Model-based matching for causal inference in observational studies

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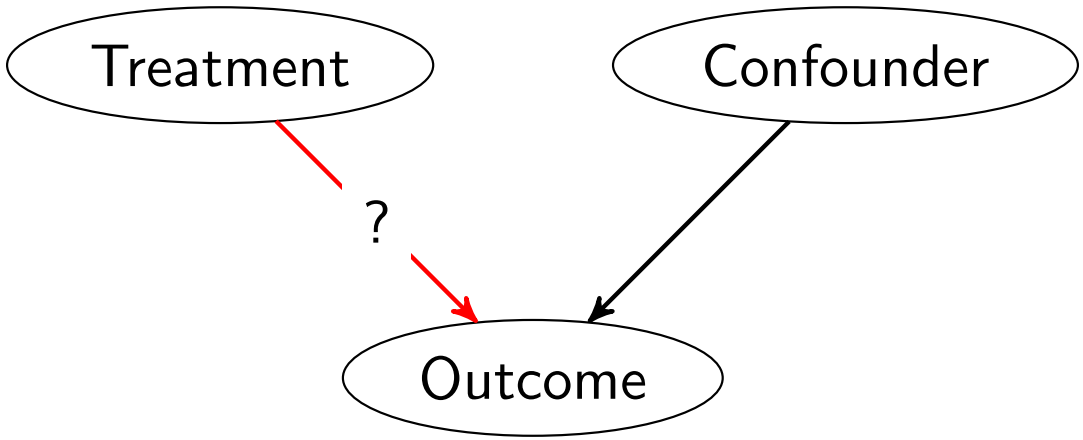
Outline

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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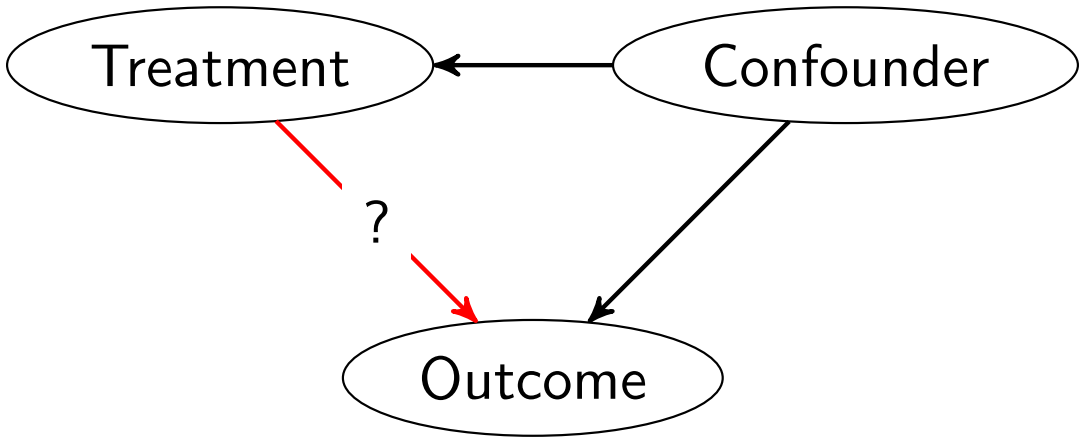
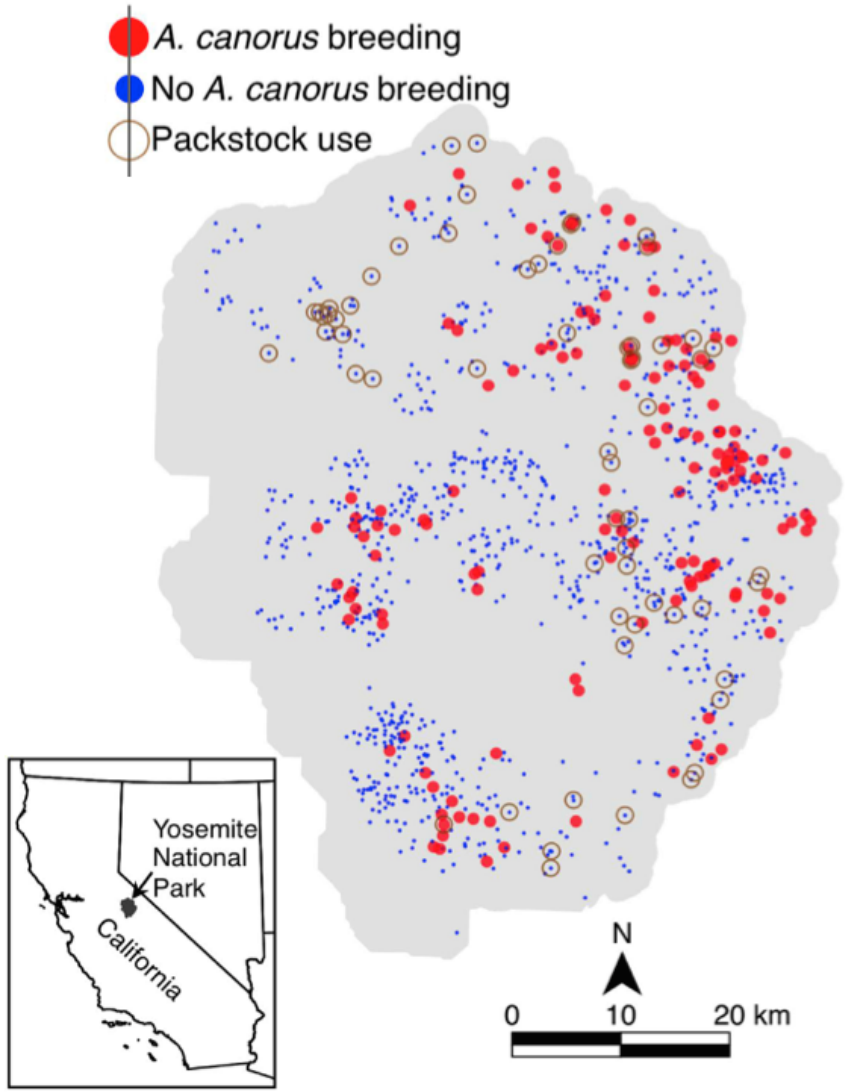


