Development of a Python Package for Matching Observational Data

Master's Thesis Presentation

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Contents

Introduction

Introduction

Problem Setting

- Observational studies frequent in econometrics, psychology, and medical research
- This presentation: binary treatment/control variable, $\mathbf{z}$.
- Goal is to estimate ATE: $\mathbb{E}[y_{i1} - y_{i0}]$
- Solve this problem via *matching* treatment observations to control observations
- We break this down into two orthogonal problems:
  - How is distance measured?
  - How are matches assigned?
- `matching`: Python package for matching observational data.

Introduction

Notation

Now, we will introduce some notation, so we can precisely talk about construction of different matching methods.

- $X \in \mathbb{R}^{(n+m)\times p}$ of features; $X_T \in \mathbb{R}^{n\times p}, X_C \in \mathbb{R}^{m\times p}$
- $\mathbf{z} \in \{0,1\}^{n+m}$ of binary treatment assignments;
- $d : \mathbb{R}^p \times \mathbb{R}^p \to \mathbb{R}^+$ is a distance measure between feature vectors, e.g. $d(\mathbf{x}_{T_i}, \mathbf{x}_{C_j})$;
- $\mathcal{D}_d : \mathbb{R}^{n\times p} \times \mathbb{R}^{m\times p} \to \mathbb{R}^{n\times m}$ produces *biadjacency matrix*;
- Some procedures use a preprocessing function f (usually: dimension reduction or coarsening of the data).

Our framework is similar to that of Iacus, King, and Porro (2011):

$$\mathcal{D}_d(f(X)_T, f(X)_C). \tag{1}$$

Literature Review

Measuring Distance

Balancing Scores

Definition (balancing score, Rosenbaum and Rubin (1983))

A function $b(X) : \mathbb{R}^{(n+m)\times p} \mapsto \mathbb{R}^{n+m}$ is a balancing score iff

$$X \perp \mathbf{z} | b(X). \tag{2}$$

- Idea: balancing score makes observational studies more like randomized studies
- If $\mathbf{y}_0, \mathbf{y}_1 \perp \mathbf{z}|X$, *then* $\mathbf{y}_0, \mathbf{y}_1 \perp \mathbf{z}|b(X)$

These methods use L^1 distance by convention:

$$\mathcal{D}_{L^1}(b(X)_T, b(X)_C). \tag{3}$$

Measuring Distance

The Propensity Score

Definition (propensity score, Rosenbaum and Rubin (1983))

The *propensity score* is the balancing score $b(X) = \mathbb{E}[\mathbf{z}|X]$.

- Even if not used for matching, a useful diagnostic (Dehejia and Wahba 1999).
- Implicitly "weights" features by heterogeneity wrt $\mathbf{z}$.
- Continuous scores: Imai and Dyk (2004).
- Often prune potential matches with a caliper c.

Measuring Distance

The Prognostic Score

Definition (prognostic score, Hansen (2008))

The *prognostic score* is the function $b(X) = \mathbb{E}_C[\mathbf{y}|X]$.

- Note that the expectation is with respect to control data C.
  - Previous attempts to match on outcomes failed, such as Miettinen (1976).
- Implicitly "weights" features by heterogeneity wrt $\mathbf{y}$.
- "conditionality principle" suggests usefulness Hansen (2008).
- Joint use of propensity and prognostic scores Leacy and Stuart (2014).

Measuring Distance

(Almost) Exact Matching

Most notable criticism of balance scores comes from King and Nielsen (2019).

- "Lower standard".
- "Paradox of Propensity Score Matching".

What do they suggest instead?

- Coarsened Exact Matching (CEM) (Iacus, King, and Porro 2012). No balance checks required!
- Observation weights:

$$w_i = \begin{cases} 1, & i \in \text{treatment group} \\ \frac{m_C}{m_T}\frac{m_T^s}{m_C^s}, & i \in \text{control group} \end{cases}. \tag{4}$$

- ML extensions (Gupta et al. 2021): DAME (Liu et al. 2019), FLAME (Wang et al. 2021)

Measuring Distance

L^P norms and Mahalanobis distance

Norm-based measurements are rarely used without some preprocessing function f. Why? Scaling.

However, Mahalanobis is often used as a *second* step.

- Initial filter: balancing score with a caliper. Then, match on Mahalanobis distance.
- "Iterative" approach performs well in practice (Baltar, Sousa, and Westphal 2014).
- `MatchIt` has limited support (Ho et al. 2011).

