Matching Methods for Causal Inference & 21 Other Topics

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1GaryKing.org
3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 76,900 articles!) sounds magical:
   – "Why Propensity Scores Should Not Be Used for Matching" (Gary King, Richard Nielsen)

2. Do powerful methods have to be complicated?
   – "Causal Inference Without Balance Checking: Coarsened Exact Matching" (PA, 2011. Stefano M 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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• Qualitative choice from unbiased estimates = biased estimator
e.g., Choosing from results of 50 randomized experiments

• Choosing based on “plausibility” is probably worse
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• People do not have easy access to their own mental processes
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• Experts overestimate their ability to control personal biases
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Without Matching:

Imbalance $\leadsto$ Model Dependence $\leadsto$ Researcher discretion
The Problems Matching Solves

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Imbalance \Rightarrow Model Dependence \Rightarrow Researcher discretion \Rightarrow Bias
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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:
  \[ TE_i = Y_i - Y_i(0) = \text{observed} - \text{unobserved} \]

- 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:
     \[ SATT = \text{Mean} \left( \sum_{i \in \{T_i = 1\}} (TE_i) \right) \]
  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
  - 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!
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Goal of Each Matching Method (in Observational Data)

- **PSM:** complete randomization
- **Other methods:** fully blocked
- **Other matching methods dominate PSM**
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$\Rightarrow$ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence, power, efficiency, bias,
Matching: Finding Hidden Randomized Experiments

Types of Experiments

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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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Matching: Finding Hidden Randomized Experiments

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

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Method 1: Mahalanobis Distance Matching
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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
12 14 16 18 20 22 24 26 28

Education (years)
20
30
40
50
60
70
80

C

T
Mahalanobis Distance Matching

Education (years)
Age
12 14 16 18 20 22 24 26 28
20
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Mahalanobis Distance Matching

Education (years)
Age
12 14 16 18 20 22 24 26 28
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CC C C C
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Mahalanobis Distance Matching

Education (years)
Age
12 14 16 18 20 22 24 26 28
20 30 40 50 60 70 80
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TTT TT
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T TT
C
C
C C
CC
C
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C CCC
C
C
CC C C C
C
Best Case: Mahalanobis Distance Matching
Best Case: Mahalanobis Distance Matching
Best Case: Mahalanobis Distance Matching

![Scatter plot showing the relationship between age and education level. The x-axis represents education (years) ranging from 12 to 28, and the y-axis represents age ranging from 20 to 80. The scatter plot includes data points marked with 'T' and 'C', indicating some form of analysis or classification.](image-url)
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 $X$
   - 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
Method 2: Coarsened Exact Matching
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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
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T TT
Coarsened Exact Matching

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HS  BA  MA  PhD  2nd PhD

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C
C C
CC
CC C CC
C
TT T T TT
TT T
T
T TT
Best Case: Coarsened Exact Matching
Best Case: Coarsened Exact Matching
Best Case: Coarsened Exact Matching

![Graph showing Education vs Age with 'C' markers at various points on the graph.]

- Education
- Age
- 12 14 16 18 20 22 24 26 28
- 20 30 40 50 60 70 80
- 'C' markers at different coordinates on the graph.
Best Case: Coarsened Exact Matching

![Graph showing scatter plot with 'C' markers indicating data points for Education vs Age. The x-axis represents Education ranging from 12 to 28, and the y-axis represents Age ranging from 20 to 80. The data points are spread out across the graph.]
Method 3: Propensity Score Matching

1. Preprocess (Matching)
   • Reduce $k$ elements of $X$ to scalar $\pi_i = \Pr(T_i = 1 | X) = \frac{1}{1 + e^{-x_i \beta}}$
   • 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)
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)

2. Estimation Difference in means or a model
Method 3: Propensity Score Matching
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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)

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     \[ \pi_i \equiv \Pr(T_i = 1|X) = \frac{1}{1+e^{-x_i\beta}} \]
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   - Match each treated unit to the nearest control unit
   - Control units: not reused; pruned if unused

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

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($X_c$, $X_t$) = $|\pi_c - \pi_t|$
   - Match each treated unit to the nearest control unit
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2. **Estimation** Difference in means or a model
Method 3: Propensity Score Matching
(Approximates Completely Randomized Experiment)

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   - Prune matches if Distance $>$ *caliper*
   - (Many adjustments available to this basic method)

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

Propensity Score

Age

Education (years)

0
1

12 16 20 24 28
20
30
40
50
60
70
80
C
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CC
C
C
C
C
C
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0
Propensity Score Matching

Age

Education (years)

Propensity Score
Propensity Score Matching

Education (years)

Age

12 16 20 24 ...

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1
0

Propensity Score

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C C C C

C C C C

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T T T T

T T T T

T T T T

T T T T

T T T T

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

- Age
- Education (years)
- Propensity Score

Graph showing the relationship between age, education, and propensity score.
Best Case: Propensity Score Matching

![Graph showing a scatter plot with Education (years) on the x-axis and Age on the y-axis. The plot includes various markers and labels indicating different data points.](image-url)
Best Case: Propensity Score Matching is Suboptimal
Random Pruning Increases Imbalance

• "Random pruning": pruning process is independent of $X$

• Discrete example

- Sex-balanced dataset: treated $M_t$, $F_t$, controls $M_c$, $F_c$
- Randomly prune 1 treated & 1 control $\Rightarrow$ 4 possible datasets: 2 balanced $\{M_t, M_c\}$, $\{F_t, F_c\}$, 2 imbalanced $\{M_t, F_c\}$, $\{F_t, M_c\}$

$\Rightarrow$ random pruning increases imbalance

• Continuous example

- Dataset: $T \in \{0, 1\}$ randomly assigned; $X$ any fixed variable; with $n$ units
- Measure of imbalance: squared difference in means $d^2$, where $d = \bar{X}_t - \bar{X}_c$
- $E(d^2) = V(d) \propto 1/n$ (note: $E(d) = 0$)
- Random pruning $\Rightarrow n$ declines $\Rightarrow E(d^2)$ increases

$\Rightarrow$ random pruning increases imbalance

• Result is completely general (see math in the paper)
Random Pruning Increases Imbalance

Deleting data only helps if you’re careful!

