Simplifying Matching Methods for Causal Inference

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University of Wisconsin, 2/7/2021

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3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 336,000 articles!) sounds magical:

2. Do powerful methods have to be complicated?
   ⇝ “Causal Inference Without Balance Checking: Coarsened Exact Matching” (PA, 2011. Stefano Iacus, Gary King, and Giuseppe Porro)

3. Matching methods optimize either imbalance (≈ bias) or # units pruned (≈ variance); users need both simultaneously:
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### Matching to Reduce Model Dependence

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<table>
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<th>Education (years)</th>
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![Graph showing data points and linear regression lines](attachment:image)
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The Problems Matching Solves

• Qualitative choice from unbiased estimates = biased estimator
  e.g., Choosing from results of 50 randomized experiments
• Choosing based on “plausibility” is probably worse
• Conscientious effort doesn’t avoid biases (Banaji 2013)
• People do not have easy access to their own mental processes or feedback to avoid the problem (Wilson and Brekke 1994)
• Experts overestimate their ability to control personal biases more than nonexperts, and more prominent experts are the most overconfident (Tetlock 2005)
• “Teaching psychology is mostly a waste of time” (Kahneman 2011)
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Without Matching:

Imbalance
The Problems Matching Solves

Without Matching:

Imbalance $\sim$ Model Dependence
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Without Matching:

Imbalance $\mapsto$ Model Dependence $\mapsto$ Researcher discretion

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A central project of statistics: Automating away human discretion
What’s Matching?

- $Y_i$, dep var,
- $T_i$ (1=treated, 0=control),
- $X_i$ confounders

Treatment Effect for treated observation $i$:

$$TE_i = Y_i - Y_i(0) = \text{observed - unobserved}$$

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

Quantities of Interest:

1. SATT: Sample Average Treatment effect on the Treated:

$$SATT = \text{Mean}_{i \in \{T_i = 1\}}(TE_i)$$

2. FSATT: Feasible SATT (prune badly matched treateds too)

- Big convenience: Follow preprocessing with whatever statistical method you’d have used without matching
- Pruning nonmatches makes control vars matter less: reduces imbalance, model dependence, researcher discretion, & bias
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Matching: Finding Hidden Randomized Experiments

Types of Experiments

- **Balance**
  - **Covariates:**
    - *Complete Randomization*
    - *Fully Blocked*
  - **Observed**
    - On average
  - **Unobserved**
    - On average

\[\Rightarrow\] Fully blocked dominates complete randomization for:
- Imbalance
- Model dependence
- Power
- Efficiency
- Bias
- Research costs
- Robustness.

E.g., Imai, King, Nall 2009: SEs 600% smaller!

Goal of Each Matching Method (in Observational Data)

- **PSM:** complete randomization
- Other methods:** fully blocked
- Other matching methods dominate PSM

(wait, it gets worse)
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Goal of Each Matching Method (in Observational Data)

- PSM: complete randomization
- Other methods: fully blocked
- Other matching methods dominate PSM (wait, it gets worse)
Matching: Finding Hidden Randomized Experiments

Types of Experiments

- Complete Randomization

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On average, fully blocked randomization dominates complete randomization for: imbalance, model dependence, power, efficiency, bias, research costs, robustness. E.g., Imai, King, Nall 2009: SEs 600% smaller!
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Goal of Each Matching Method (in Observational Data)

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Other matching methods dominate PSM (wait, it gets worse)

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Matching: Finding Hidden Randomized Experiments

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#### Goal of Each Matching Method (in Observational Data)
Matching: Finding Hidden Randomized Experiments

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Goal of Each Matching Method (in Observational Data)

- PSM: complete randomization
Matching: Finding Hidden Randomized Experiments

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Goal of Each Matching Method (in Observational Data)

- PSM: complete randomization
- Other methods: fully blocked
Matching: Finding Hidden Randomized Experiments

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Goal of Each Matching Method (in Observational Data)

- PSM: complete randomization
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Goal of Each Matching Method (in Observational Data)

- PSM: complete randomization
- Other methods: fully blocked
- Other matching methods dominate PSM (wait, it gets worse)
Method 1: Mahalanobis Distance Matching

1. Preprocess (Matching)
   - \[ \text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)'S^{-1}(X_c - X_t)} \]
   - (Mahalanobis is for methodologists; in applications, use Euclidean!)
   - Match each treated unit to the nearest control unit
   - Control units: not reused; pruned if unused
   - Prune matches if Distance > caliper
   - (Many adjustments available to this basic method)

2. Estimation
   - Difference in means or a model
Method 1: Mahalanobis Distance Matching
(Approximates Fully Blocked Experiment)

