Simplifying Matching Methods for Causal Inference

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(Talk at Princeton University, Center for Statistics and Machine Learning, 2/6/2015)

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3 Problems, 3 Solutions

Current practice, matching as preprocessing:
violates current statistical theory.
So let's change the theory:
⇝ "A Theory of Statistical Inference for Matching Methods in Applied Causal Research" (Stefano Iacus, Gary King, Giuseppe Porro)

The most popular method (propensity score matching, used in 49,600 articles!) sounds magical:
⇝ "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)

Matching methods optimize either imbalance (≈ bias) or # units pruned (≈ variance); users need both simultaneously:
⇝ "The Balance-Sample Size Frontier in Matching Methods for Causal Inference" (Gary King, Christopher Lucas and Richard Nielsen)
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![Graph showing the relationship between Education (years) and Outcome.](image)
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The Advantage of Matching

Without Matching:
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Without Matching:

Imbalance
The Advantage of Matching

Without Matching:

Imbalance $\leadsto$ Model Dependence
The Advantage of Matching

Without Matching:

Imbalance $\rightsquigarrow$ Model Dependence $\rightsquigarrow$ Researcher discretion
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Imbalance $\leadsto$ Model Dependence $\leadsto$ Researcher discretion $\leadsto$ Bias
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\[ \text{Imbalance} \sim \text{Model Dependence} \sim \text{Researcher discretion} \sim \text{Bias} \]
Current Practice: Matching as Preprocessing

- $Y_i$ dependent variable, $T_i$ (1=treated, 0=control), $X_i$ confounders

- Treatment Effect for treated observation $i$:
  \[ \text{TE}_i = Y_i - Y_i(0) = \text{observed} - \text{unobserved} \]

- Quantities of Interest:
  1. SATT: Sample Average Treatment effect on the Treated:
     \[ \text{SATT} = \text{mean}_{i \in \{T_i=1\}}(\text{TE}_i) \]
  2. FSATT: Feasible Average Treatment effect on the Treated

- Estimate $Y_i(0)$ with $Y_j$ from matched ($X_i \approx X_j$) control

- Prune nonmatches: reduces imbalance & model dependence

- Big convenience: Follow preprocessing with whatever statistical method you'd have used without matching
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Existing Theory of Inference:

- Framework: simple random sampling from a population
- Exact matching: Rarely possible; but would make estimation easy

- Assumptions:
  - Unconfoundedness: $T \perp Y(0) | X$ (Healthy & unhealthy get meds)
  - Common support: $Pr(T = 1 | X) < 1$ ($T = 0, 1$ are both possible)

- Approximate matching (bias correction, new variance estimation):
  - common, but all current practices would have to change

Alternative Theory of Inference:

- Framework: stratified random sampling from a population
- Define $A$: a stratum in a partition of the product space of $X$ (“continuous” variables have natural breakpoints)
- We already know and use these procedures: Group strong and weak partisans; Don’t match college dropout with 1st year grad student

- Assumptions:
  - Set-wide Unconfoundedness: $T \perp Y(0) | A$
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- Fits all common matching methods & practices; no asymptotics
- Easy extensions for: multi-level, continuous, & mismeasured treatments; $A$ too wide, $n$ too small
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Approximating Randomized Experiments

Types of experiments:

1. Compete Randomization: Treatment assignment by coin flips
   - Balance on $X$: only on average
   - Balance on unmeasured vars: only on average

2. Fully Blocked: Match pairs on $X$ (exactly), then flip coins
   - Balance on $X$: perfect in sample
   - Balance on unmeasured vars: only on average

Fully blocked dominates complete randomization for: imbalance, model dependence, power, efficiency, bias, research costs, and robustness.

Matching methods approximate which experiment?

