Model-based matching for causal inference in observational studies

Kellie Ottoboni
with Philip B. Stark

Department of Statistics, UC Berkeley
Berkeley Institute for Data Science

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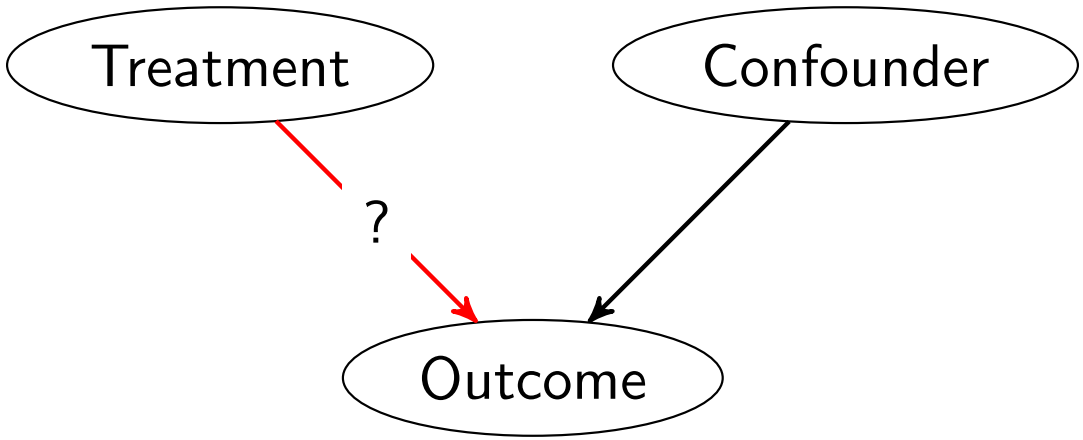
Outline

Observational Studies vs Experiments

- **Problem:** Estimate the causal effect of a treatment on outcome of interest
- In randomized experiments, treatment is assigned to individuals at random.
- In observational studies, the way individuals select into treatment groups is unknown.



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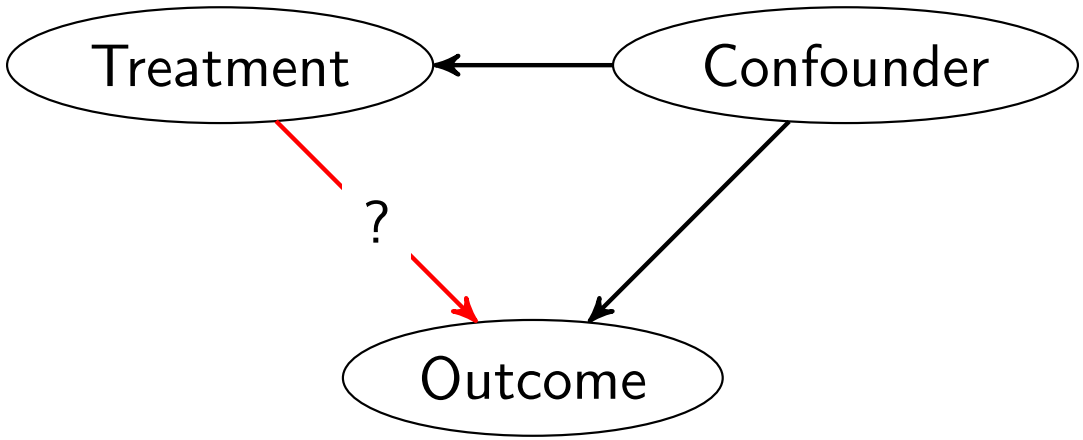


Neyman-Rubin Causal Model

- Population of $i = 1, \ldots, N$ individuals. Each individual has two **potential outcomes**.
- $Y_i(1)$ is individual i's outcome if he receives treatment
- $Y_i(0)$ is individual i's outcome if he is in the control group
- The treatment effect for individual i is $\tau_i = Y_i(1) - Y_i(0)$

