



LUND
UNIVERSITY

Matching and synthetic controls

Nils Droste

2022 ClimBEco course



Causal Inference from observational data

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- model comparison
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Synopsis: Today, we will be looking into methods that help us find (aka *match*) or simulate (aka *synthesize*) a control group for inferring causal effects from observational data, and its recent developments

In particular, we will develop an understanding of



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- matching approaches



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 - classical
 - machine-based learning



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- matching approaches
 - classical
 - machine-based learning
- synthetic controls



Intuition

Consider a situation where the untreated are very different from the treated:

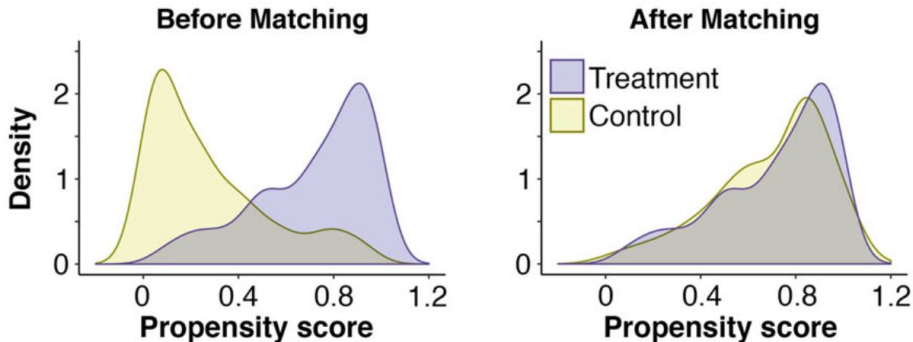


Image source: Schleicher et al. 2020



Intuition

Consider a situation where the untreated are very different from the treated:

Matching, def: any method that strategically subsamples dataset to balance covariate distribution in treated and control groups such that after matching both groups share an equal probability of treatment.

**Non-Random
Treatment
Assignment**

Matching Methods
→
to Subsample

**Average Treatment Effect on
the Treated + ~~Selection Bias~~**

Image source: [Image source: Sizemore and Alkurdi 2019](#)

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Matching Methods
→
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**Average Treatment Effect on
the Treated + ~~Selection Bias~~**

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→ matching is a ***pre-analytical procedure***, allowing unbiased inference.

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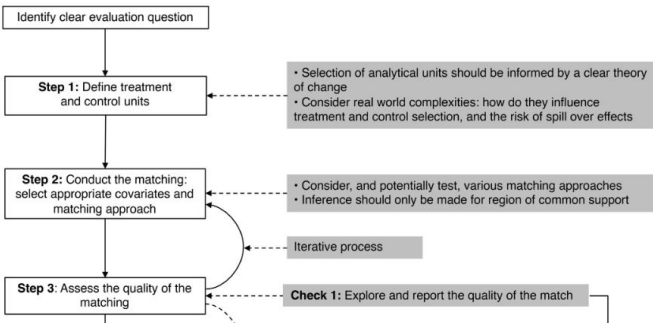
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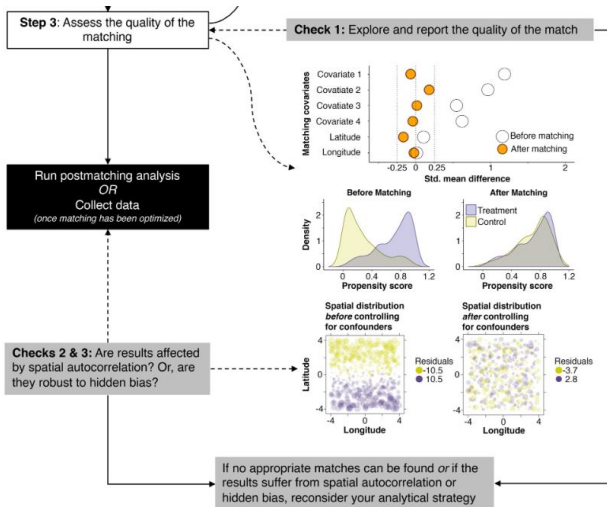