- PSMT: complete randomization
- Other methods: fully blocked

$\Rightarrow$ As we show, other methods usually dominate PSM (but wait, it gets worse for PSM)
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  - PSM: complete randomization
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Approximating Randomized Experiments

- Types of experiments:
  1. *Compete Randomization*: Treatment assignment by coin flips
     - Balance on $X$: only on average

- Fully blocked dominates complete randomization for:
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  - power,
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1. Preprocess (Matching)
   - $\text{Distance}(X_i, X_j) = \sqrt{(X_i - X_j)' S^{-1} (X_i - X_j)}$
   - Match each treated unit to the nearest control unit
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2. Estimation Difference in means or a model

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Mahalanobis Distance Matching

Age vs. Education (years)
Mahalanobis Distance Matching

Age
12 14 16 18 20 22 24 26 28
20
30
40
50
60
70
80

Education (years)
Method 2: Coarsened Exact Matching

1. Preprocess (Matching)
   - Temporarily coarsen $X$ as much as you're willing
   - e.g., Education (grade school, high school, college, graduate)
   - Apply exact matching to the coarsened $X$, $C(X)$
   - Sort observations into strata, each with unique values of $C(X)$
   - Prune any stratum with 0 treated or 0 control units
   - Pass on original (uncoarsened) units except those pruned

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   - Need to weight controls in each stratum to equal treateds

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   - Easier, but still iterative
Coarsened Exact Matching
Coarsened Exact Matching

Age
12 14 16 18 20 22 24 26 28

Education

Graph showing the relationship between age and education with various symbols indicating data points.
Coarsened Exact Matching

- Old
- Retirement
- Senior Discounts
- The Big 40
- Don't trust anyone over 30
- Drinking age

Education:
- HS
- BA
- MA
- PhD
- 2nd PhD

Senior Discounts

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Education
Coarsened Exact Matching

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Education

HS  BA  MA  PhD  2nd PhD

C  C  C  CC  CC  C  C  CC  CC  C  TT  T  T  TT  TT  T  T  TT
Method 3: Propensity Score Matching

1. Preprocess (Matching)
   - Reduce \( k \) elements of \( X \) to scalar \( \pi_i \equiv \Pr(T_i = 1 \mid X) = \frac{1}{1 + e^{-X_i \beta}} \)
   - Distance (\( X_i, X_j \)) = \| \pi_i - \pi_j \|
   - Match each treated unit to the nearest control unit
   - Control units: not reused; pruned if unused
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Propensity Score Matching

Education (years) vs. Age

- Education levels: 12, 16, 20, 24, 28
- Age levels: 20, 30, 40, 50, 60, 70, 80

Symbols:
- C: Control
- T: Treatment
Propensity Score Matching

Age

Propensity Score

Education (years)
Propensity Score Matching

Age

Propensity Score

Education (years)
Propensity Score Matching

- Age
- Education (years)
- Propensity Score

The diagram shows a scatter plot with Age on the y-axis and Education (years) on the x-axis. Lines connect points with different education levels, indicating matching in the propensity score.
Propensity Score Matching

The graph above illustrates the relationship between Education (years) and Age. The data points are color-coded, with different symbols representing different categories or treatments. The x-axis represents Education (years), ranging from 12 to 28 years, and the y-axis represents Age, ranging from 20 to 80 years. The scatter plot shows how the data points are distributed across these variables.
PSM’s Statistical Properties

• PSM is Inefficient:
  • Efficient relative to complete randomization, but
  • Inefficient relative to full blocking (Imai, King, and Nall: up to 600% difference in SEs in experiments)

• The PSM Paradox:
  • If data are balanced to begin with, or after some pruning, \( \hat{\pi} \approx 0.5 \) (or constant within strata)
  • Random matching increases imbalance!
  • Approximating complete randomization (by pruning) \( \Rightarrow \) higher imbalance \( \Rightarrow \) more inefficiency
  • If the data have no good matches, the paradox won’t be a problem but you’re cooked anyway

• PSM is Biased:
  • Imbalance \( \Rightarrow \) Inefficency \( \Rightarrow \) Model dependence \( \Rightarrow \) Bias