Bipartite Matching Algorithms

Define a matching $\mathcal{M}$ as a set of tuples (i, j) indicating a matching between observations T_i and C_j. "Optimal" matching via the Hungarian algorithm (Munkres 1957).

$$\min_{\mathcal{M}} \sum_{(i,j)\in\mathcal{M}} d\left(\mathbf{x}_{T_i}, \mathbf{x}_{C_j}\right), \text{ s.t. } \forall (i,j),(k,l) \in \mathcal{M}, i = k \iff j = l. \tag{5}$$

- Extendable to $1 : k$ matching via b-matching.
- Slow: $O((n+m)^3)$; approximation: b-SUITOR (Khan et al. 2016).

Greedy matching: sort edges by distance, pop matches off the top.

- No optimality assured.
- Problems when matching $1 : k$ (Rosenbaum 1989).

`matching`: a Python Package for Matching Observational Data

matching

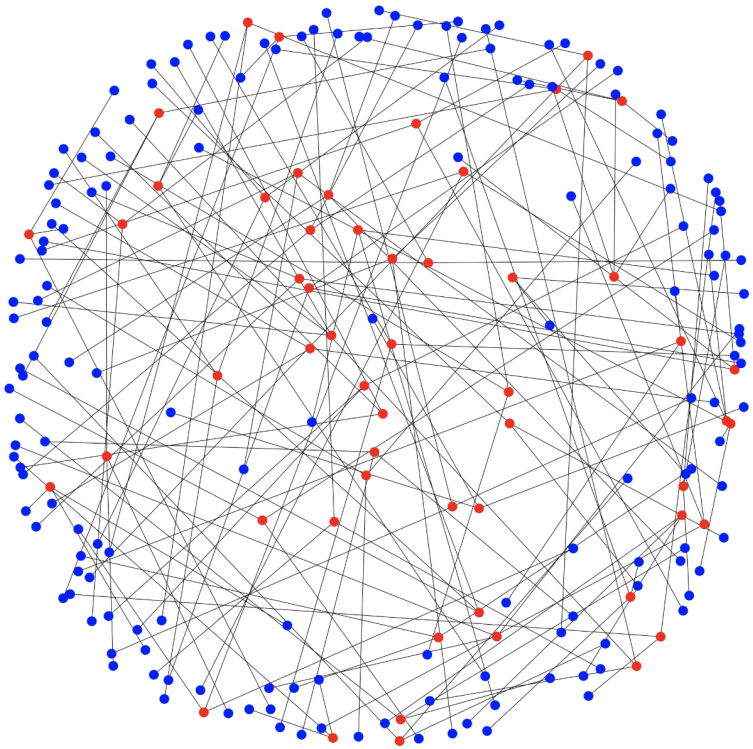
Design Goals

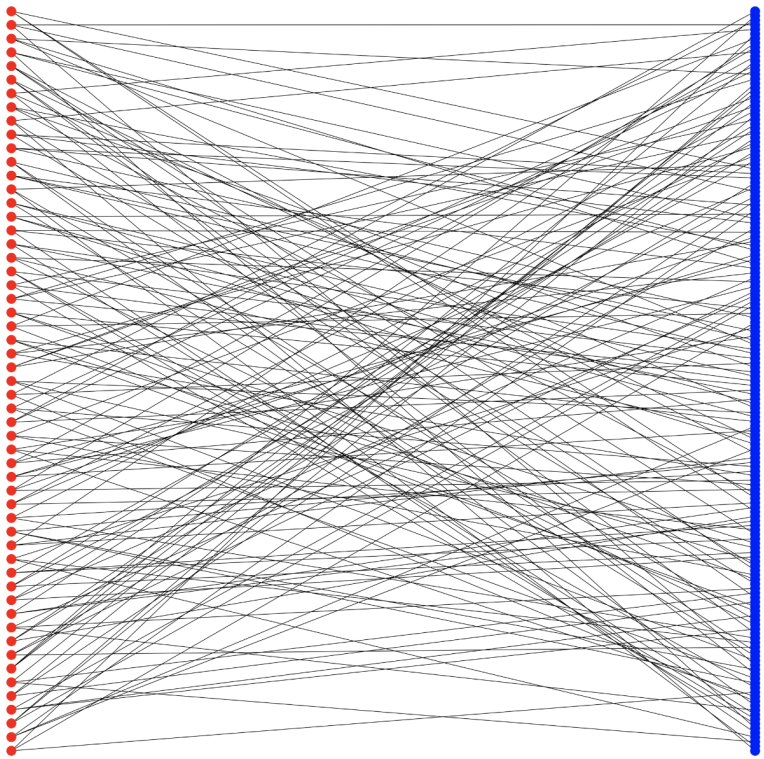
- The main data structure used is a bipartite graph.
- It supports iterative distance measures of arbitrary length/complexity.
- It supports filtering by individual matches (edge), observation (node), and match-group/strata (subgraphs)
- Includes a `preprocessing` module for coarsening data and a `balance` assessment module.

matching

Drawing Graphs

Example graphs after conducting 1 : 3 optimal matching.