Image source: Schleicher et al. 2020

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Basic conditions

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The classical overarching conditions for robust causal inference:

- stable unit treatment value assumption (SUTVA)
 - treating one individual unit does not affect another's (potential) outcome
 - treatment is comparable [no (strong) variation in treatment]



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The classical overarching conditions for robust causal inference:

- stable unit treatment value assumption (SUTVA)
 - treating one individual unit does not affect another's (potential) outcome
 - treatment is comparable [no (strong) variation in treatment]
- unconfoundedness (strong ignorability)
 - $(Y(1), Y(0)) \perp D$: treatment assignment is independent of the outcomes
 - i.e. no omitted variable bias (recall the storch example)
 - or, at least, conditional unconfoundedness $(Y(1), Y(0)) \perp D|X$

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→ $\pi(X_i) = Pr(D_i = 1|X_i)$ or *propensity score* can be used for matching

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 - or, at least, conditional unconfoundedness $(Y(1), Y(0)) \perp D|X$
- $\pi(X_i) = Pr(D_i = 1|X_i)$ or *propensity score* can be used for matching
- but should maybe not (King and Nielsen 2019), we will see alternatives

Overview

Here is a general overview of possible matching methods

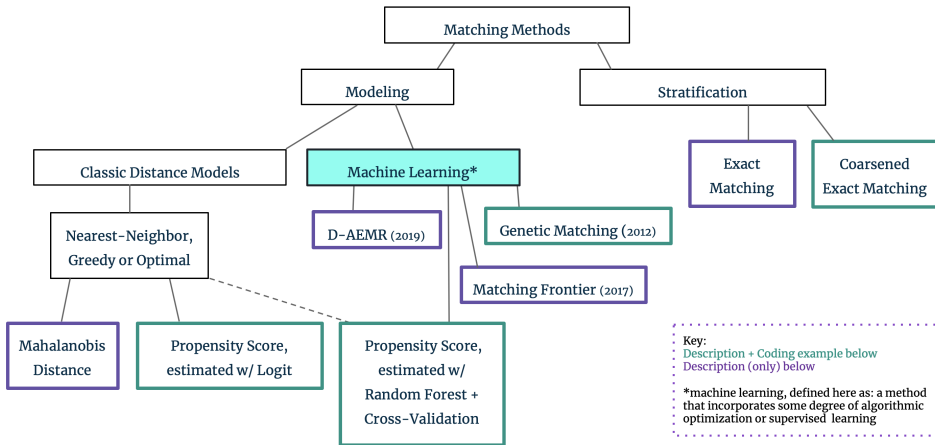


Image source: Sizemore and Alkurdi 2019

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Consider that we aim to estimate *conditional average treatment effect* (CATE) (cf. Abrevaya, Hsu and Lieli 2015)

$$CATE = E(Y(1) - Y(0)|X = x) \quad (1)$$



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Consider that we aim to estimate *conditional average treatment effect* (CATE) (cf. Abrevaya, Hsu and Lieli 2015)

$$CATE = E(Y(1) - Y(0)|X = x) \quad (1)$$

How to find the sufficiently similar subsamples?



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Consider that we aim to estimate *conditional average treatment effect* (CATE) (cf. Abrevaya, Hsu and Lieli 2015)

$$CATE = E(Y(1) - Y(0)|X = x) \quad (1)$$

King and Nielsen (2019) formulate a general pruning (*matching*) function M :

$$X_\ell = M(X|A_\ell, T_i = 1, T_j = 0, \delta) \equiv M(X|A_\ell) \subseteq X \quad (2)$$

providing X_ℓ , subset of matched observation based on condition A_ℓ .

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providing X_ℓ , subset of matched observation based on condition A_ℓ .

→ in what follows we will look at different pruning method ℓ
to produce the best matched subset δ .

Exact matching

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For exact matching we find exactly equal pairs

$$X_{EM} = M(X|X_i = X_j) \quad (3)$$

Note: X can be a vector of covariates.