• Curse of Dimensionality Problems:
  • The Promise: avoid it by balancing on \( \pi \) rather than \( X \)
  • The Reality: The PSM Paradox is bigger with more covariates
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  - Approximating complete randomization (by pruning)$\Rightarrow$ higher imbalance$\Rightarrow$ more inefficiency
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  - If data are balanced to begin with, or after some pruning, $\hat{\pi} \approx 0.5$ (or constant within strata) $\Rightarrow$ matching is at random
  - Random matching increases imbalance!
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  - Imbalance $\Rightarrow$ Inefficiency $\Rightarrow$ Model dependence $\Rightarrow$ Bias

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  - The Promise: avoid it by balancing on $\pi$ rather than $X$
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PSM is Blind Where Other Methods Can See
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PSM is Blind Where Other Methods Can See
What Does PSM Match?

MDM Matches

PSM Matches

Controls: \(X_1, X_2 \sim \text{Uniform}(0,5)\)
Treateds: \(X_1, X_2 \sim \text{Uniform}(1,6)\)
PSM Increases Model Dependence & Bias

Model Dependence

Bias

\[ Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i \]
\[ \epsilon_i \sim N(0, 1) \]
The Propensity Score Paradox

Finkle et al. (2012)

Nielsen et al. (2011)
The Matching Frontier

- Bias-Variance trade off $\Rightarrow$ Imbalance Trade Off
- Frontier = matched dataset with lowest imbalance for each n
- (Maybe we can beat MDM/CEM for a given #pruned?)
- To use, make 2 choices:
  1. Quantity of interest: SATT (prune Cs only) or FSATT
  2. Fixed- or variable-ratio matching
- Result:
  - Simple to use
  - No need to choose or use a matching method
  - All solutions are optimal
  - No iteration or diagnostics required
  - No cherry picking possible; you see everything optimal
The Matching Frontier

- Bias-Variance trade off $\leadsto$ Imbalance-$n$ Trade Off

  Frontier $=$ matched dataset with lowest imbalance for each $n$
The Matching Frontier

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How hard is the frontier to calculate?

Consider 1 point on the SATT frontier:

- Start with matrix of $N$ control units $X_0$
- Calculate imbalance for all $(N\times n)$ subsets of rows of $X_0$
- Choose subset with lowest imbalance

Evaluations needed to compute the entire frontier:

- $(N\times n)$ evaluations for each sample size $n = N, N-1, \ldots, 1$
- The combination is the (gargantuan) “power set”
- e.g., $N > 300$ requires more imbalance evaluations than elementary particles in the universe

$\Rightarrow$ It’s hard to calculate!

We develop algorithms for the (optimal) frontier which:

- runs very fast
- operate as “greedy” but we prove are optimal
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185 Ts; pruning most 16,252 Cs won’t increase variance much

Huge bias-variance trade-off after pruning most Cs

Estimates converge to experiment after removing bias

No mysteries: basis of inference clearly revealed
Constructing the FSATT Mahalanobis Frontier
Constructing the FSATT Mahalanobis Frontier

Remaining Data

- Covariate 1
- Covariate 2

Frontier

- Treated
- Control
- Next to remove

Number of Observations Dropped

Average Mahalanobis Discrepancy

0 5 10 15 20

0.0
0.1
0.2
0.3
0.4
Constructing the FSATT Mahalanobis Frontier

Remaining Data

Frontier

- Covariate 1
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- Treated
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- Next to remove

- Average Mahalanobis Discrepancy
- Number of Observations Dropped
Constructing the FSATT Mahalanobis Frontier

Remaining Data

- Covariate 1
- Covariate 2

Frontier

- Number of Observations Dropped
- Average Mahalanobis Discrepancy

Treated
Control
Next to remove
Constructing the FSATT Mahalanobis Frontier

Remaining Data

- Covariates 1 and 2
- Treated
- Control
- Next to remove

Frontier

- Average Mahalanobis Discrepancy
- Number of Observations Dropped
Constructing the FSATT Mahalanobis Frontier