Experiments

Experiments

Overview

- Hyperparameters n, m, p, θ_0, θ_1, and ρ.

$$\boldsymbol{\mu}_0 \sim \mathcal{N}(\theta_0, 0.25), \boldsymbol{\mu}_1 \sim \mathcal{N}(\theta_1, 0.25) \tag{6}$$

$$\{\mathbf{x}_C\}_{j=1}^{m} \sim \mathcal{N}(\boldsymbol{\mu}_0, \Sigma), \{\mathbf{x}_T\}_{i=1}^{n} \sim \mathcal{N}(\boldsymbol{\mu}_1, \Sigma) \tag{7}$$

$$\text{where } \Sigma_{ab} = \begin{cases} 1 & \text{if } a = b \\ \rho & \text{otherwise.} \end{cases} \tag{8}$$

- Balance metrics: mean ASMD[1], maximum ASMD, proportion of treatment observations matched.
  - In practice: use more robust metrics (Basu, Polsky, and Manning 2008; Zhu, Savage, and Ghosh 2018).
- Vary calipers $c \in \{0.05, 0.10, 0.15, \ldots, 0.50\}$.

[1] Absolute Standardized Mean Difference

Experiments

Caliper vs. Imbalance

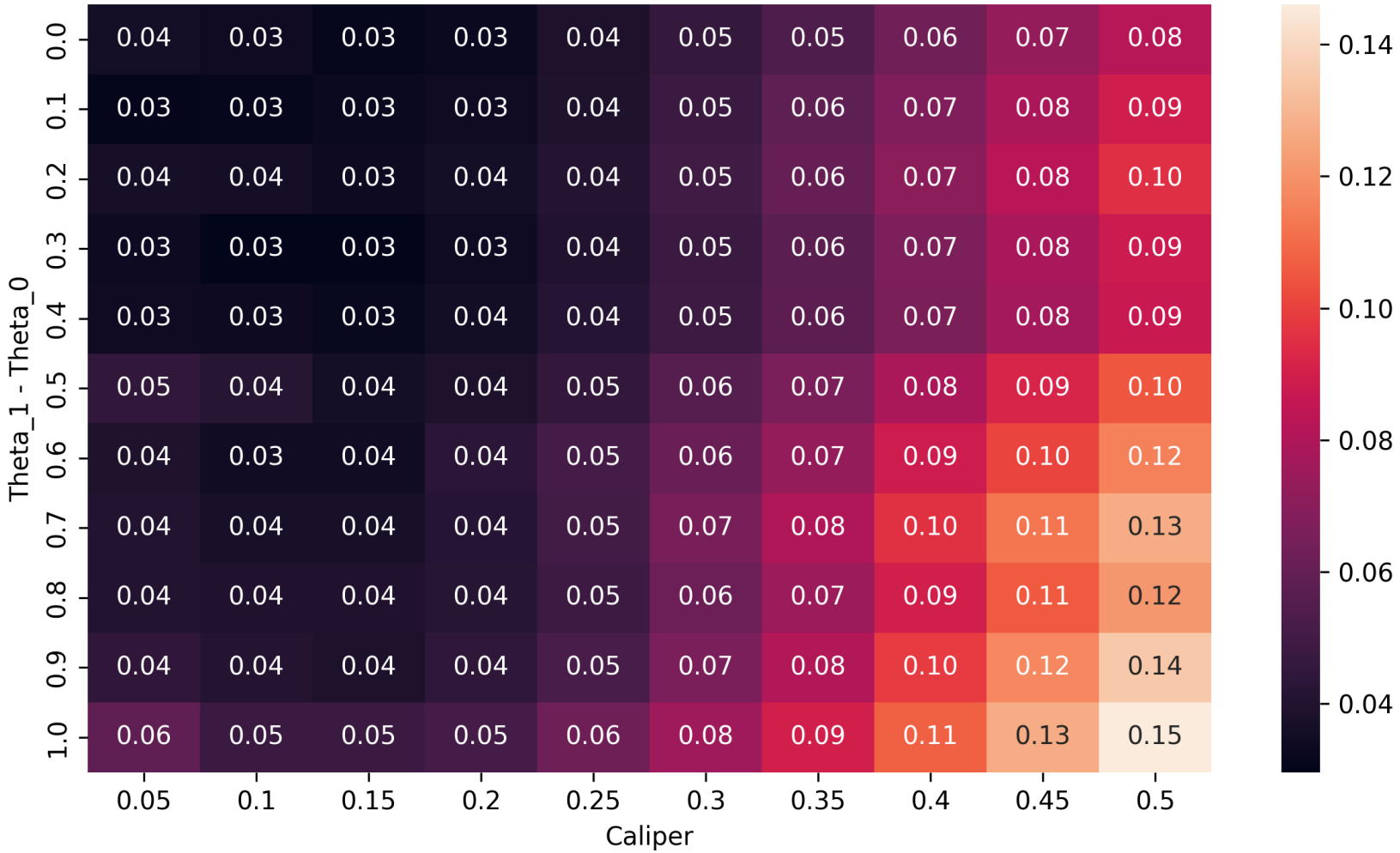
This will consider the effects of increased heterogeneity between T and C.