Coarsened Exact Matching (CEM)

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For coarsened exact matching we approximate

$$X_{CEM} = M(X | C_{\delta}(X_i) = C_{\delta}(X_i)) \quad (4)$$

where C_{δ} is a vector of same dimensions as X , but coarsened values, e.g. at "*natural breakpoints*" such as years in one school type, levels of income, etc.

Mahalanobis Distance Method (MDM)

For multidimensional data, we can identify nearest neighbours in an n-dimensional space.

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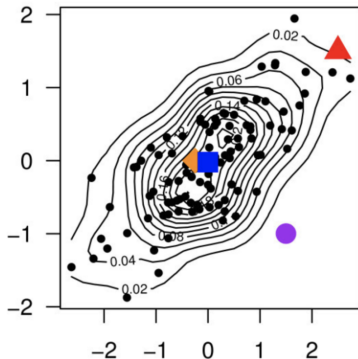
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$$md(X_i, X_j) = \{(X_i - X_j)^\top S^{-1}(X_i - X_j)\}^{\frac{1}{2}}$$

(Above) Mahalanobis distance measure, where S denotes the covariance matrix of X . [24]

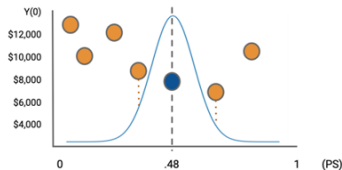
(Left) A contour plot is overlaid on a Mahalanobis distance scatter plot of 100 observations randomly drawn from a bivariate normal distribution. The centroid, in blue, is the reference point for distance between two points.

Image credit and description: Statistics How To: Mahalanobis Distance, Simple Definitions, Examples. Retrieved 10-08-2019 from: <https://www.statisticshowto.datasciencecentral.com/mahalanobis-distance/>

Image source: Sizemore and Alkurdi 2019

Propensity score matching (PSM)

Else, we can estimate probability of being treated, aka propensity score $\pi(X_i) = Pr(D_i = 1 | X_i)$ by logistic regression



T ●
C ●

Advantages

solves matching problem for high dimensions

many available R packages for easy implementation

Disadvantages

misspecification of PS model = bad matches

matched pairs may be dissimilar across X

Image source: Sizemore and Alkurdi 2019



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```
library(tidyverse)
library(MatchIt)
```

```
data("lalonde")
lalonde <- lalonde %>% as_tibble()
```

```
m.out <- matchit(treat ~ age + educ + race + married +
                 nodegree + re74 + re75, data = lalonde,
                 method = "full")
```



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```
> m.out
```

A matchit object

- method: Optimal full matching
- distance: Propensity score
 - estimated with logistic regression
- number of obs.: 614 (original), 614 (matched)
- target estimand: ATT
- covariates: age, educ, race, married, nodegree, re74, re75

example

```
plot(m.out, type = "ecdf", which.xs = c("age", "re74", "married"))
```

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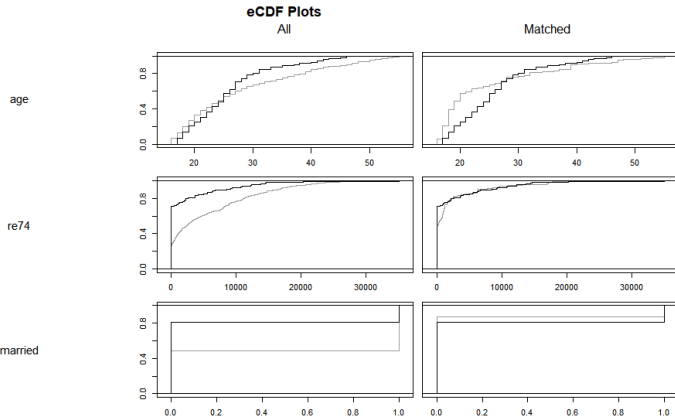
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Code source: [Greifer 2020](#)

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```
psFormula <- formula(treat ~ age + educ + race  
                      + married + nodegree + re74 + re75)
```

