LUND UNIVERSITY

Matching and synthetic controls

Nils Droste

2023 ClimBEco course

Causal Inference from observational data

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
  - classical
  - machine-based learning
- synthetic controls

Intuition

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

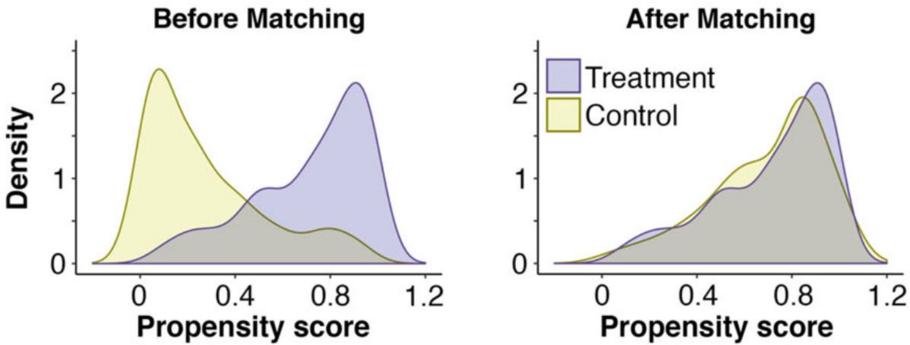

Image source: Schleicher et al. 2020

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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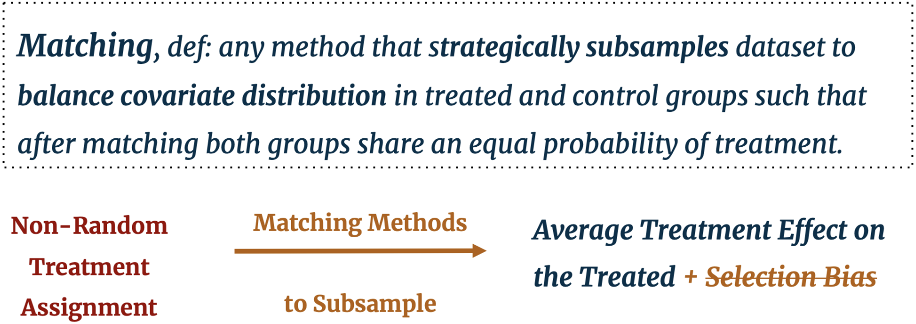
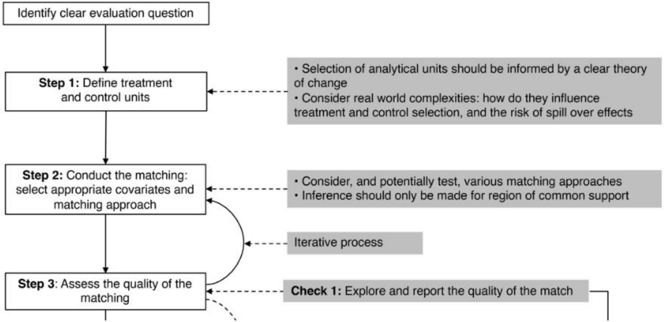


Image source: Image source: Sizemore and Alkurdi 2019

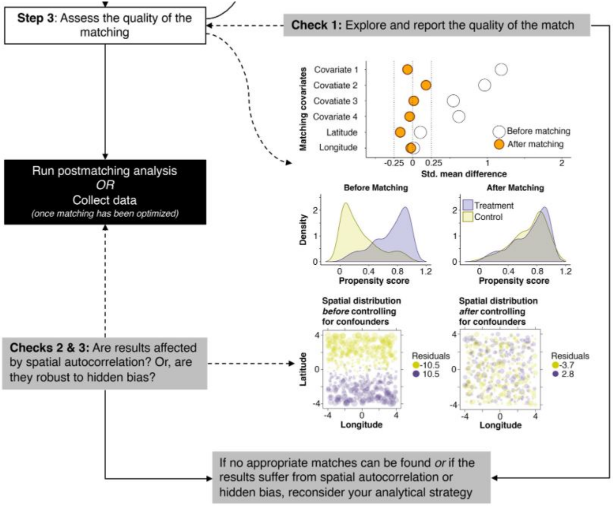
→ matching is a ***pre-analytical procedure***, allowing unbiased inference.