- $m = 750$
- $n = 250$
- $p = 5$
- $\rho = 0$
- $\theta_0 = 0$

We vary $\theta_1 \in \{0, 0.1, 0.2, \ldots, 1\}$.

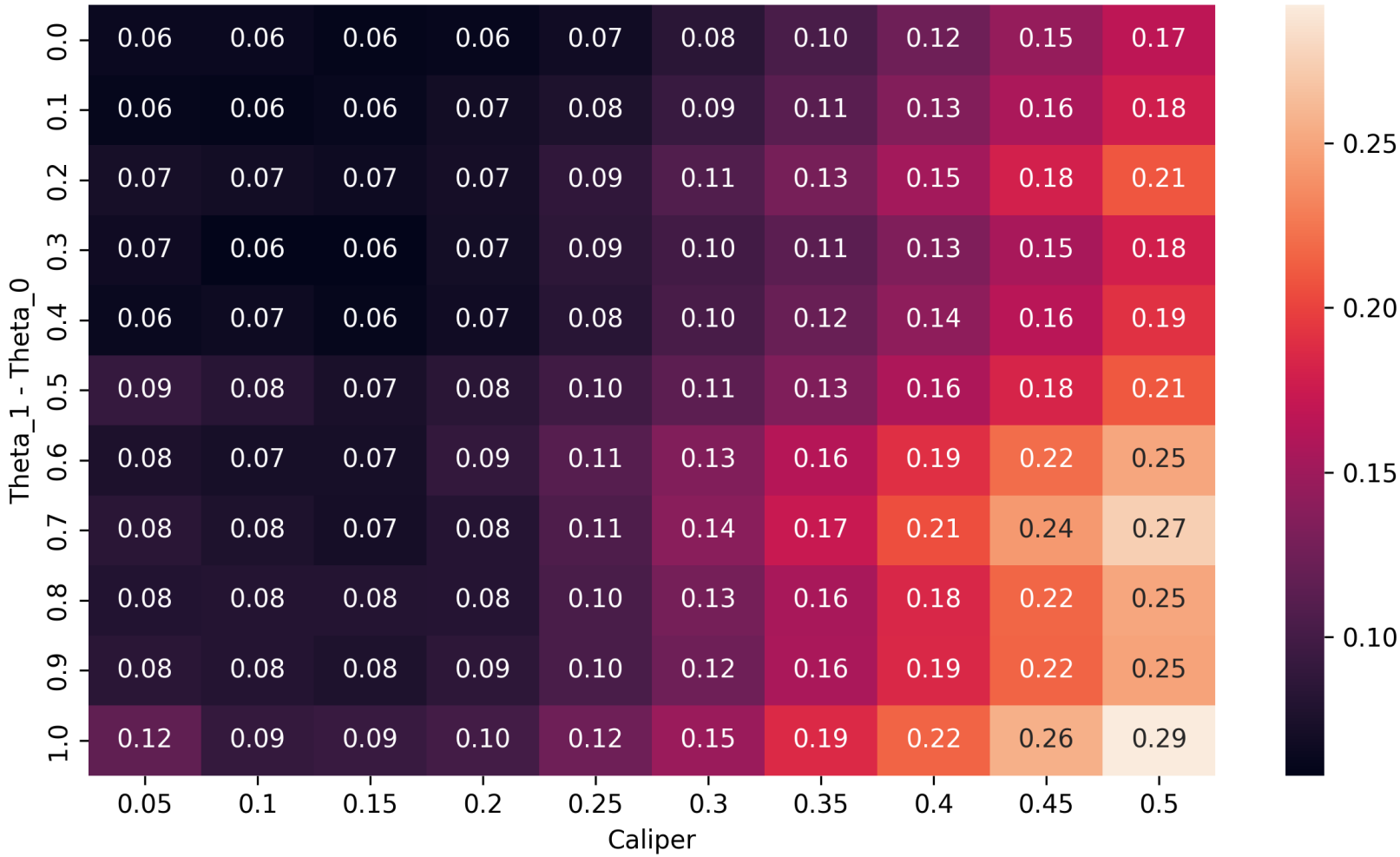
Experiments

Caliper vs. Imbalance: Mean Absolute Standardized Mean Difference