Motivating Example: Toads and Packstock



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Motivating Example: Toads and Packstock

- The response is rare (few meadows have toads).
- The treatment is rare (few meadows are used by packstock).
- Randomized experiment is impossible, and toad/packstock presence is not random across meadows.
- We're interested in detecting any effect, no matter how small. If treatment effect varies across meadows, then averages might not be informative.

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 $\tau_i = Y_i(1) - Y_i(0)$

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

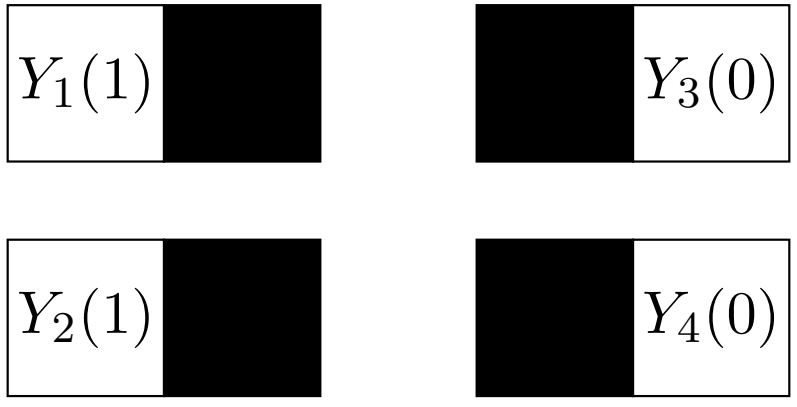
$Y_3(1)$	$Y_3(0)$

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

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

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 $Y_i = T_i Y_i(1) + (1 - T_i) Y_i(0)$



Goal

Goal: test the **strong null hypothesis** of no treatment effect whatsoever.

$$H_0 : Y_i(1) = Y_i(0) \text{ for all } i$$
$$H_1 : Y_i(1) \neq Y_i(0) \text{ for some } i$$