$Y_1(1)$	$Y_1(0)$

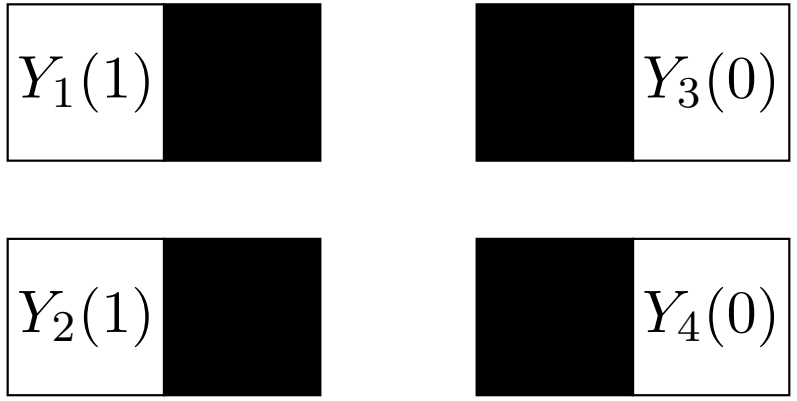
$Y_3(1)$	$Y_3(0)$

$Y_2(1)$	$Y_2(0)$

$Y_4(1)$	$Y_4(0)$

Fundamental Problem of Causal Inference [Holland, 1986]

- We may never observe both $Y_i(1)$ and $Y_i(0)$
- T_i is a treatment indicator: 1 if i is treated, 0 if i is control
- The observed outcome for individual i is $Y_i = T_i Y_i(1) + (1 - T_i) Y_i(0)$



Estimands

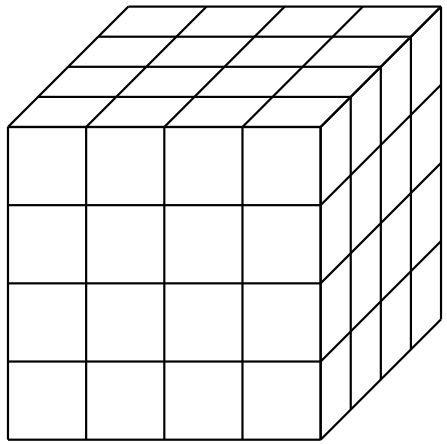
- Average treatment effect
$$\mathbb{E}(Y_i(1) - Y_i(0))$$
- Average treatment effect on the treated
$$\mathbb{E}(Y_i(1) - Y_i(0) \mid T_i = 1)$$
- Conditional average treatment effect
$$\mathbb{E}(Y_i(1) - Y_i(0) \mid X_i)$$
- If treatment effect varies by covariates X, then averages might not be informative

Outline

Matching

How can we estimate the counterfactual for treated individuals?

- **Ideal:** group individuals by X_i to estimate subgroup treatment effects and then average over subgroups
- **Reality:** many covariates, perhaps continuous, make it difficult to stratify

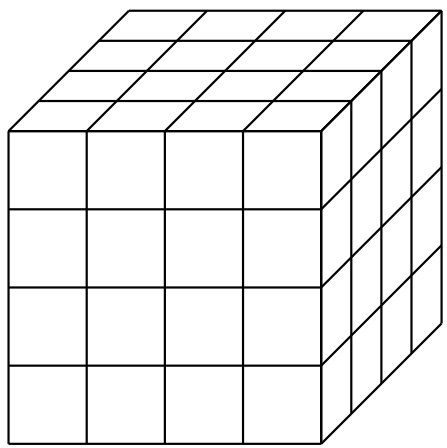


Aside... the curse of dimensionality

- If d covariates are split into k bins, we have d^k groups.
- To guarantee that we have at least one treated and one control in each group with 95% probability, we need

$$n \geq \frac{2\log(1-(0.95)^{1/k^{d+1}})}{\log(\frac{k^d-1}{k^d})}$$

- If $d = 5$ and $k = 2$, $n \geq 225$.
- If $d = 10$ and $k = 2$, $n \geq 10,844$.



Matching

- **Solution:** use a one-dimensional score to match or group individuals

Propensity score matching

- The **propensity score** is an individual's probability of being assigned treatment, conditional on their covariates

$$p(x) = \mathbb{P}(T = 1 \mid X = x)$$

- The propensity score is a balancing score: $X \perp\!\!\!\perp T \mid p(X)$
- For individuals with the same propensity score, treatment assignment is as if random

Propensity score matching

Theorem (Rosenbaum and Rubin [1983])

If treatment assignment is independent of potential outcomes given X*,*

$$(Y(1), Y(0)) \perp\!\!\!\perp T \mid X$$

and if every unit has a chance of receiving treatment,

$$0 < p(X) < 1 \text{ for all } X$$

then $(Y(1), Y(0)) \perp\!\!\!\perp T \mid p(X)$*.*

In particular, treated units can serve as the counterfactual for controls with the same $p(X)$

$$\mathbb{E}(Y(t) \mid T = 1, p(X)) = \mathbb{E}(Y(t) \mid T = 0, p(X)) \text{ for } t = 0, 1$$