```
lalonge$p.score <-  
  glm(psFormula, data = lalonge,  
       family = "binomial")$fitted.values
```

```
lalonge$att.weights <-  
  with(lalonge, treat + (1-treat)*p.score/(1-p.score))
```

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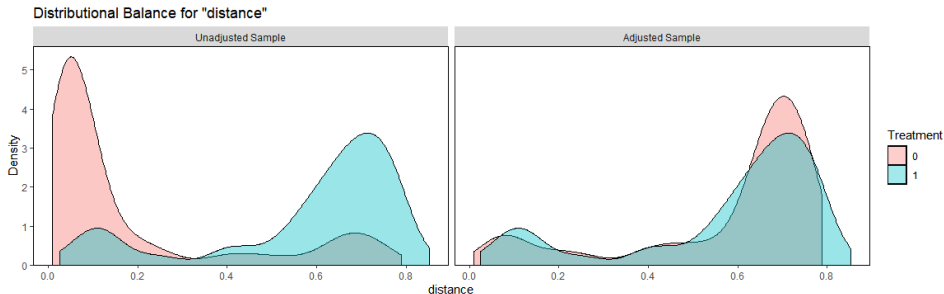
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```
bal.plot(f.build("treat", covs0),  
        data = lalonde, var.name = "p.score",  
        weights = "att.weights", distance = "p.score",  
        method = "weighting", which = "both")
```



Code source: [Greifer 2020](#)

Intermediate discussion

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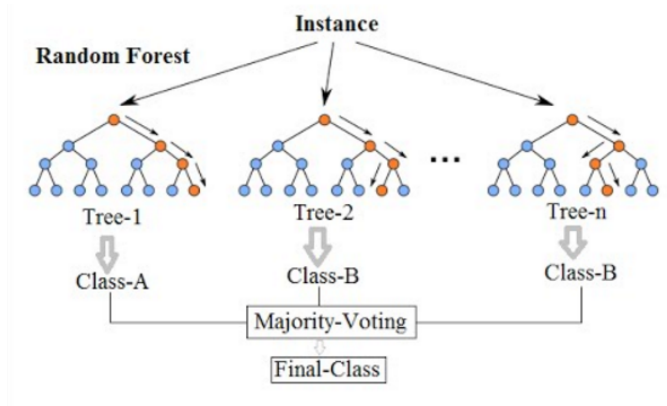
There is a bit of critique on PSM

- King and Nielsen (2019)
 - *"PSM is ... uniquely blind to the often large portion of imbalance"*
 - *"easy to avoid by switching to one of the other popular methods of matching"*
 - i.e.: CEM and MDM
- Sizemore and Alkurdi (2019)
 - test PSM against machine learning based methods
 - logistic PSM \succ random forest PSM \succ genetic matching
 - CEM ???



Random forest (RF)

RF are multiple regression trees classifying the data by partitioning



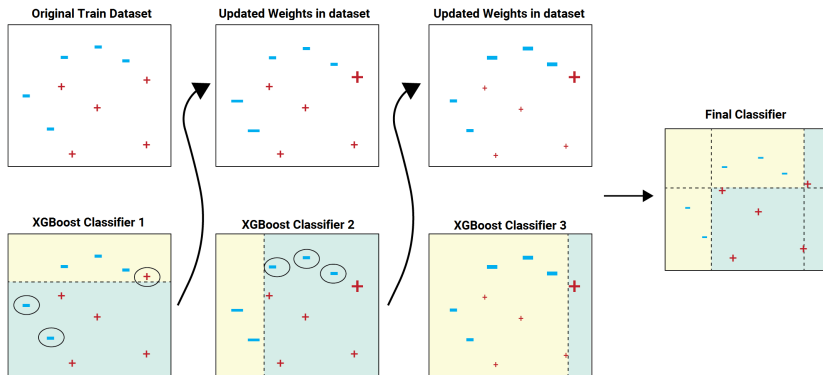
Code source: [Wikipedia](#)