Remaining Data

- Covariate 1
- Covariate 2

Frontier

- Number of Observations Dropped
- Average Mahalanobis Discrepancy

○ Treated
○ Control
○ Next to remove
Constructing the FSATT Mahalanobis Frontier

Remaining Data

Frontier

- Covariate 1
- Covariate 2

- Treated
- Control
- Next to remove

- Number of Observations Dropped
- Average Mahalanobis Discrepancy
Constructing the FSATT Mahalanobis Frontier

### Remaining Data

- **Covariate 1**
- **Covariate 2**

### Frontier

- **Average Mahalanobis Discrepancy**
- **Number of Observations Dropped**

- "Treated"
- "Control"
- "Next to remove"
Constructing the FSATT Mahalanobis Frontier

Remaining Data

- Covariate 1
- Covariate 2
- Treated
- Control
- Next to remove

Frontier

- Number of Observations Dropped
- Average Mahalanobis Discrepancy
Constructing the FSATT Mahalanobis Frontier

**Remaining Data**

- Covariate 1
- Covariate 2

**Frontier**

- Treated
- Control
- Next to remove

**Average Mahalanobis Discrepancy**

- Number of Observations Dropped

<table>
<thead>
<tr>
<th>Number of Observations Dropped</th>
<th>Average Mahalanobis Discrepancy</th>
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</thead>
<tbody>
<tr>
<td>0</td>
<td>0.4</td>
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<tr>
<td>5</td>
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<tr>
<td>10</td>
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</tr>
<tr>
<td>15</td>
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</tr>
<tr>
<td>20</td>
<td>0.0</td>
</tr>
</tbody>
</table>
Constructing the FSATT Mahalanobis Frontier

Remaining Data

Frontier

Remaining Data

Covariate 1

Covariate 2

-1.0 −0.5 0.0 0.5 1.0

-1.0

-0.5

0.0

0.5

1.0

●

●

●

●

●

●

●

Treated

Control

Next to remove

Number of Observations Dropped

Average Mahalanobis Discrepancy

0 5 10 15 20

0.0

0.1

0.2

0.3

0.4

●

●

●

●

●

●

●

●

●
Constructing the FSATT Mahalanobis Frontier

Remaining Data

Frontier

Covariate 1
Covariate 2

-1.0 -0.5 0.0 0.5 1.0

-1.0 -0.5 0.0 0.5 1.0

0 5 10 15 20

0.0 0.1 0.2 0.3 0.4

0.0 0.1 0.2 0.3 0.4

Treated
Control
Next to remove

Number of Observations Dropped
Constructing the FSATT Mahalanobis Frontier

**Remaining Data**

- **Covariate 1**
- **Covariate 2**

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<th>Values</th>
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<tr>
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<td></td>
<td></td>
<td></td>
</tr>
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</tr>
</tbody>
</table>

**Frontier**

- Treated
- Control
- Next to remove

**Average Mahalanobis Discrepancy**

<table>
<thead>
<tr>
<th>Number of Observations Dropped</th>
<th>0.4</th>
<th>0.3</th>
<th>0.2</th>
<th>0.1</th>
<th>0.0</th>
</tr>
</thead>
<tbody>
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<td>●</td>
<td>●</td>
<td>●</td>
<td>●</td>
<td>●</td>
</tr>
<tr>
<td>5</td>
<td></td>
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<tr>
<td>10</td>
<td></td>
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<td></td>
</tr>
<tr>
<td>15</td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>20</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Constructing the FSATT Mahalanobis Frontier