We'd like our test to have power to detect

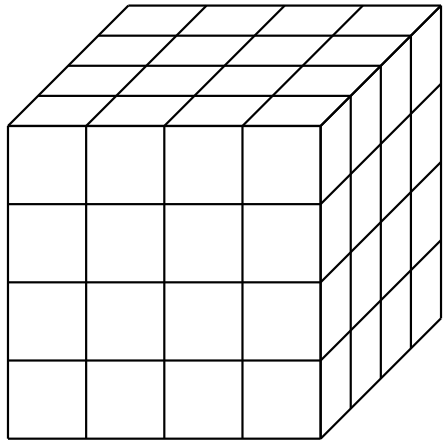
- non-constant effects
- non-linear effects
- effects with non-constant sign

Outline

Matching

Individuals with similar covariates should have similar outcomes, but for the treatment.

- **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

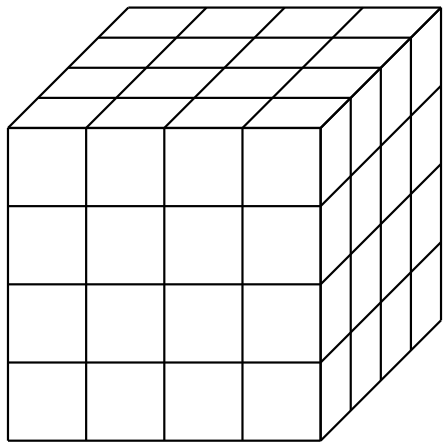


Aside... the curse of dimensionality

- 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 complicates inference

- Standard errors are difficult to compute for matching estimators [Abadie and Imbens, 2006, 2008]
- Rarely used in hypothesis testing procedures
- There's no "optimal" way to match [Austin, 2014]

Model-based Matching

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

Computing $\hat{Y}$, the "best" prediction of the outcome based on all covariates except for the treatment, buys us two things:

- $\hat{Y}$ is a score on which to stratify observations
- Using residuals $Y - \hat{Y}$ improves precision by removing variation due to X [Rosenbaum, 2002]

Model-based Matching

Suppose that outcomes have the form

$$Y_i(t) = f(t, X_i) + \varepsilon_i$$

for $i = 1, \ldots, N$ and $t = 0, 1$. Let X_i be fixed and suppose that $\mathbb{E}(\varepsilon_i) = 0$, independent of X_i and of $\varepsilon_j, j \neq i$.

We observe $Y_i = T_i Y_i(1) + (1 - T_i) Y_i(0)$.

Under the strong null hypothesis, $f(0, X_i) = f(1, X_i)$ for each i.

Thus, our best guess of Y_i needn't involve the treatment:

$$\hat{Y}_i = \hat{f}(X_i)$$

Model-based Matching

Stratify or match units on their $\hat{Y}_i = \hat{f}(X_i)$.

- Let $S_i = j$ if unit i is in stratum j, where $j \in \{1, \ldots, J\}$. Stratum j contains N_j units, n_j of which are treated. (For now, don't worry about how to select J strata.)
- **Under the null**, we expect units in the same strata to have the similar responses.
- **Under the alternative**, the treatment adds additional information about the responses beyond $\hat{f}$.
  The residuals will capture some of the effect of treatment:
  $$Y_i - \hat{Y}_i \not\perp\!\!\!\perp T_i$$

Test statistic

If treatment is binary, we will use the average difference in means across strata as our test statistic:

$$\tau(Y,T) = \sum_{j=1}^{J} \frac{N_j}{N} \left| \frac{1}{n_j} \sum_{\substack{i:S_i=j \\ T_i=1}} \left(Y_i - \hat{Y}_i\right) - \frac{1}{N_j - n_j} \sum_{\substack{i:S_i=j \\ T_i=0}} \left(Y_i - \hat{Y}_i\right) \right|$$

If treatment is continuous, we will use the average correlation across strata as our test statistic:

$$\tau(Y,T) = \sum_{j=1}^{J} \frac{N_j}{N} \left| \rho_j(Y_i - \hat{Y}_i, T_i) \right|$$

NB: we can use any other test statistic that measures association between $Y_i - \hat{Y}_i$ and T_i

Permutation tests

Basic idea: Under the null hypothesis, the probability distribution of the data is invariant under permutation of treatment assignments within strata.