We can use this to predict treatment (aka propensity scores)



eXtreme Gradient Boosting (XGBoost)

Machine learning such as XGBoost or even ensembles can also be used to



Code source: [Quant Insti](#)

→ predict treatment (aka propensity scores)

Causal Inference

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Genetic matching

Genetic Matching combines PSM and MDM

$$GMD(X_i, X_j, W) = \sqrt{(X_i)^T (S^{-\frac{1}{2}})^T W S^{-\frac{1}{2}} (X_i - X_j)} \quad (5)$$

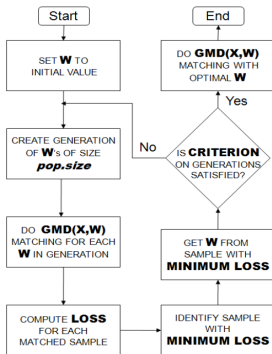


Image source: Sizemore and Alkurdi 2019

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comparison - fitting distributions

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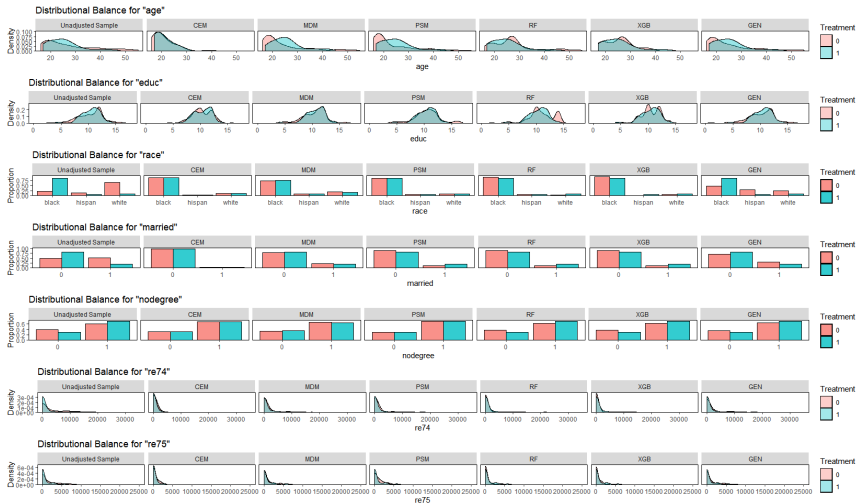
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plotting model comparisons for covariates of the lalonde data set

comparison - mean absolute error

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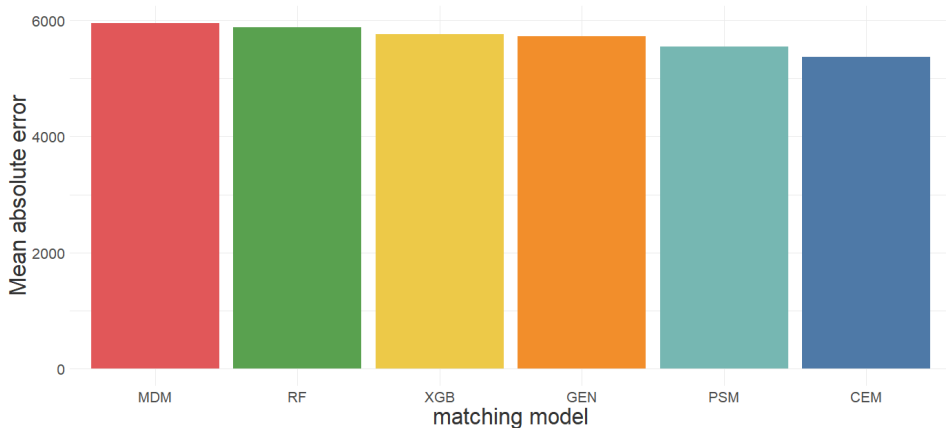
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plotting model comparisons for the lalonde data set, cf. Colson et al. 2016

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- for the comparison above I used nearest neighbour matching, reducing sample size