• “Random pruning”: pruning process is independent of \( X \)

• Discrete example

  Sex-balanced dataset: treateds \( M_t, F_t \), controls \( M_c, F_c \)

  Randomly prune 1 treated & 1 control

  \( \Rightarrow \) 4 possible datasets:
  
  2 balanced \{ \( M_t, M_c \), \( F_t, F_c \) \}

  2 imbalanced \{ \( M_t, F_c \), \( F_t, M_c \) \}

  \( \Rightarrow \) random pruning increases imbalance

• Continuous example

  Dataset: \( T \in \{ 0, 1 \} \) randomly assigned; \( X \) any fixed variable; with \( n \) units

  Measure of imbalance: squared difference in means \( d^2 \), where

  \( d = \overline{X}_t - \overline{X}_c \)

  \( E(d^2) = V(d) \propto 1/n \) (note: \( E(d) = 0 \))

  Random pruning \( \Rightarrow n \) declines \( \Rightarrow E(d^2) \) increases

  \( \Rightarrow \) random pruning increases imbalance

• Result is completely general (see math in the paper)
Random Pruning Increases Imbalance
Deleting data only helps if you’re careful!

• “Random pruning”: pruning process is independent of $X$

- Discrete example
  - Sex-balanced dataset: treated $M_t$, $F_t$, controls $M_c$, $F_c$
  - Randomly prune 1 treated & 1 control $\Rightarrow$ 4 possible datasets:
    - 2 balanced: $\{M_t, M_c\}$, $\{F_t, F_c\}$
    - 2 imbalanced: $\{M_t, F_c\}$, $\{F_t, M_c\}$
  - $\Rightarrow$ random pruning increases imbalance

- Continuous example
  - Dataset: $T \in \{0, 1\}$ randomly assigned; $X$ any fixed variable; with $n$ units
  - Measure of imbalance: squared difference in means $d^2$, where $d = \bar{X}_t - \bar{X}_c$
  - $E(d^2) = V(d) \propto 1/n$ (note: $E(d) = 0$)
  - Random pruning $\Rightarrow n$ declines $\Rightarrow E(d^2)$ increases
  - $\Rightarrow$ random pruning increases imbalance

- Result is completely general (see math in the paper)
Random Pruning Increases Imbalance
Deleting data only helps if you’re careful!

- “Random pruning”: pruning process is independent of $X$
- Discrete example

**Sex-balanced dataset: treated $M_t$, $F_t$, controls $M_c$, $F_c$**

Randomly prune 1 treated & 1 control
\[ \Rightarrow 4 \text{ possible datasets:} \]
- 2 balanced: \{ $M_t$, $M_c$ \}, \{ $F_t$, $F_c$ \}
- 2 imbalanced: \{ $M_t$, $F_c$ \}, \{ $F_t$, $M_c$ \}

\[ = \Rightarrow \text{random pruning increases imbalance} \]

**Continuous example**

- Dataset: $T \in \{ 0, 1 \}$ randomly assigned; $X$ any fixed variable;
  with $n$ units

- Measure of imbalance: squared difference in means $d^2$, where
  \[ d = \bar{X}_t - \bar{X}_c \]

\[ E(d^2) = V(d) \propto 1/n \text{ (note: } E(d) = 0) \]

- Random pruning \[ \Rightarrow n \text{ declines} \]
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- Result is completely general (see math in the paper)
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1. Low Standards:
   • Sometimes helps, never optimizes
   • Efficient relative to complete randomization, but
     • Inefficient relative to (the more powerful) full blocking
   • Other methods dominate:

2. The PSM Paradox:
   • When you do “better,” you do worse
   • Background: Random matching increases imbalance
   • When PSM approximates complete randomization (to begin
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     \[ \hat{\pi}_c \approx \hat{\pi}_t \]
     \[ \Rightarrow \]
   • Imbalance
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   • Model dependence
   • Bias
   • If the data have no good matches, the paradox won’t be a
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     Nope.
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![Diagram showing scatter plots and bar charts comparing Mahalanobis and Propensity Score methods.]
What Does PSM Match?

MDM Matches

![MDM Matches Chart]

PSM Matches

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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 in Real Data

[Diagram showing results for real data sets, indicating similar patterns across 20 other real data sets checked.]
The Propensity Score Paradox in Real Data

Finkel et al. (JOP, 2012)

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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

• Bias-Variance trade off ⇝ 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:

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

Evaluations needed to compute the entire frontier:

- $\binom{N}{n}$ evaluations for each sample size $n = N, N-1, ..., 1$

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
- do not require evaluating every subset
- work with very large data sets
- is the exact frontier (no approximation or estimation)

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  - $\binom{N}{n}$ 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
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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;
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• A New General Approach: The Matching Frontier
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