Once we observe the actual data, we know other possible data sets that are equally likely.

There are

$$\prod_{j=1}^{J} \binom{N_j}{n_j}$$

equally likely assignments to treatment, conditional on the strata and number treated in each stratum.

Permutation tests

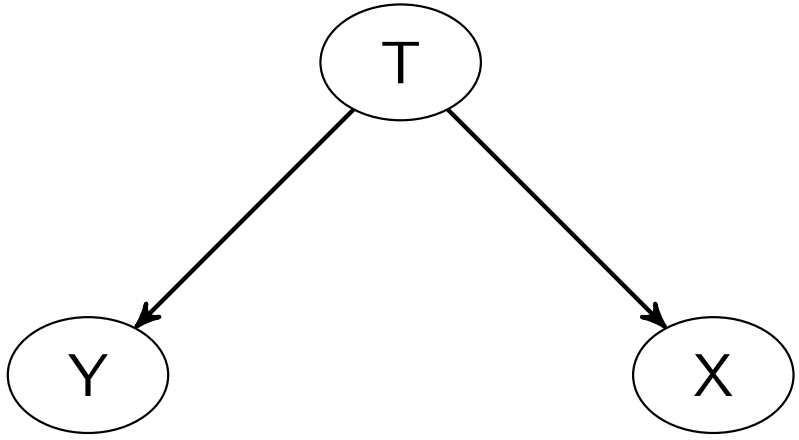
We approximate the null distribution using this invariance principle.

- Within strata, permute treatment assignments to obtain new treatment vector T_1^*.
- Compute the test statistic $\tau(Y, T_1^*)$.
- Repeat a large number B times to get a distribution $\tau(Y, T_1^*), \ldots, \tau(Y, T_B^*)$.
- The p-value of the test is

$$p = \mathbb{P}(\tau(Y, T) \geq \tau(Y, t)) \approx \frac{\sum_{i=1}^{B} \mathbb{I}(\tau(Y, T_b^*) \geq \tau(Y, T))}{B}$$

Association or Causation?

- Pathological example: suppose $Y_i = cT_i + \varepsilon_i$, $X_i = T_i$. A model-based matching test will find no treatment effect.

