Matching Methods for Causal Inference

Gary King

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National Taiwan University, 5/30/2018
1. The most popular method (propensity score matching, used in 103,000 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: “The Balance-Sample Size Frontier in Matching Methods for Causal Inference” (In press, AJPS; Gary King, Christopher Lucas and Richard Nielsen)
3 Problems, 3 Solutions

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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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Imbalance
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Imbalance $\leadsto$ Model Dependence $\leadsto$ Researcher discretion

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Without Matching:

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

• 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:
     $$SATT = \text{Mean}_{i \in \{T_i = 1\}}(TE_i)$$
  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**
  - **Unobserved**

- On average, 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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⇒ *Fully blocked* dominates *complete randomization* for: imbalance, model dependence,
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~ Fully blocked dominates complete randomization for: imbalance, model dependence, power, efficiency,
Matching: Finding Hidden Randomized Experiments

Types of Experiments

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### Matching: Finding Hidden Randomized 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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- 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
- Other matching methods dominate PSM (wait, it gets worse)
Method 1: Mahalanobis Distance Matching

1. Preprocess (Matching)
   - 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 $> caliper$

2. Estimation Difference in means or a model
Method 1: Mahalanobis Distance Matching
(Approximates Fully Blocked Experiment)
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   - (Many adjustments available to this basic method)

2. Estimation Difference in means or a model
Mahalanobis Distance Matching

Education (years)

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

8 / 25
Best Case: Mahalanobis Distance Matching
Best Case: Mahalanobis Distance Matching
Best Case: Mahalanobis Distance Matching
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 $X$, $C(X)$
   • 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

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

$10 / 25$
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Coarsened Exact Matching

Age

Education

12 14 16 18 20 22 24 26 28

20 30 40 50 60 70 80

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

T
Coarsened Exact Matching

Don't trust anyone over 30
The Big 40
Senior Discounts
Retirement
Old
Coarsened Exact Matching

Education

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

Drinking age
Don't trust anyone over 30
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Coarsened Exact Matching

Education

HS BA MA PhD 2nd PhD

Drinking age
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C C C C
C CC C C C C
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Coarsened Exact Matching

Education:
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Best Case: Coarsened Exact Matching
### Best Case: Coarsened Exact Matching

#### Education vs. Age

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[Diagram showing a scatter plot with markers indicating data points]
Best Case: Coarsened Exact Matching
Best Case: Coarsened Exact Matching

![Graph showing the relationship between Education and Age. The graph displays a scatter plot with points marked at various Education levels and Age values. The scatter plot suggests a trend where Education increases with Age, with a higher concentration of points in the upper right quadrant, indicating a positive correlation.](image-url)
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
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   - Prune matches if Distance $>$ caliper

2. Estimation
   - Difference in means or a model
Method 3: Propensity Score Matching
(Approximates Completely Randomized Experiment)
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   - (Many adjustments available to this basic method)

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

Age

Education (years)

Propensity Score

1

0
Best Case: Propensity Score Matching
Best Case: Propensity Score Matching
Best Case: Propensity Score Matching
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:

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

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)
  \[ \Rightarrow \hat{\pi} \approx 0 \] (or constant within strata)
  \[ \Rightarrow \text{pruning at random} \Rightarrow \text{imbalance} \Rightarrow \text{Inefficency} \Rightarrow \text{Model dependence} \Rightarrow \text{Bias} \]
- 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?
  \[ \text{Nope.} \]
  \[ \text{The PSM Paradox gets worse with more covariates} \]
PSM’s Statistical Properties

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   - *Efficient* relative to complete randomization, but
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   - Other methods usually dominate:
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PSM is Blind Where Other Methods Can See
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What Does PSM Match?

MDM Matches

PSM Matches

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

Treated: $X_1, X_2 \sim \text{Uniform}(1,6)$
**PSM Increases Model Dependence & Bias**

**Model Dependence**

**Bias**

\[
Y_i = 2T_i + X_{1i} + X_{2i} + \epsilon_i
\]

\[
\epsilon_i \sim \mathcal{N}(0, 1)
\]
The Propensity Score Paradox in Real Data

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:

- 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 $n = N, N-1, \ldots, 1$

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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Job Training Data: Frontier and Causal Estimates

- 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
- No need to choose among matching methods
- Optimal results from your choice of imbalance metric

Using more information is simpler and more powerful
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• A New General Approach: The Matching Frontier
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  • No need to choose among matching methods
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Conclusions

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  - Ignores information; exacerbates model dependence
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- ☞ Using more information is simpler and more powerful
For more information, articles, & software

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