Propensity score matching

This result identifies the average treatment effect in terms of quantities we can estimate:

$$\begin{aligned}
\mathbb{E}(Y(1) - Y(0)) &= \mathbb{E}_{p(x)}\left[\mathbb{E}(Y(1) - Y(0) \mid p(x))\right] \\
&= \mathbb{E}_{p(x)}\left[\mathbb{E}(Y(1) \mid p(x)) - \mathbb{E}(Y(0) \mid p(x))\right] \\
&= \mathbb{E}_{p(x)}\left[\mathbb{E}(Y \mid p(x), T = 1) - \mathbb{E}(Y \mid p(x), T = 0)\right]
\end{aligned}$$

Propensity score matching

$p(x)$ is usually unknown and estimated by $\hat{p}(x)$ using logistic or probit regressions

- Assumes a simple functional form for relationship between covariates and treatment
- Assumes that probability of treatment takes same form for all individuals
- May actually worsen balance if estimated incorrectly [Diamond and Sekhon, 2012]

Matching introduces bias

- Standard errors are difficult to compute for matching estimators [Abadie and Imbens, 2006, 2008]
- There's no "optimal" way to match

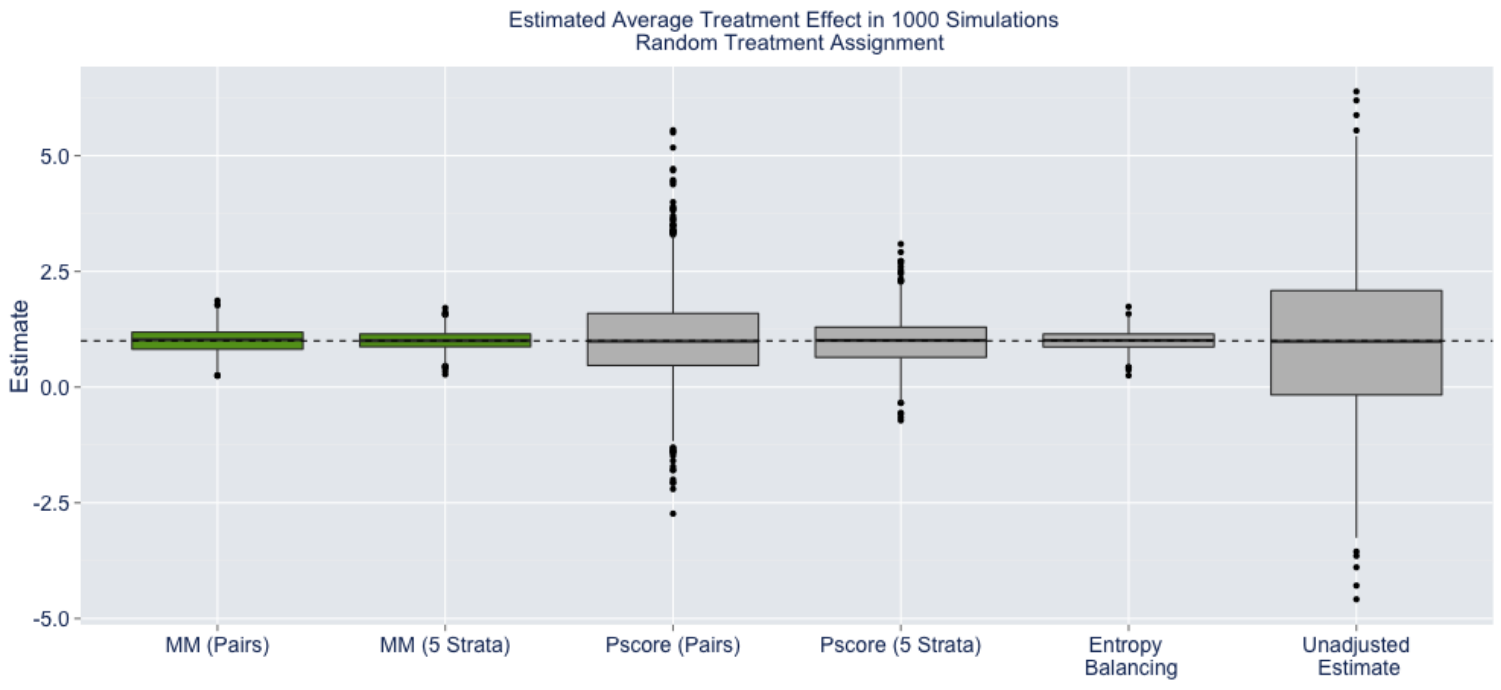
Model-based Matching

Idea: Instead of modeling the propensity score, model the outcome

Stratify on $\hat{Y}$, the "best" prediction of the outcome based on all covariates except for the treatment