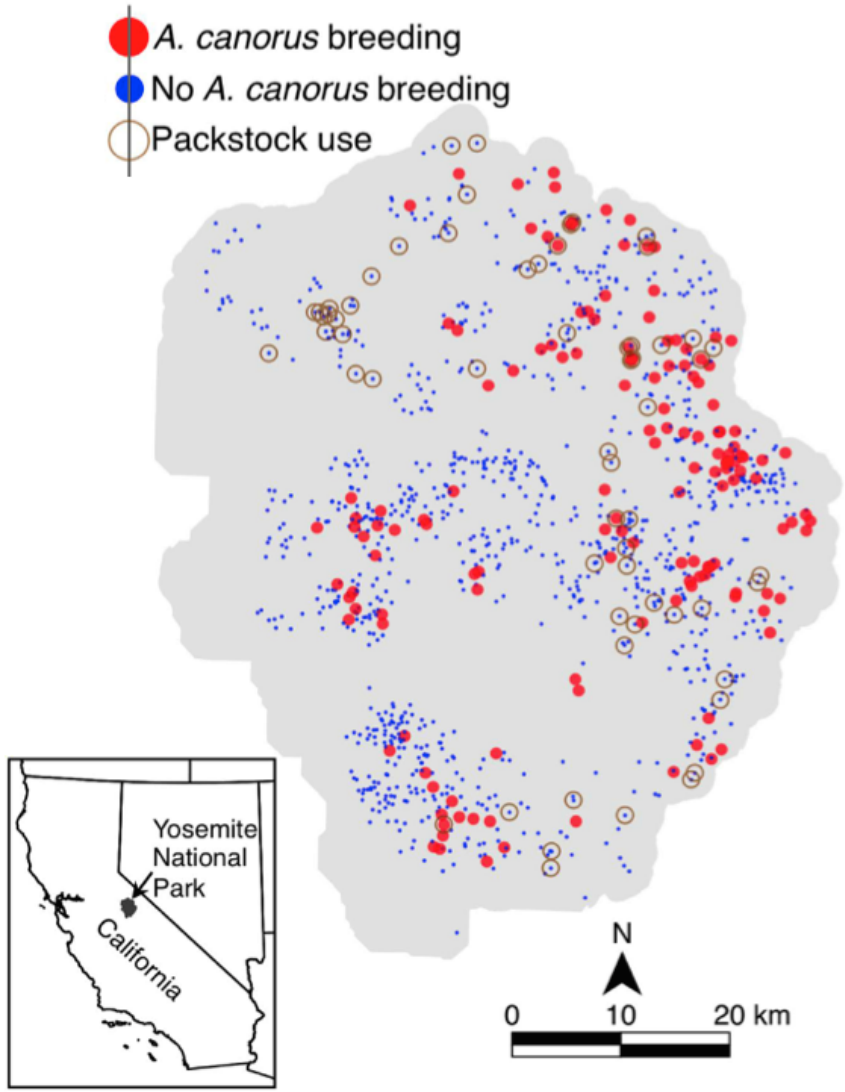


- Difference with predictive statistics: covariates included in fitting $\hat{f}$ must be pretreatment!

- Causal inference requires more assumptions than we've made.

Outline

Toads and Packstock



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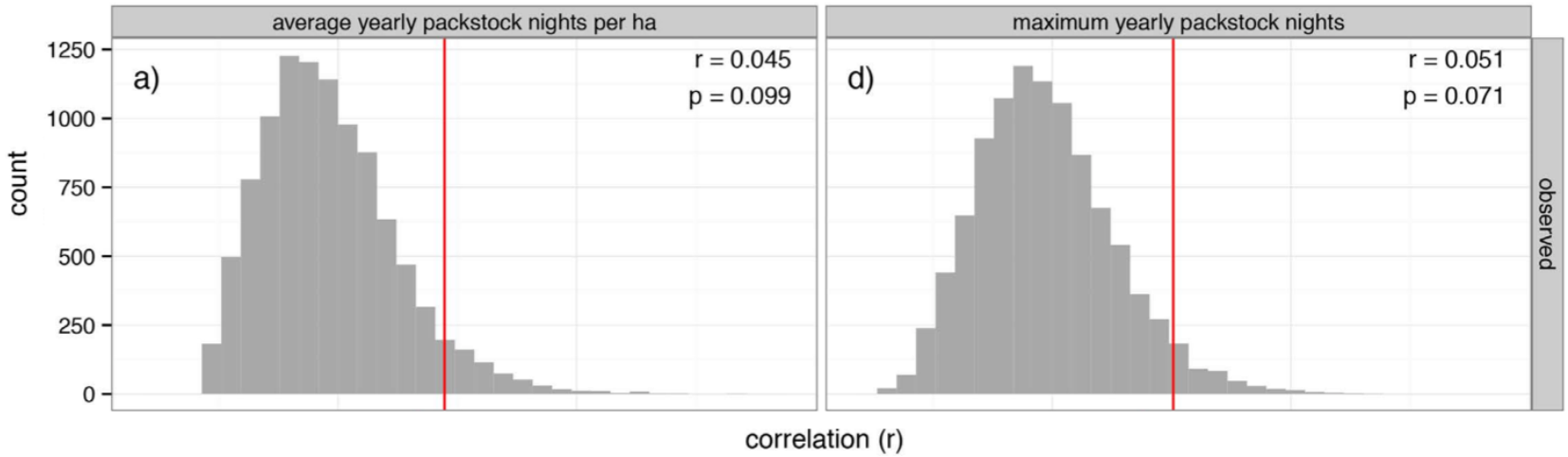
Toads and Packstock

- Response is binary: did toads breed in the meadow or not?
- Treatment is continuous: average or maximum packstock nights in each meadow
- Prediction: probability of toad presence according to meadow characteristics
- Test statistic: within-stratum absolute value of correlation between treatment and residuals, averaged over strata

Toads and Packstock

Intensity of packstock use appears to be **weakly correlated** with toad presence. The correlation is not significant.