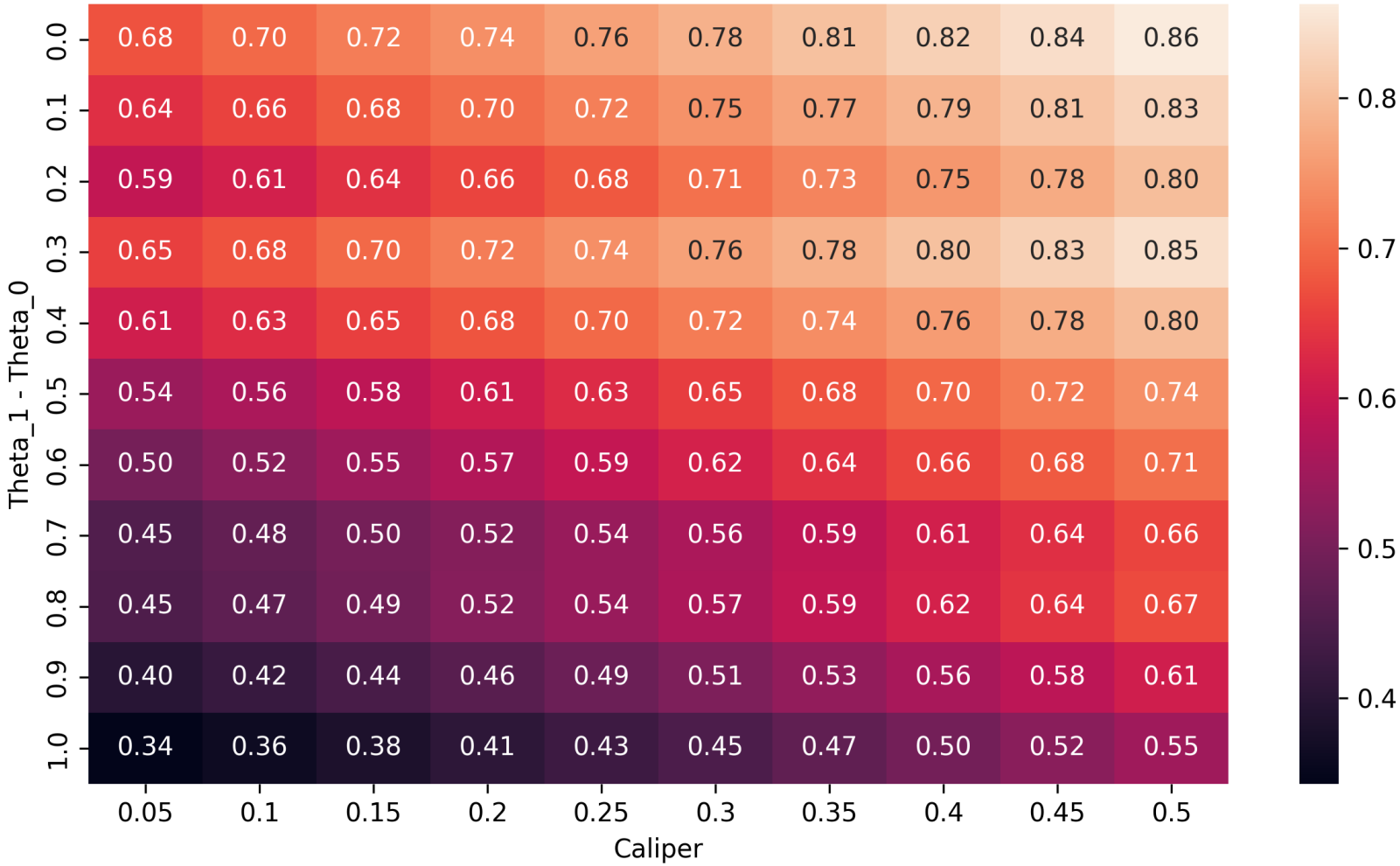
Experiments

Caliper vs. Imbalance: Maximum Absolute Standardized Mean Difference



Experiments

Caliper vs. Imbalance: Proportion of Treatment Observations Matched



Experiments

Caliper vs. Correlation