1. Preprocess (Matching)
   - $\text{Distance}(X_c, X_t) = \sqrt{(X_c - X_t)^T S^{-1} (X_c - X_t)}$
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2. **Estimation** Difference in means or a model
Mahalanobis Distance Matching

Age
12 14 16 18 20 22 24 26 28

Education (years)
Mahalanobis Distance Matching

Age

Education (years)

12 14 16 18 20 22 24 26 28

20

30

40

50

60

70

80

T T

T T

TT TT T TT

TTT TT

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T TT

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C

C C

CC

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Mahalanobis Distance Matching

Age
12 14 16 18 20 22 24 26 28
20
30
40
50
60
70
80
T T
T T
TT TT T TT
TTT TT
T
T TT
C
C
C C
CC
C
C
C CCC
C
C
CC C C C
C

Education (years)
Best Case: Mahalanobis Distance Matching
Best Case: Mahalanobis Distance Matching
Best Case: Mahalanobis Distance Matching

![Graph showing data points scattered across the diagram with labels for Age and Education (years).]
Method 2: Coarsened Exact Matching
(Most powerful easy-to-use approach)

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 $X$
   - 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

2. Estimation
   - Difference in means or a model
   - Weight controls in each stratum to equal treateds

10 / 25
Method 2: Coarsened Exact Matching
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   - Weight controls in each stratum to equal treateds
Coarsened Exact Matching
Coarsened Exact Matching

Education

- HS
- BA
- MA
- PhD
- 2nd PhD

Drinking age

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

CCC C
CC CC
C CC C CCC CCCC CCC CC CCC CCCCCC
C CCC CC C
T T
T T
TT TT T TT
TTT TT
T
T TT

Education
Coarsened Exact Matching

Education

Don't trust anyone over 30
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Education

HS  BA  MA  PhD  2nd PhD
Coarsened Exact Matching

Education

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Old
Coarsened Exact Matching

Age

Education

12 14 16 18 20 22 24 26 28

20

30

40

50

60

70

80

C

C

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Best Case: Coarsened Exact Matching
Best Case: Coarsened Exact Matching
Best Case: Coarsened Exact Matching
Best Case: Coarsened Exact Matching

![Diagram showing a scatter plot with age on the y-axis and education on the x-axis. The data points are represented by 'C' and 'T'.]
Method 3: Propensity Score Matching

1. Preprocess (Matching)
   - Reduce $k$ elements of $X$ to scalar $\pi_i \equiv \Pr(T_i = 1 | X) = \frac{1}{1 + e^{-X_i \beta}}$
   - Distance($X_c, X_t$) = $|\pi_c - \pi_t|$
   - Match each treated unit to the nearest control unit
   - Control units: not reused; pruned if unused
   - Prune matches if Distance > caliper

   (Many adjustments available to this basic method)

2. Estimation
   - Difference in means or a model
Method 3: Propensity Score Matching
(Approximates Completely Randomized Experiment)

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2. Estimation Difference in means or a model
Method 3: Propensity Score Matching
(Approximates Completely Randomized Experiment)

1. **Preprocess** (Matching)

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2. **Estimation** Difference in means or a model
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   - Control units: not reused; pruned if unused
   - Prune matches if Distance $>$ caliper
   - (Many adjustments available to this basic method)

2. Estimation  Difference in means or a model
Propensity Score Matching

Age
12 16 20 24 ...

Education (years)
Propensity Score Matching

Age

Education (years)

Propensity Score
Propensity Score Matching
Propensity Score Matching

Education (years)

Age

Education (years)

Age
Best Case: Propensity Score Matching
Best Case: Propensity Score Matching

The image shows a scatter plot with the x-axis labeled "Education (years)" ranging from 12 to 28, the y-axis labeled "Age" ranging from 20 to 80, and the z-axis labeled "Propensity Score" ranging from 0 to 1. The plot visualizes the relationship between education, age, and propensity scores.
Best Case: Propensity Score Matching

Age

Education (years)

Propensity Score

0 1

0 20 30 40 50 60 70 80

12 16 20 24 28
Best Case: Propensity Score Matching

Age

Education (years)
Best Case: Propensity Score Matching is Suboptimal
PSM’s Statistical Properties

1. Low Standards:
   - Sometimes helps, never optimizes
   - Efficient relative to complete randomization, but
     Inefficient relative to (the more powerful) full blocking
   - Other methods usually dominate:

2. The PSM Paradox:
   - When you do “better,” you do worse
   - Background: Random matching increases imbalance
   - When PSM approximates complete randomization (to begin
     with or, after some pruning)
     \[ \hat{\pi} = \pi \text{ (or constant within strata)} \]
     \[ \Rightarrow \] pruning at random
     \[ \Rightarrow \] Imbalance
     \[ \Rightarrow \] Inefficency
     \[ \Rightarrow \] Model dependence
     \[ \Rightarrow \] Bias
   - If the data have no good matches, the paradox won’t be a
     problem but you’re cooked anyway.
   - Doesn’t PSM solve the curse of dimensionality problem?
     Nope. The PSM Paradox gets worse with more covariates
PSM’s Statistical Properties

1. **Low Standards:** Sometimes helps, never optimizes
PSM’s Statistical Properties

1. **Low Standards**: Sometimes helps, never optimizes
   - *Efficient* relative to complete randomization, but

\[ X_c = X_t \Rightarrow \pi_c = \pi_t \]

\[ X_c = X_t \neq \Rightarrow X_c = X_t \]

2. **The PSM Paradox**: When you do “better,” you do worse
   - Background: Random matching increases imbalance
   - When PSM approximates complete randomization (to begin with or, after some pruning)
     - \( \hat{\pi} \approx 0 \) (or constant within strata)
     - \( \Rightarrow \) pruning at random
     - \( \Rightarrow \) Imbalance
     - \( \Rightarrow \) Inefficency
     - \( \Rightarrow \) Model dependence
     - \( \Rightarrow \) Bias
   - If the data have no good matches, the paradox won’t be a problem but you’re cooked anyway.
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     - *Nope.*
     - The PSM Paradox gets worse with more covariates
PSM’s Statistical Properties

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   - *Efficient* relative to complete randomization, but
   - *Inefficient* relative to (the more powerful) full blocking

2. **The PSM Paradox:** When you do “better,” you do worse
   - Background: Random matching increases imbalance
   - When PSM approximates complete randomization (to begin with or, after some pruning)
     \[ \hat{\pi}_c = \hat{\pi}_t \Rightarrow \pi_c = \pi_t \neq \pi_t \Rightarrow X_c = X_t \]
   - All \( \hat{\pi} \approx 0 \) (or constant within strata)
   - Pruning at random
   - Imbalance
   - Inefficency
   - Model dependence
   - Bias

   - If the data have no good matches, the paradox won’t be a problem but you’re cooked anyway.

   - Doesn’t PSM solve the curse of dimensionality problem?
     Nope.

   - The PSM Paradox gets worse with more covariates
1. Low Standards: Sometimes helps, never optimizes
   - *Efficient* relative to complete randomization, but
   - *Inefficient* relative to (the more powerful) full blocking
   - Other methods usually dominate:

\[
\begin{align*}
\pi_c &= \pi_t \\
\Rightarrow 
\pi_c &= \pi_t \\
\not\Rightarrow 
\end{align*}
\]

2. The PSM Paradox: When you do “better,” you do worse
   - Background: Random matching increases imbalance
   - When PSM approximates complete randomization (to begin with or, after some pruning) 
     \[
     \hat{\pi} \approx 0 \quad \text{or constant within strata}
     \]
     \[
     \Rightarrow \quad \text{pruning at random} \\
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PSM is Blind Where Other Methods Can See
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What Does PSM Match?

MDM Matches

Controls: $X_1, X_2 \sim \text{Uniform}(0,5)$

Treated: $X_1, X_2 \sim \text{Uniform}(1,6)$

PSM Matches
PSM Increases Model Dependence & Bias

Model Dependence

Bias

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

Nielsen et al. (AJPS, 2011)

Similar pattern for >20 other real data sets we checked
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The Matching Frontier

- Frontier = matched dataset with lowest imbalance for each $n$
- Bias-Variance trade off $\Rightarrow$ Imbalance-$n$ Trade Off
- 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
- Choose an imbalance metric, then run.
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How hard is the frontier to calculate?

Consider 1 point on the SATT frontier:

1. Start with matrix of $N$ control units $X_0$.
2. Calculate imbalance for all $\binom{N}{n}$ subsets of rows of $X_0$.
3. Choose subset with lowest imbalance.

Evaluations needed to compute the entire frontier:

- $\binom{N}{n}$ 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.

It’s hard to calculate!

We develop algorithms for the (optimal) frontier which:

- Run very fast.
- Operate as “greedy” but are proven to be optimal.
- Do not require evaluating every subset.
- Work with very large data sets.
- Is the exact frontier (no approximation or estimation).

It’s easy to calculate!
How hard is the frontier to calculate?

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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
Conclusions

• 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.

• A Simple and Powerful Method: CEM
• A New General Approach: The Matching Frontier
  • Fast; easy; no iteration; Software: MatchingFrontier
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  • Optimal results from your choice of imbalance metric

⇝ Using more information is simpler and more powerful
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• \(\rightsquigarrow\) Using more information is simpler and more powerful
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