Procedure



Identify clear evaluation question
Step 1: Define treatment and control units
• Selection of analytical units should be informed by a clear theory of change
• Consider real world complexities: how do they influence treatment and control selection, and the risk of spill over effects
Step 2: Conduct the matching: select appropriate covariates and matching approach
• Consider, and potentially test, various matching approaches
• Inference should only be made for region of common support
Iterative process
Step 3: Assess the quality of the matching
Check 1: Explore and report the quality of the match

Procedure



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Basic conditions

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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  - $(Y(1), Y(0)) \perp D$: treatment assignment is independent of the outcomes
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$\rightarrow$ but should maybe not (King and Nielsen 2019), we will see alternatives

Overview

Here is a general overview of possible matching methods

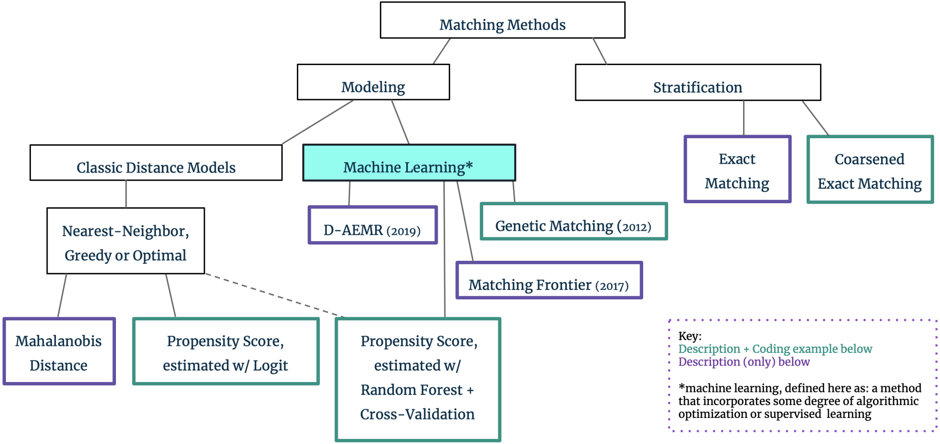

Image source: Sizemore and Alkurdi 2019

Notation

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

$$CATE = E(Y(1) - Y(0)|X = x) \tag{1}$$

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How to find the sufficiently similar subsamples?

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

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

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

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

Exact matching

For exact matching we find exactly equal pairs

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

Note: X can be a vector of covariates.

Coarsened Exact Matching (CEM)

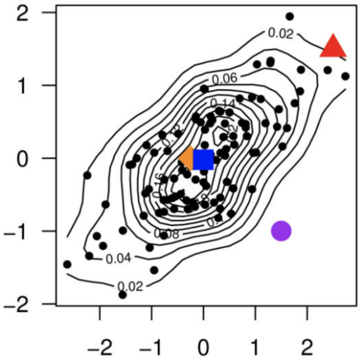
For coarsened exact matching we approximate

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

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.



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

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

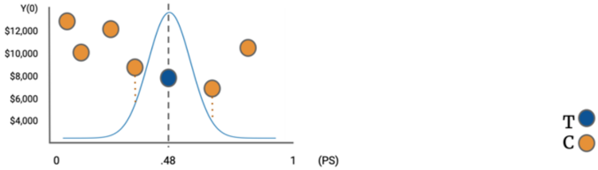
(Left) A contour plot is overlaid on a Mahalanobis distance scatter plot of 100 observations randomly drawn from a bivariate normal distribution. The centroid, in blue, is the reference point for distance between two points.