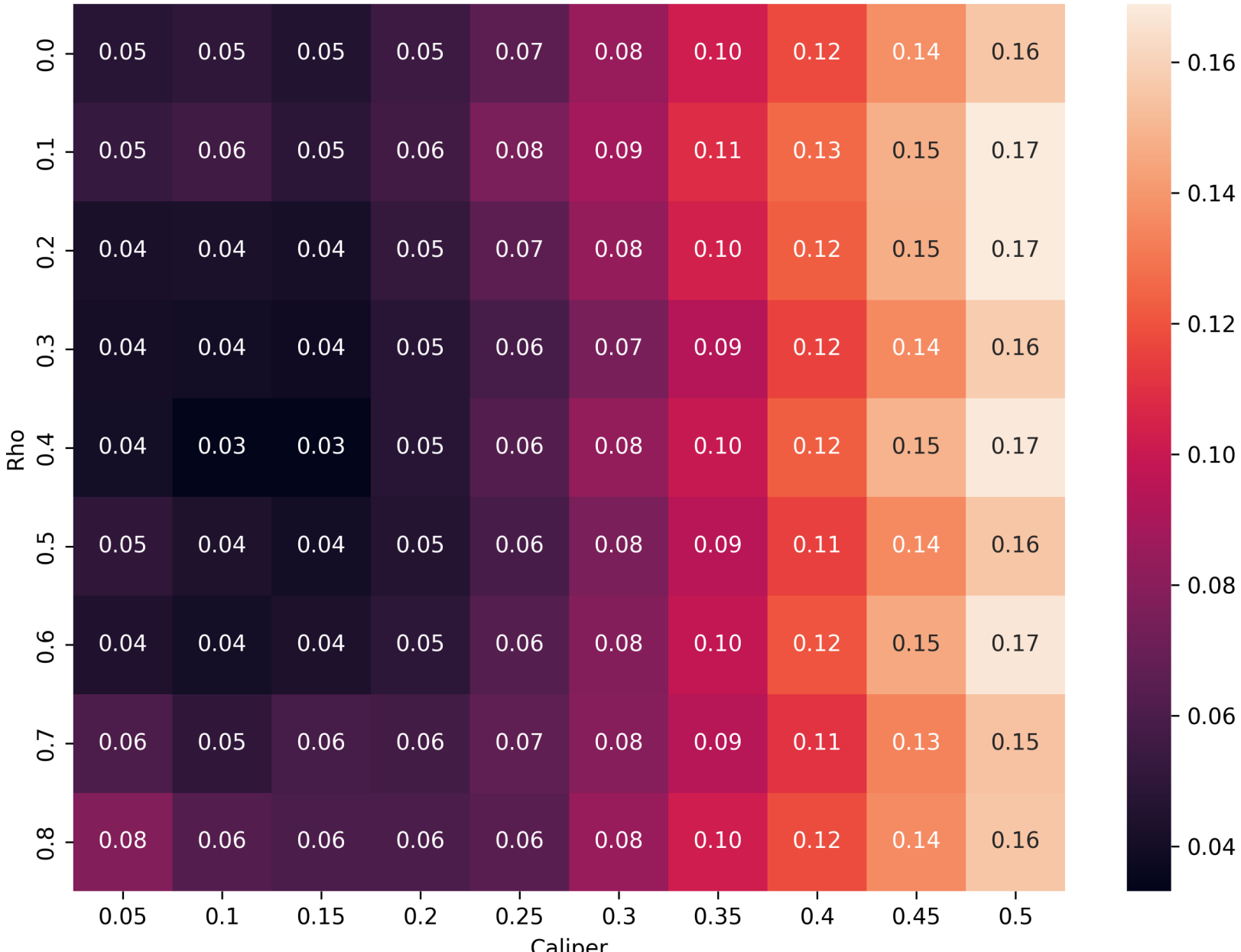
This will consider the effects of increased correlation between the features of X

- $m = 750$
- $n = 250$
- $p = 5$
- $\theta_0 = 0$
- $\theta_1 = 1$

We vary $\rho \in \{0, 0.1, 0.2, \ldots, 0.8\}$.