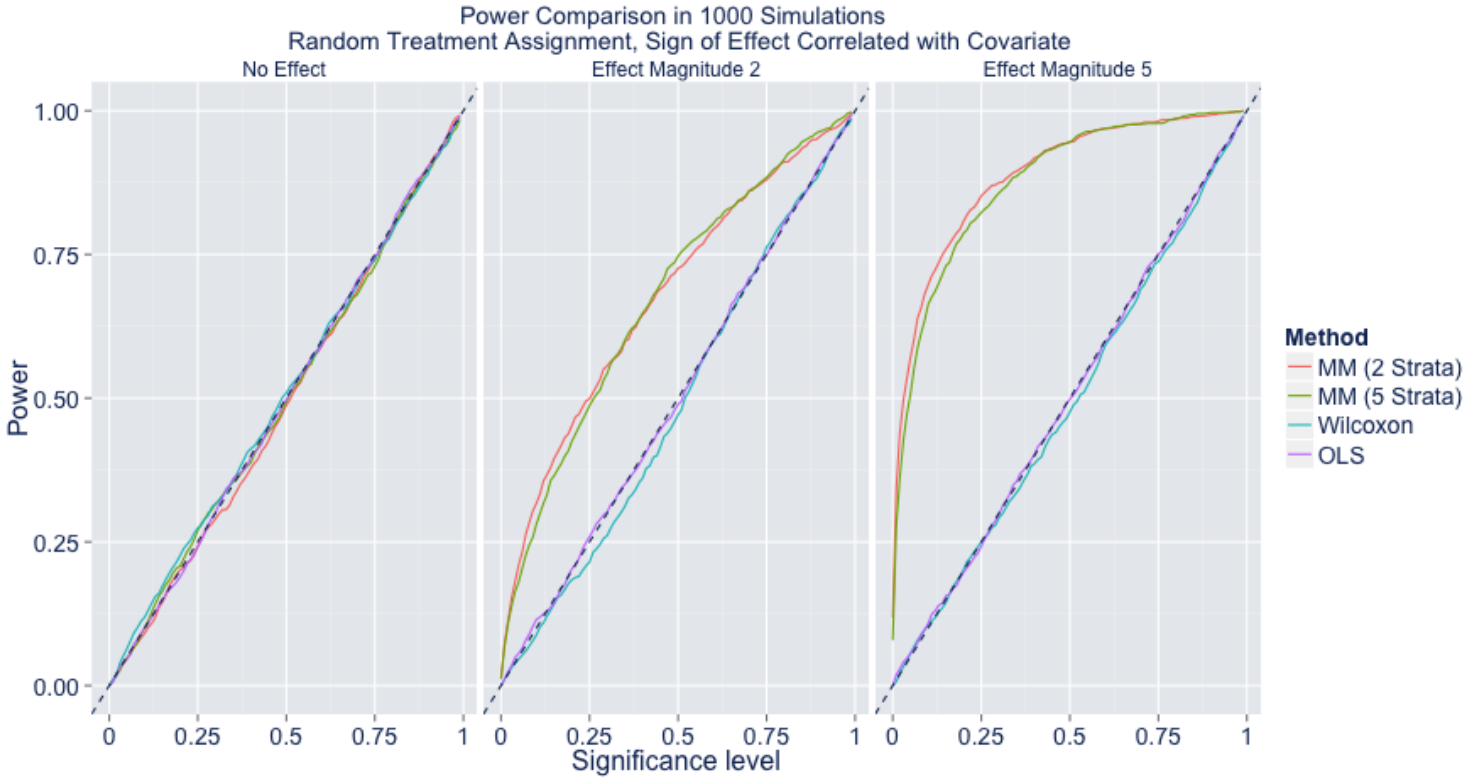
Model-based Matching

- Under standard assumptions (conditional independence of treatment and potential outcomes given X), the **average treatment effect** is nonparametrically identified
- Estimate it using the difference in average residuals, $Y - \hat{Y}$, between treated and controls