Remaining Data

Frontier

Covariate 1

Covariate 2

-1.0 -0.5 0.0 0.5 1.0

-1.0

-0.5

0.0

0.5

1.0

●

●

●

●

●

Treated

Control

Next to remove

Number of Observations Dropped

Average Mahalanobis Discrepancy

0 5 10 15 20

0.0

0.1

0.2

0.3

0.4

0.0

0.1

0.2

0.3

0.4

0 5 10 15 20
Constructing the FSATT Mahalanobis Frontier

Remaining Data

- Covariate 1
- Covariate 2
- Treated
- Control
- Next to remove

Frontier

- Average Mahalanobis Discrepancy
- Number of Observations Dropped
Constructing the FSATT Mahalanobis Frontier

Remaining Data

- Covariate 1
- Covariate 2

-1.0   -0.5   0.0   0.5   1.0

-1.0

-0.5

0.0

0.5

1.0

Treated

Control

Next to remove

Frontier

Number of Observations Dropped

Average Mahalanobis Discrepancy

0 5 10 15 20

0.0

0.1

0.2

0.3

0.4
Constructing the FSATT Mahalanobis Frontier

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- Covariate 2

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- Control
- Next to remove

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- Average Mahalanobis Discrepancy
Constructing the FSATT Mahalanobis Frontier

- Warning: figure omits details and the proof!
Constructing the FSATT Mahalanobis Frontier

Remaining Data

Frontier

- Treated
- Control
- Next to remove

• Warning: figure omits details and the proof!
• Very fast; works with any continuous imbalance metric
Constructing the L1/L2 SATT Frontier

![Graph showing frequency bars for different bins labeled Bin1 to Bin6 with Treatment and Control categories. A scatter plot on the right shows the number of observations dropped along the x-axis and L2 values along the y-axis.]

- Frequency bars indicate the number of observations in each bin for Treatment (blue) and Control (red) categories.
- Number of observations dropped in each bin are as follows:
  - Bin1: Treatment 5, Control 4
  - Bin2: Treatment 6, Control 7
  - Bin3: Treatment 2, Control 3
  - Bin4: Treatment 3, Control 3
  - Bin5: Treatment 3, Control 2
  - Bin6: Treatment 1, Control 2

- Scattered points on the right graph show the L2 values against the number of observations dropped.
Constructing the L1/L2 SATT Frontier

![Bar chart showing frequency by bin for Treatment and Control groups.]

![Graph showing number of observations dropped vs. L2 norm.]

Number of Observations Dropped: 23 / 26
Constructing the L1/L2 SATT Frontier

![Bar chart showing frequency distribution across different bins for Treatment and Control groups.]

- Bin 1: Treatment 5, Control 4
- Bin 2: Treatment 6, Control 7
- Bin 3: Treatment 2, Control 3
- Bin 4: Treatment 3, Control 5
- Bin 5: Treatment 3, Control 2
- Bin 6: Treatment 1, Control 2

![Graph showing number of observations dropped against L2 value.]

L2 values: 0.12, 0.10, 0.08, 0.06, 0.04, 0.02, 0.00
Number of observations dropped: 0, 2, 4, 6, 8, 10
Constructing the L1/L2 SATT Frontier

Frequency

<table>
<thead>
<tr>
<th>Bin</th>
<th>Treatment</th>
<th>Control</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bin_1</td>
<td>5</td>
<td>4</td>
</tr>
<tr>
<td>Bin_2</td>
<td>6</td>
<td>3</td>
</tr>
<tr>
<td>Bin_3</td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>Bin_4</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>Bin_5</td>
<td>4</td>
<td>2</td>
</tr>
<tr>
<td>Bin_6</td>
<td>1</td>
<td>2</td>
</tr>
</tbody>
</table>

Number of Observations Dropped

L2

<table>
<thead>
<tr>
<th>Number of Observations Dropped</th>
<th>L2</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0.12</td>
</tr>
<tr>
<td>2</td>
<td>0.10</td>
</tr>
<tr>
<td>4</td>
<td>0.08</td>
</tr>
<tr>
<td>6</td>
<td>0.06</td>
</tr>
<tr>
<td>8</td>
<td>0.04</td>
</tr>
<tr>
<td>10</td>
<td>0.02</td>
</tr>
</tbody>
</table>
Constructing the L1/L2 SATT Frontier

![Graph showing frequency and number of observations dropped in different bins.]