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- maximizing post-match balance does not necessarily improve explanatory model power (Colson et al. 2016)



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- maximizing post-match balance does not necessarily improve explanatory model power (Colson et al. 2016)
- possibly both sample size and balance need to be taken into account (King, Lucas and Nielsen 2017)



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- latest approaches include almost exact matching (Dieng et al. 2018; Dieng et al. 2021), text matching (Roberts, Stewart and Nielsen 2020), generalized optimal matching (Kallus 2020)



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- R packages include MatchIt, Matching, and PanelMatch



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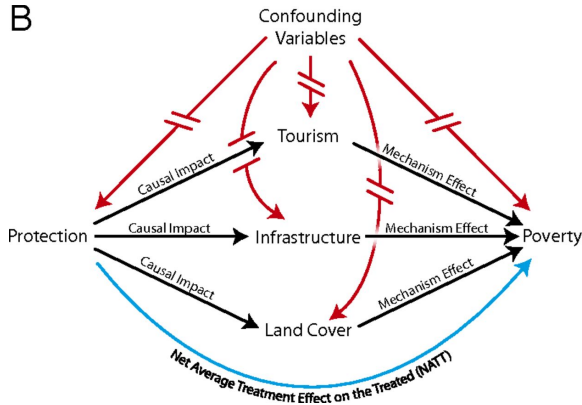
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- latest approaches include almost exact matching (Dieng et al. 2018; Dieng et al. 2021), text matching (Roberts, Stewart and Nielsen 2020), generalized optimal matching (Kallus 2020)
- R packages include MatchIt, Matching, and PanelMatch
- for the debate around propensity score matching (King and Nielsen 2019), see also Hünermund, (2019)



an example

Ferraro and Hanauer (2014) use matching approach (MDM) to assess the effect of protected areas on poverty reduction



Causal model of PA on poverty effects, source: Ferraro and Hanauer 2014

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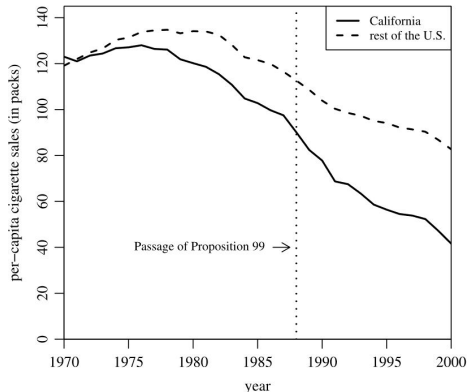
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Synthetic Controls

What if we do only have *one* treated unit?



California introduces tobacco control in 1988, cf. Abadie et al. 2010

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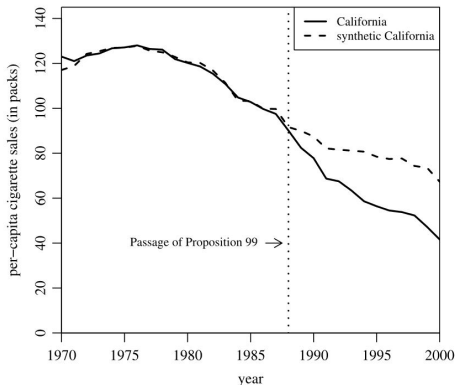
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a case and an idea

How about we compare to a weighted average of untreated?



California introduces tobacco control in 1988, cf. Abadie et al. 2010

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and a notation

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$$\hat{Y}_{t,post}(0) = \mu + \sum_{i=1}^N w_i Y_{i,T}^{obs} \quad (6)$$

"In other words, the imputed control outcome for the treated unit is a linear combination of the control units, with intercept μ and weights w_i for control unit i ." (Doudchenko and Imbens 2020: 7)

the process

We compare the treated to the non-treated

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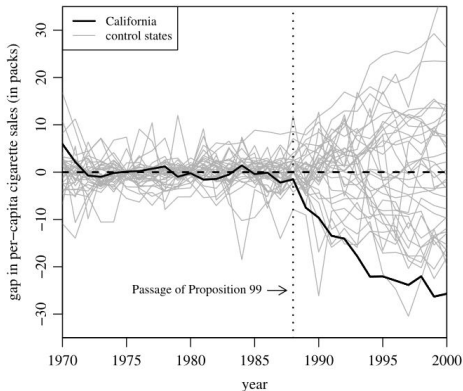