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



Advantages	Disadvantages
solves matching problem for high dimensions	misspecification of PS model = bad matches
many available R packages for easy implementation	matched pairs may be dissimilar across X

Image source: Sizemore and Alkurdi 2019

example

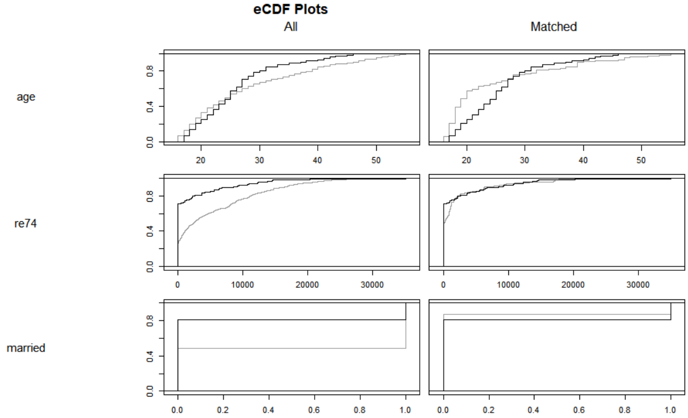

```
library(tidyverse)
library(MatchIt)

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

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

example


```
> 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"))
```



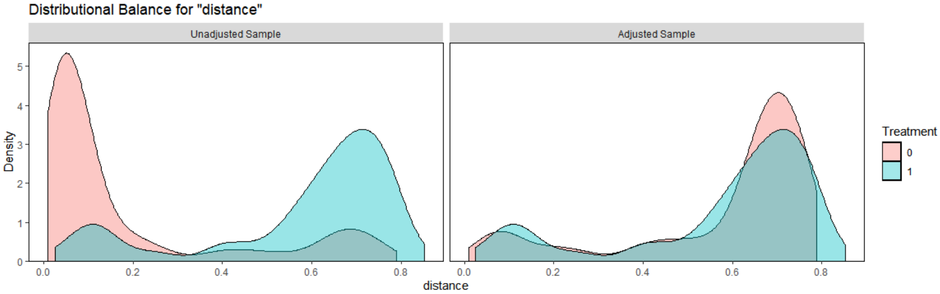
Code source: Greifer 2020

example


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

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

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

example

```
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

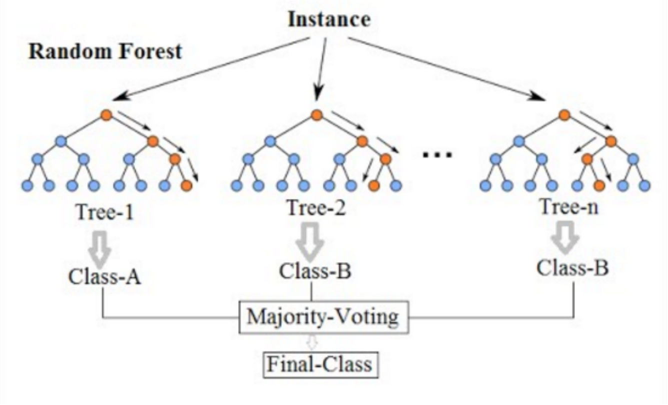
Intermediate discussion

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

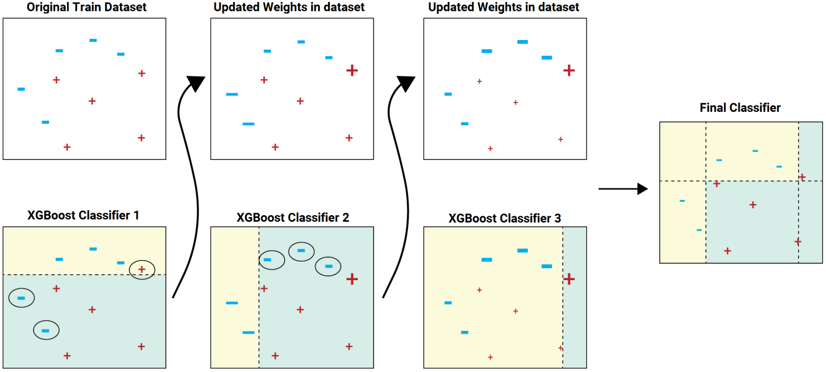


Code source: [Wikipedia]

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)

