Matching Methods for Causal Inference

Gary King\textsuperscript{1}

Institute for Quantitative Social Science
Harvard University

Microsoft Research, 1/19/2018

\textsuperscript{1}GaryKing.org
3 Problems, 3 Solutions

1. The most popular method (propensity score matching, used in 93,700 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 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)
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![Graph showing relationship between education and outcome](image_url)
Matching to Reduce Model Dependence

(Ho, Imai, King, Stuart, 2007: fig.1, *Political Analysis*)

![Graph showing the relationship between education (years) and outcome. The graph includes data points labeled 'C' and 'T'.]
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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)
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Imbalance
The Problems Matching Solves

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Imbalance $\leadsto$ Model Dependence
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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

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Matching: Finding Hidden Randomized Experiments

Types of Experiments

- Balance
- Covariates:
  - Complete Randomization
  - Fully Blocked

Observed: On average
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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Goal of Each Matching Method (in Observational Data)

- **PSM:** Complete randomization
- **Other methods:** Fully blocked
- **Other matching methods dominate PSM**
Matching: Finding Hidden Randomized Experiments

Types of Experiments

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

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Types of Experiments

- Complete Randomization
- Fully Blocked

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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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E.g., Imai, King, Nall 2009: SEs 600% smaller!
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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 \( \left( X_c, X_t \right) = \sqrt{(X_c - X_t)'S^{-1}(X_c - X_t)} \)
   - (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)
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Mahalanobis Distance Matching

Education (years)

Age

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

Education (years)

Age

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8 / 25
Mahalanobis Distance Matching

Age
12 14 16 18 20 22 24 26 28

Education (years)
20
30
40
50
60
70
80
Mahalanobis Distance Matching

Age
12 14 16 18 20 22 24 26 28

Education (years)
20
30
40
50
60
70
80

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

Age

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
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
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Coarsened Exact Matching

Education

HS  BA  MA  PhD  2nd PhD

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Senior Discounts

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C C
CC
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Best Case: Coarsened Exact Matching
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Age
12 14 16 18 20 22 24 26 28

Education
20
30
40
50
60
70
80

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C CC CC

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T TT TT
Best Case: Coarsened Exact Matching
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
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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

![Graph showing the relationship between Education (years) and Propensity Score. The x-axis represents Education (years) ranging from 12 to 28, the y-axis represents Age ranging from 20 to 80. The graph includes a scatter plot with lines connecting data points, indicating the matching process.]

- **Education (years):** 12, 16, 20, 24, 28
- **Age:** 20, 30, 40, 50, 60, 70, 80

The graph illustrates the matching process where each point on the scatter plot represents an individual's education level and age, with lines connecting similar education levels to represent matched pairs.
Propensity Score Matching

Propensity Score

Education (years)

Age

12 16 20 24 28

20

30

40

50

60

70

80

1

0

Propensity Score
Propensity Score Matching

Age

Education (years)

Propensity Score
Propensity Score Matching

Age

Education (years)
Best Case: Propensity Score Matching
Best Case: Propensity Score Matching
Best Case: Propensity Score Matching

Propensity Score
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)
   - \( \Rightarrow \) all \( \hat{\pi} \approx 0 \) (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.
   - Doesn’t PSM solve the curse of dimensionality problem?
   - No. PSM Paradox gets worse with more covariates
PSM’s Statistical Properties

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

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\[
x = x \Rightarrow \pi_c = \pi_t \ni \pi_c = \pi_t \neq \Rightarrow x = x
\]
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     X_c = X_t \implies \pi_c = \pi_t \quad \text{but} \quad \pi_c = \pi_t \nRightarrow X_c = X_t
     \]
PSM’s Statistical Properties

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     \[ \pi_c = \pi_t \not\implies X_c = X_t \]

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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

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

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

Similar pattern for > 20 other real data sets we checked
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- 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

→ 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; caliper on propensity score; not switching to other methods.

- A Simple and Powerful Method: CEM
- A New General Approach: The Matching Frontier
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  - Optimal results from your choice of imbalance metric

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For more information, articles, & software

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