Figure 5. Per-capita cigarette sales gaps in California and placebo gaps in 34 control states (discards states with pre-Proposition 99 MSPE twenty times higher than California's).



the process

and compute the difference to a counterfactual weighted set of untreated

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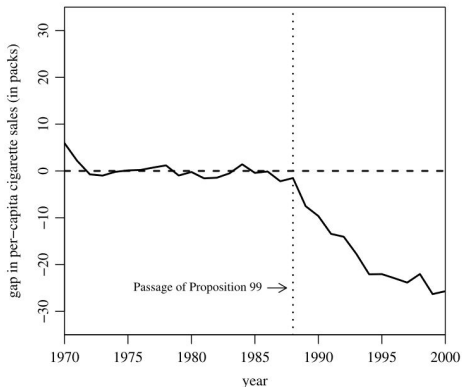
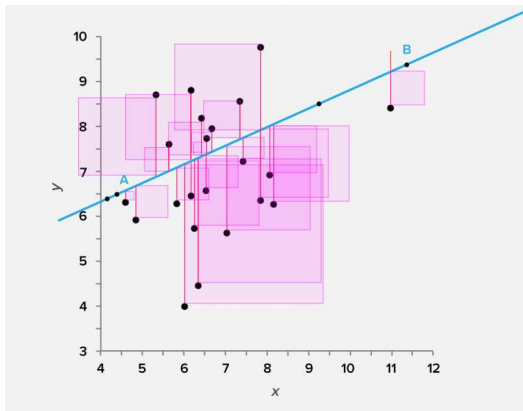


Figure 3. Per-capita cigarette sales gap between California and synthetic California.



estimation

Recall the ordinary least square estimate (OLS)



OLS, img source: [Gavrilova, 2020](#)

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For $\hat{Y}_{t,post}(0) = \mu + \sum_{i=1}^N w_i Y_{i,T}^{obs}$

μ and w_i can, in principle, be estimate with OLS (cf. Doudchenko and Imbens 2020)

$$(\hat{\mu}^{ols}, \hat{w}^{ols}) = \arg \min_{\mu, w} \sum_{s=1}^{T_0} \left(Y_{0, T_0-s+1}^{obs} - \mu - \sum_{i=1}^N w_i \cdot Y_{0, T_0-s+1}^{obs} \right)^2 \quad (7)$$

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For $\hat{Y}_{t,post}(0) = \mu + \sum_{i=1}^N w_i Y_{i,T}^{obs}$

μ and w_i can, in principle, be estimate with OLS (cf. Doudchenko and Imbens 2020)

$$(\hat{\mu}^{ols}, \hat{w}^{ols}) = \arg \min_{\mu, w} \sum_{s=1}^{T_0} \left(Y_{0, T_0-s+1}^{obs} - \mu - \sum_{i=1}^N w_i \cdot Y_{0, T_0-s+1}^{obs} \right)^2 \quad (7)$$

Abadie et al. 2010 impose conditions, $\mu = 0$, $\sum_{i=1}^N w_i = 1$, and $w_i \geq 0 \forall i$.

estimation

For covariate vector X we would want to minimize (cf. Doudchenko and Imbens 2020)

$$\|Y_{t,pre}^{obs} - \mu - w^T Y_{c,pre}^{obs}\|_2^2 = (Y_{t,pre}^{obs} - \mu - w^T Y_{c,pre}^{obs})^T (Y_{t,pre}^{obs} - \mu - w^T Y_{c,pre}^{obs}) \quad (8)$$

This mathing is often performed on lagged outcomes $Y_{t-(1,...,T)}$ and other covariates.