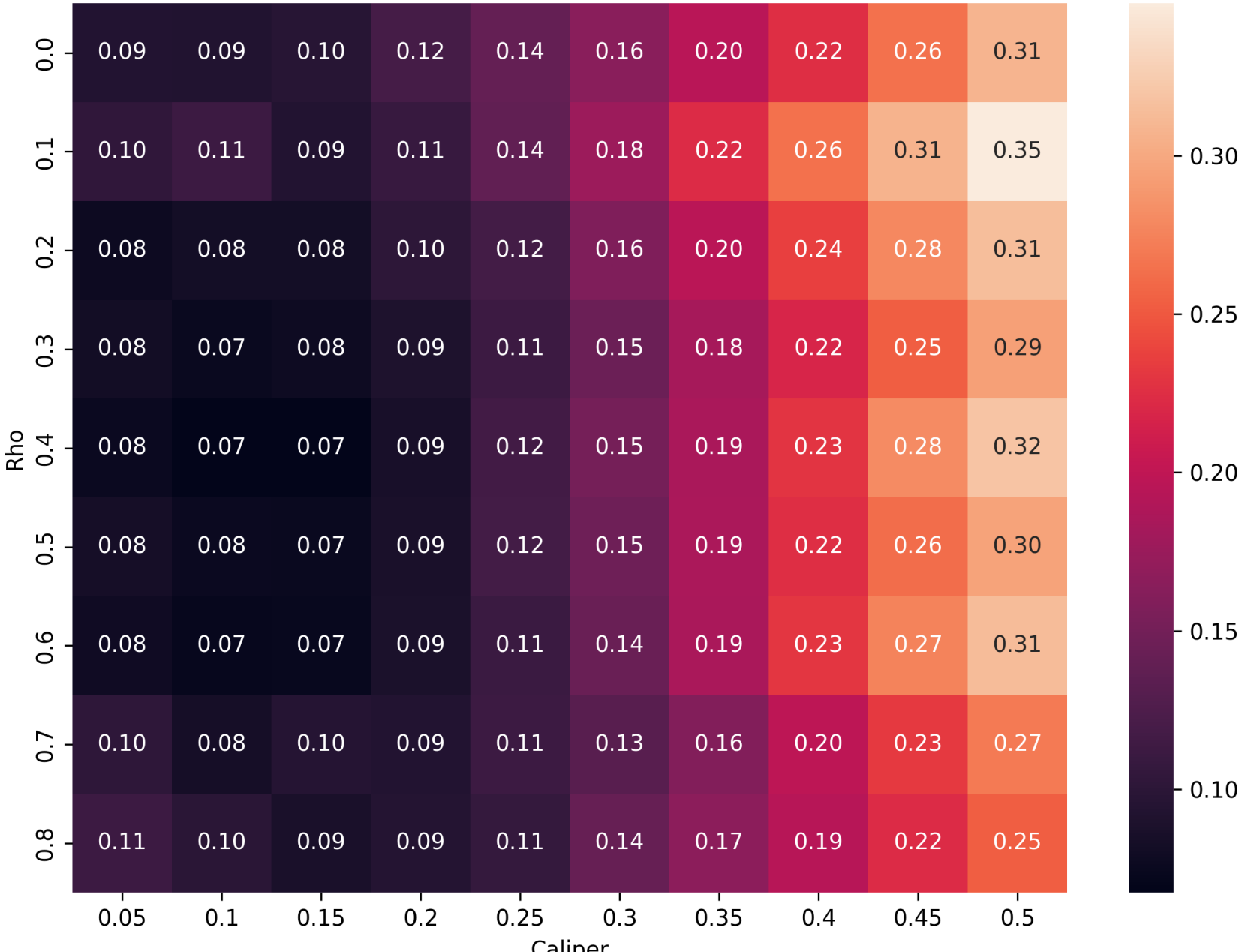
Experiments

Caliper vs. Correlation: Mean Absolute Standardized Mean Difference



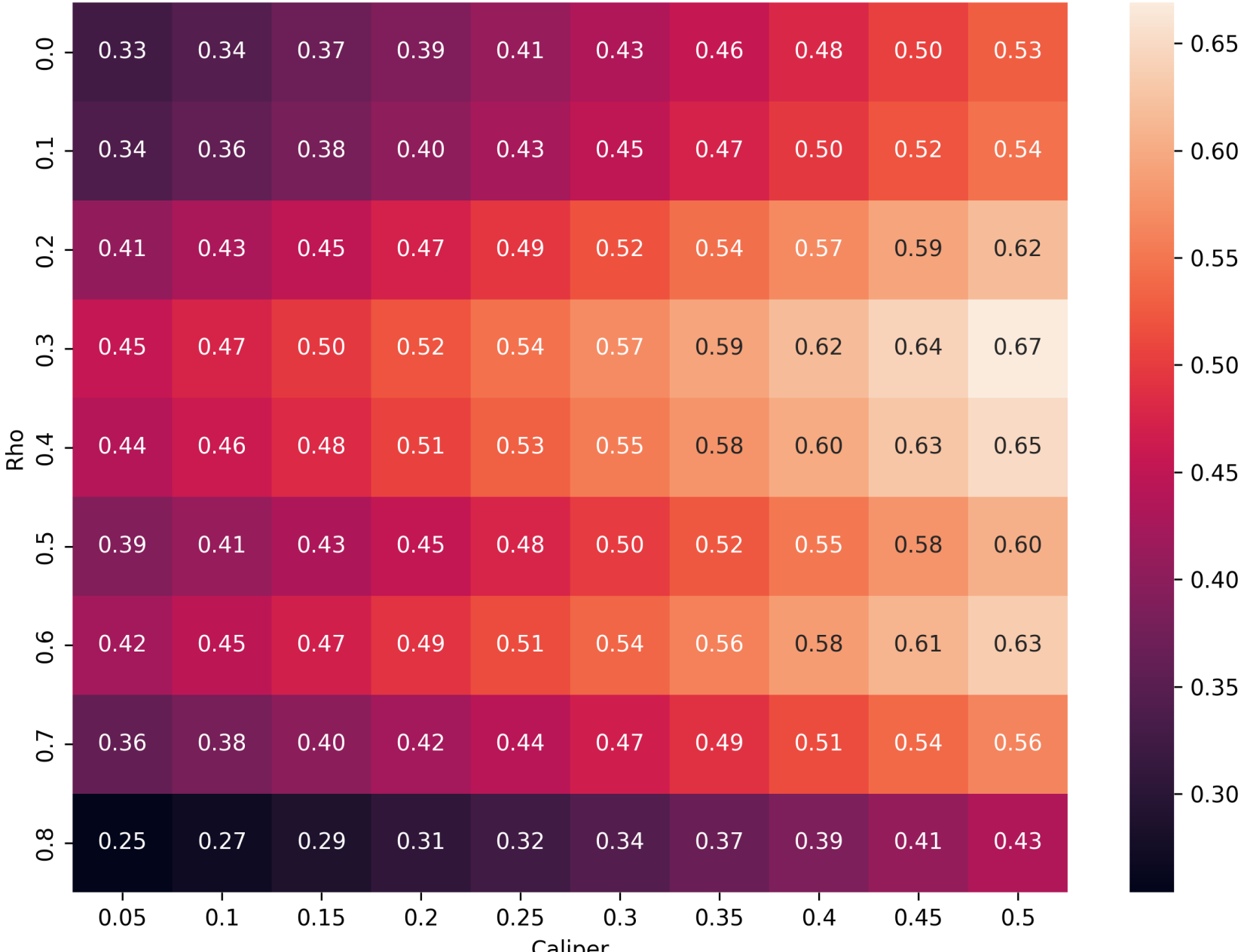
Experiments

Caliper vs. Correlation: Maximum Absolute Standardized Mean Difference



Experiments

Caliper vs. Correlation: Proportion of Treatment Observations Matched



Conclusion

Conclusion

- Common theme of numerical studies: data-dependence.
- Emphasizes the importance of
  - quality of balance metrics;
  - inspectability of matching.
- `matching` offers extreme flexibility in design of matching process.
  - The current state of the graph is always inspectable.
  - Can easily tune matches.

matching Example Code

```
1  from matplotlib import pyplot as plt
2  from matching.distance import Exact, L1Norm
3  from matching.graph import MatchingGraph
4  from matching.preprocessing import propensity_score
5
6  # Take `caliper_width` as given
7  # `X` has columns "score" and "is_nice", `z` is treatment assignments
8  mg = MatchingGraph(X, z)
9
10 # NOTE: there is also a keyword argument "exclude"
11 mg.set_edges(distance=L1Norm(max_distance=caliper_width), include=["score"])
12 mg.filter_edges(distance=Exact(), include=["is_nice"])
13
14 # Conduct optimal matching
15 mg.match(n_match=3, min_match=3, method="optimal")
16
17 # Get the matched data as a `pandas.DataFrame`
18 match_df = mg.match_data.frame
19
20 # Draw the graph of matches
21 mg.draw()
22 plt.show()
```