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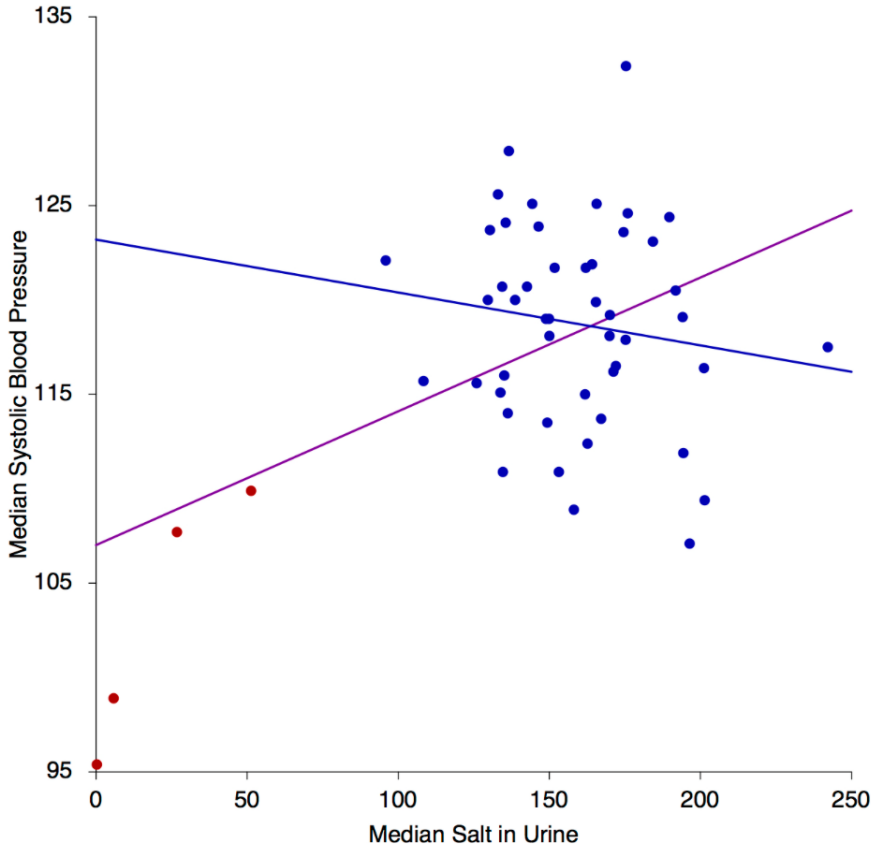
Salt

- There is a major campaign by the World Health Organization (WHO) to reduce salt consumption worldwide
  [World Health Organization, 2014]
- WHO assumes a causal pathway between eating salt and mortality. Main sources of evidence that salt is bad come from observational studies on hypertension
  [Intersalt Cooperative Research Group, 1986]
- **Goal:** test whether changes in sodium intake are associated with changes in life expectancy, after controlling for other major predictors of health.

Salt

An example of faulty analysis of salt and morbidity:

After excluding indigenous tribes (red points) from the sample, the association between salt and hypertension **changes sign** [Freedman and Petitti, 2001].