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estimation

For covariate vector X we would want to minimize (cf. Doudchenko and Imbens 2020)

$$\|Y_{t,pre}^{obs} - \mu - w^T Y_{c,pre}^{obs}\|_2^2 = (Y_{t,pre}^{obs} - \mu - w^T Y_{c,pre}^{obs})^T (Y_{t,pre}^{obs} - \mu - w^T Y_{c,pre}^{obs}) \quad (8)$$

This mathing is often performed on lagged outcomes $Y_{t-(1,...,T)}$ and other covariates. So, in simpler terms, $\|X_{treat} - X_{control} W\|$ which resembles a balancing approach (à la matching).

See Doudchenko and Imbens (2020) for a balanced, cross-validated, elastic net type penalty approach, combining Lasso and ridge regressions to regularize w .

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current development

Arkhangelsky et al. 2019 suggest a synthetic diff-in-diff approach, where W denotes binary treatment, and

SynthControl:

$$(\hat{\mu}, \hat{\beta}, \hat{\tau}^{sc}) = \arg \min_{\mu, \beta, \tau} \sum_{i=1}^N \sum_{t=1}^T (Y_{it} - \mu - \beta_t - W_{it}\tau)^2 \hat{w}_i^{sc} \quad (9)$$

DiD:

$$(\hat{\mu}, \hat{\alpha}, \hat{\beta}, \hat{\tau}^{did}) = \arg \min_{\mu, \alpha, \beta, \tau} \sum_{i=1}^N \sum_{t=1}^T (Y_{it} - \mu - \alpha_i - \beta_t - W_{it}\tau)^2 \quad (10)$$

SynthDiD:

$$(\hat{\mu}, \hat{\alpha}, \hat{\beta}, \hat{\tau}^{sdid}) = \arg \min_{\mu, \beta, \tau} \sum_{i=1}^N \sum_{t=1}^T (Y_{it} - \mu - \alpha_i - \beta_t - W_{it}\tau)^2 \hat{w}_i \hat{\lambda}_t \quad (11)$$

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intermediate summary

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A synthetic control approach allows us to

- compare a single treated unit group with an untreated quasi-counterfactual
- you can compute placebo tests for the effect on an untreated unit
- so far, has not been widely applied (for examples see Abadie 2020)
- I think it is so far underestimated (i.e. by applied researchers)



software

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available packages

- Synth
- synthdid
- scul
- gsynth



an example

Bayer and Aklin (2020) use synthetic controls to assess the effect of EU Emission Trading System (ETS) on CO₂ emissions

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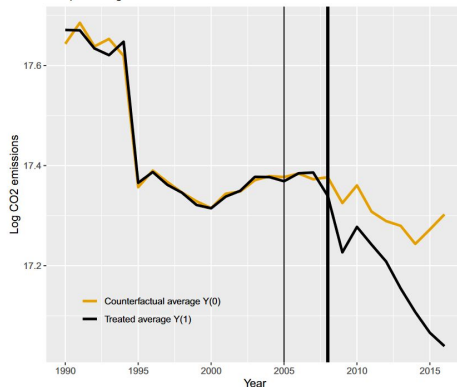
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A Treated and Counterfactual Emission Paths
Sample averages



Effect of the EU ETS over time, source: Bayer and Aklin 2020

2022 ClimBEco course

an example

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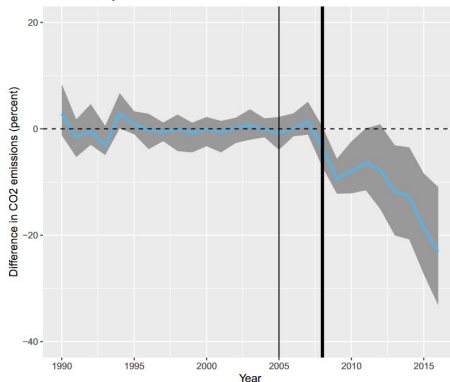
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B ATT Estimates for EU ETS, 2008–2016
Generalized synthetic control



Effect of the EU ETS over time, source: Bayer and Aklin 2020



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