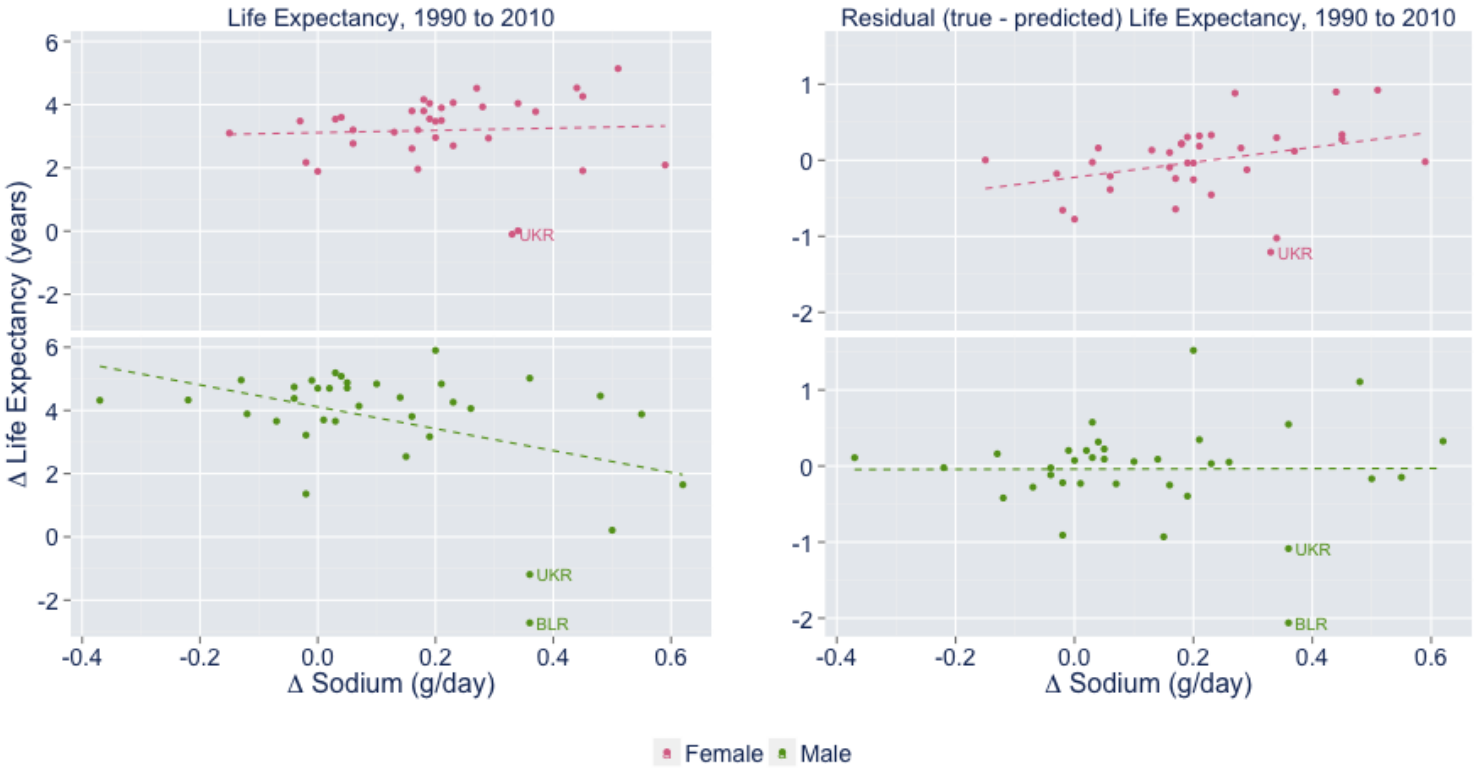
Model-based Matching

- Use stratified permutation test to test the **strong null hypothesis** of no treatment effect whatsoever
- Stratifying on $\hat{Y}$ allows us to detect non-constant and non-linear treatment effects



Outline

Salt


Life Expectancy, 1990 to 2010
Residual (true - predicted) Life Expectancy, 1990 to 2010
Δ Life Expectancy (years)
Δ Sodium (g/day)
Δ Sodium (g/day)
UKR
UKR
BLR
UKR
UKR
BLR
Female
Male

Outline

Future Directions

- Do different test statistics give greater power when the treatment effect is nonlinear?
- What is the optimal way to stratify?
- How to quantify uncertainty – standard errors and confidence intervals?

Outline

References

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