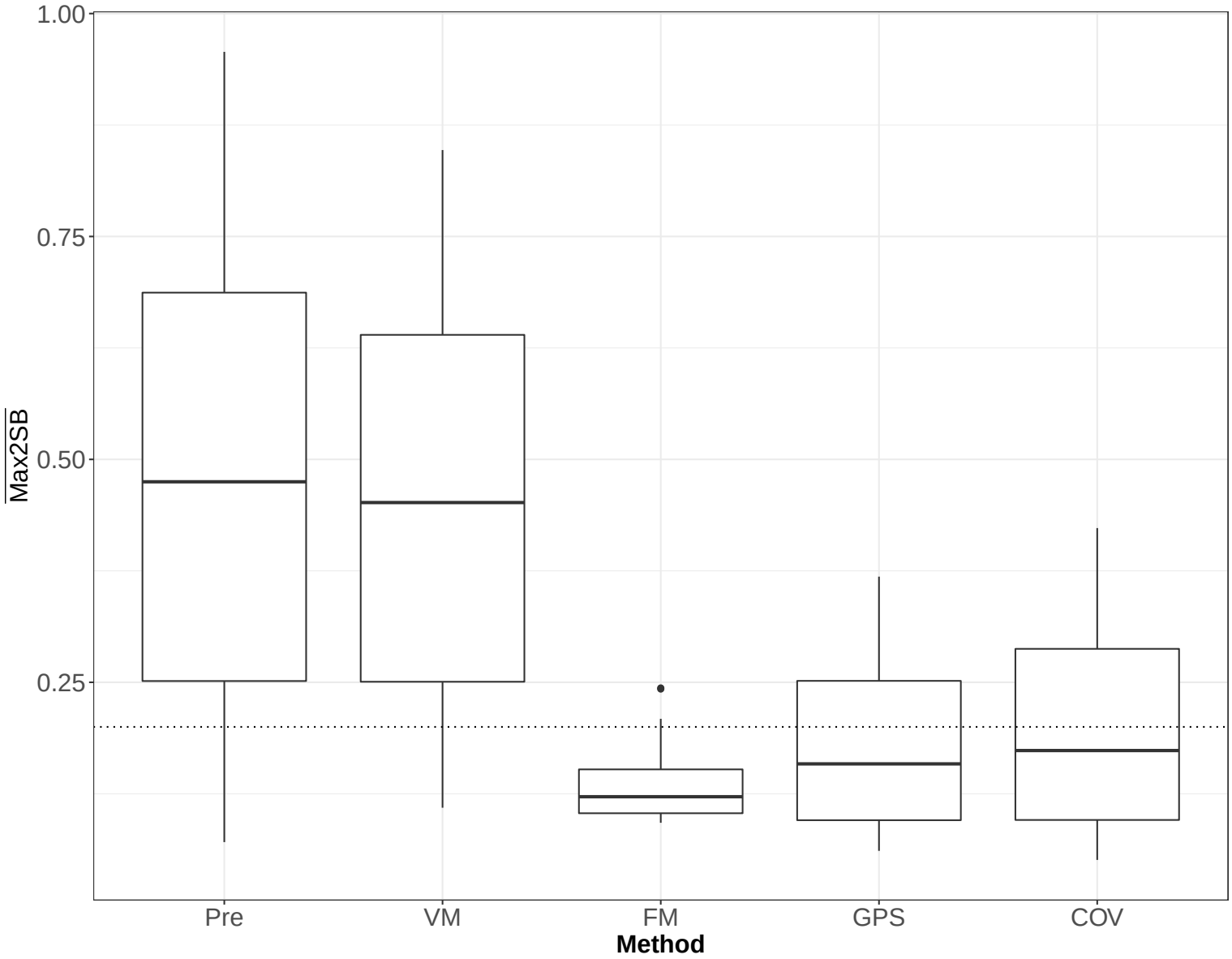
$$\overline{Max2SB} = \frac{1}{P} \sum_{p=1}^{P} Max2SB_p$$

  - Past literature advocates a cutoff of 0.20–0.25.

Results: $Z = 5$ Treatments



Results: $Z = 10$ Treatments



Discussion

- Matching on the GPS vector as a novel and effective approach to generating a well-balanced matched cohort
- Importance of study population and causal estimand
- Importance of setting
  - Number of covariates?
  - Number of treatment groups?

Contact

- Email: anthony_scotina@brown.edu
- Website: scotinastats.github.io
- Twitter: @ScotinaStats

Thank you!

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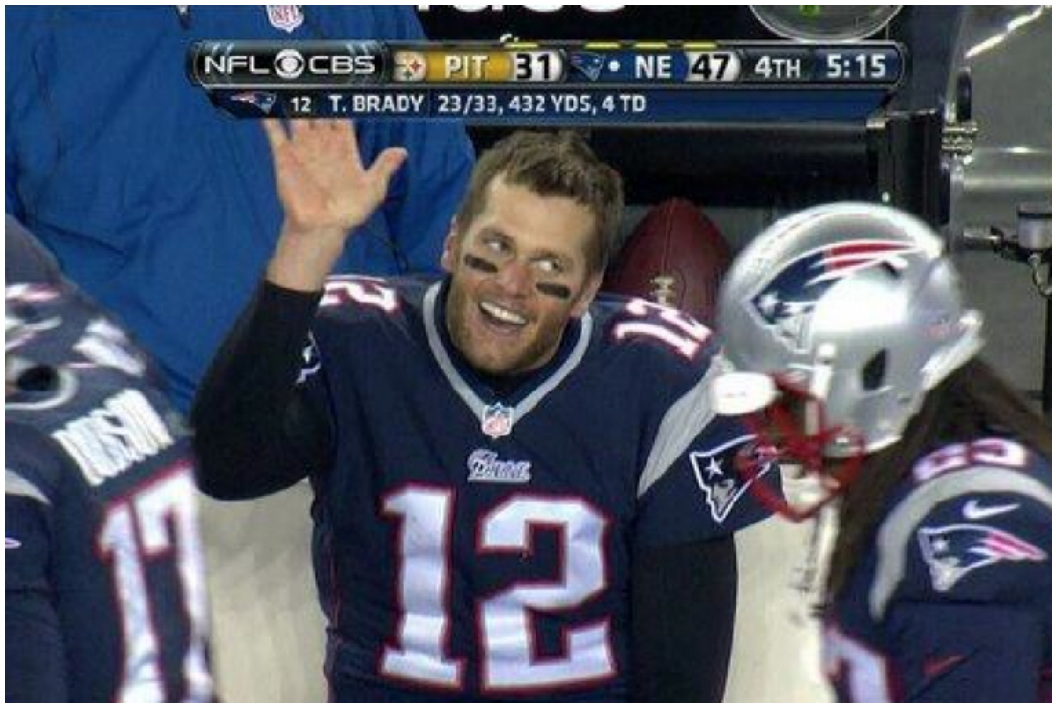

Any questions?