- **Bin 1**: Frequency: 4, Treatment: 4, Control: 4
- **Bin 2**: Frequency: 6, Treatment: 7, Control: 6
- **Bin 3**: Frequency: 2, Treatment: 3, Control: 2
- **Bin 4**: Frequency: 3, Treatment: 4, Control: 3
- **Bin 5**: Frequency: 3, Treatment: 2, Control: 2
- **Bin 6**: Frequency: 1, Treatment: 1, Control: 2

- **Number of Observations Dropped**: L2
  - Frequency: 0.12
  - Number of Observations Dropped: 0, 2, 4, 6, 8, 10
Constructing the L1/L2 SATT Frontier

![Bar chart showing frequency in bins for Treatment and Control groups.

![Graph showing the number of observations dropped against L2 values.]}
Constructing the L1/L2 SATT Frontier

![Graph showing frequency distribution across different bins.

- Bin 1: 4 Treatment, 4 Control
- Bin 2: 6 Treatment, 6 Control
- Bin 3: 2 Treatment, 2 Control
- Bin 4: 3 Treatment, 4 Control
- Bin 5: 3 Treatment, 2 Control
- Bin 6: 1 Treatment, 2 Control]

![Graph showing L2 value against number of observations dropped.

- L2 value decreases as the number of observations dropped increases.

- Number of observations dropped range from 0 to 10.

- L2 value range from 0.12 to 0.00.

Legend:
- □ Treatment
- ■ Control
Constructing the L1/L2 SATT Frontier

Frequency

Number of Observations Dropped

L2

Treatment Control

Bin1  Bin2  Bin3  Bin4  Bin5  Bin6

4   4   2   2   3   3   2   2   2   2   1   1

0.00  0.02  0.04  0.06  0.08  0.10  0.12

0  2  4  6  8  10
Constructing the L1/L2 SATT Frontier

![Bar chart and line graph showing frequency and L2 values for different bins.]

- **Bin 1**: Frequency 4, Treatment 4, Control 4
- **Bin 2**: Frequency 6, Treatment 6, Control 6
- **Bin 3**: Frequency 2, Treatment 2, Control 2
- **Bin 4**: Frequency 3, Treatment 3, Control 3
- **Bin 5**: Frequency 2, Treatment 2, Control 2
- **Bin 6**: Frequency 1, Treatment 1, Control 2

![Line graph showing L2 values against the number of observations dropped.]

- Number of Observations Dropped: 0 to 10
- L2 Values: 0 to 0.12
Constructing the L1/L2 SATT Frontier

![Bar chart showing frequency for different bins labeled Bin1 to Bin6. Bars are color-coded to represent Treatment and Control groups.](image)

![Graph showing L2 values against number of observations dropped.](image)
Constructing the L1/L2 SATT Frontier

Warning: This figure omits some technical details too!

Works very fast, even with very large data sets
Constructing the L1/L2 SATT Frontier

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Conclusions

• The Matching Frontier
  - Fast; easy; no iteration; Software: MatchingFrontier
  - No need to choose among matching methods
  - Optimal results from your choice of imbalance metric

• Propensity score matching:
  - Approximates complete, not fully blocked, experiments
  - Ignores information; exacerbates model dependence

  • Some mistakes with PSM:
    - Controlling for irrelevant covariates;
    - Adjusting experimental data;
    - Reestimating propensity score after eliminating noncommon support;
    - 1/4 caliper on propensity score;
    - Not switching to other methods.

• Theory of Inference for Matching
  - Switch from simple to stratified random sampling
  - Justifies current practices
  - Clarifies how to improve inferences

  ⇝ Using more information is simpler and more powerful
Conclusions

• The Matching Frontier
Conclusions

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For more information, papers, & software

GaryKing.org