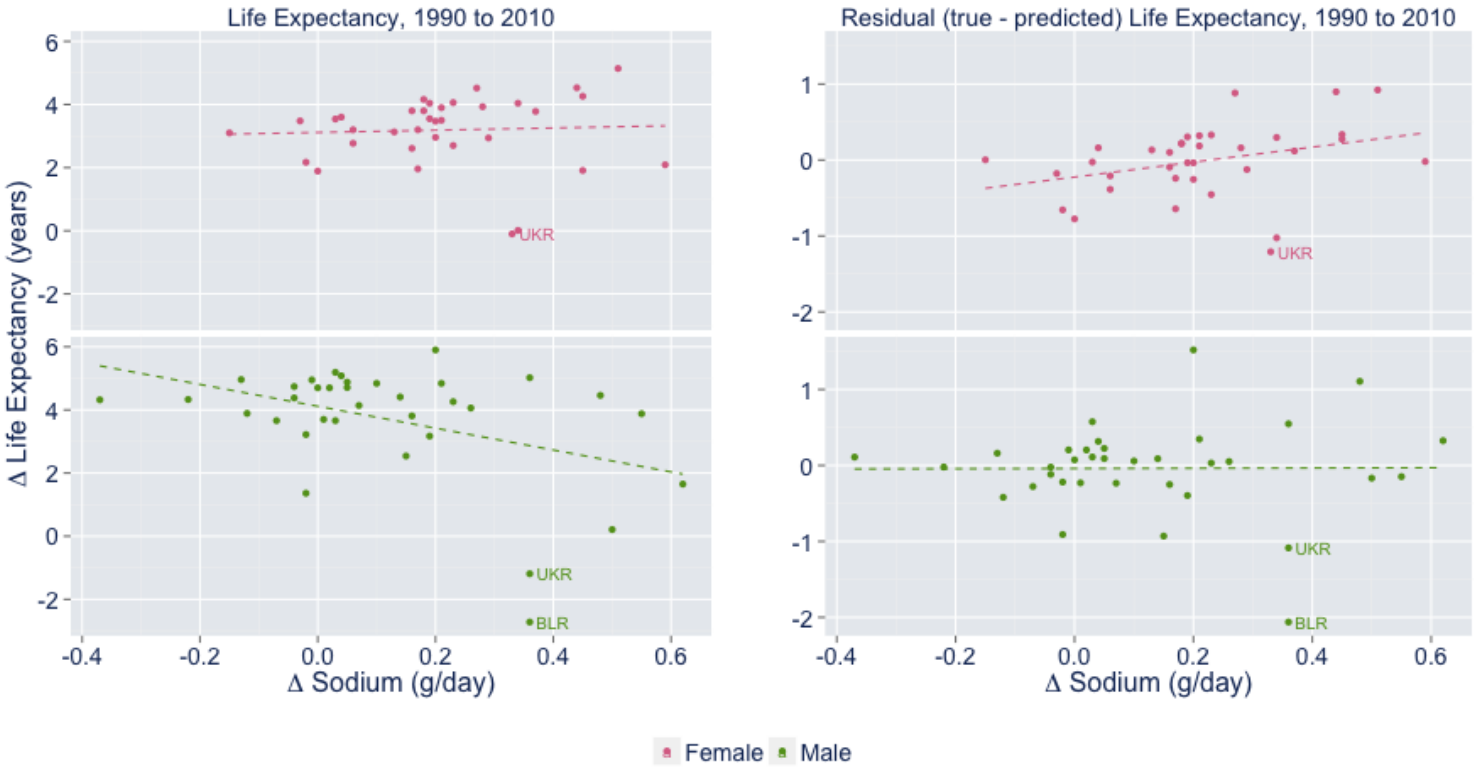
Salt

- Response is continuous: life expectancy at age 30
- Treatment is continuous: mean daily sodium intake
- Prediction: life expectancy at age 30, given alcohol consumption per capita per year, cigarettes per capita per year, and per capita GDP using random forests
- Test statistic: Pearson correlation between treatment and residuals
- All variables are differenced from 1990 to 2010 to control for baseline levels. Analyses are separate for males and females.

Salt

Sodium consumption appears to be

- **uncorrelated** with life expectancy for males
- **positively correlated** with life expectancy for females



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Conclusions

- We've developed a novel nonparametric test for treatment effects in observational studies.
- Model-based matching is more flexible than traditional methods: it has power to detect non-constant effects and can be used when treatment is non-binary.
- Stronger assumptions are needed to assert causation instead of just association.

Future Directions

- Do different test statistics give greater power? Under what conditions?
- What is the optimal way to stratify?
- How to quantify uncertainty – standard errors and confidence intervals?

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