Genetic matching

Genetic Matching combines PSM and MDM

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

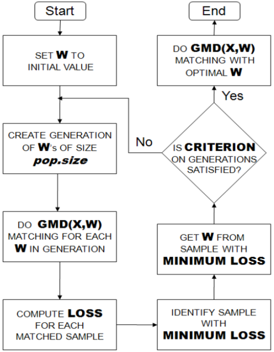
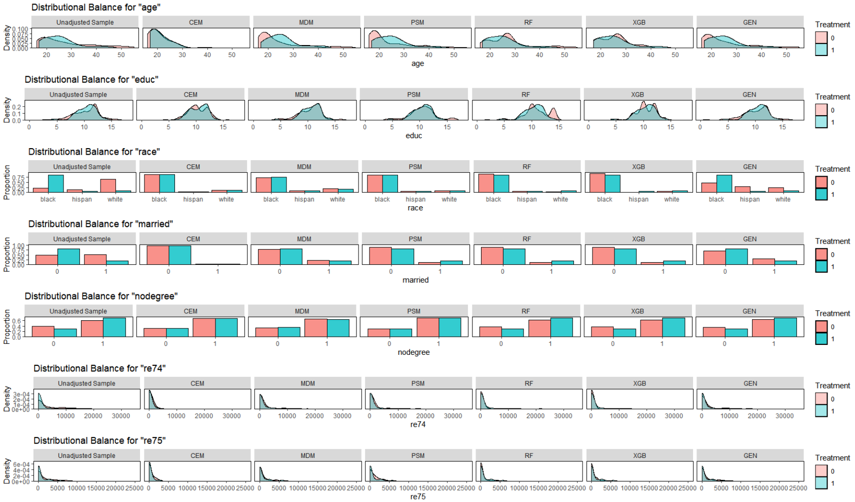


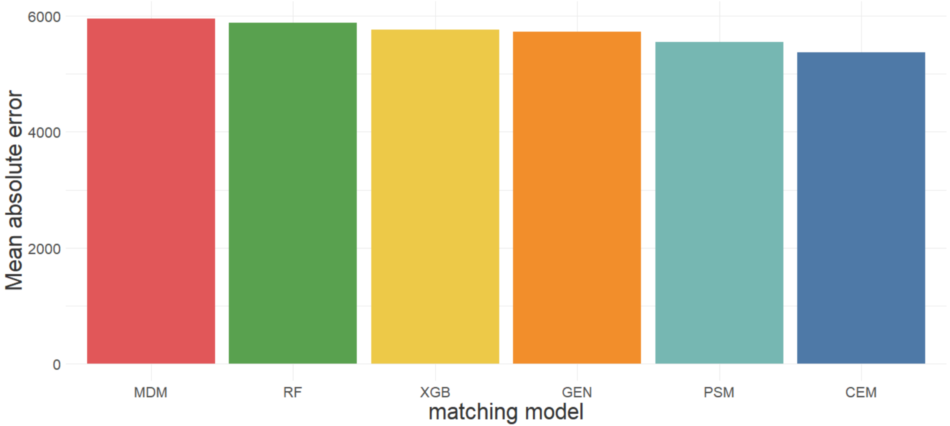
Image source: Sizemore and Alkurdi 2019

comparison - fitting distributions



plotting model comparisons for coviarates of the lalonde data set

comparison - mean absolute error



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

comparison - summary

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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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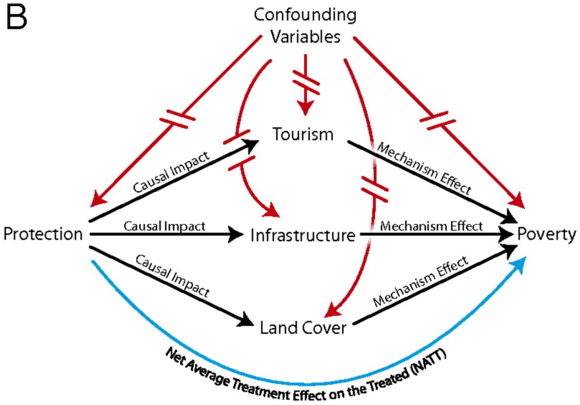
- R packages include MatchIt, Matching, and PanelMatch
- for the debate around propensity score matching (King and Nielsen 2019), see also Hünermund, (2019)

an example

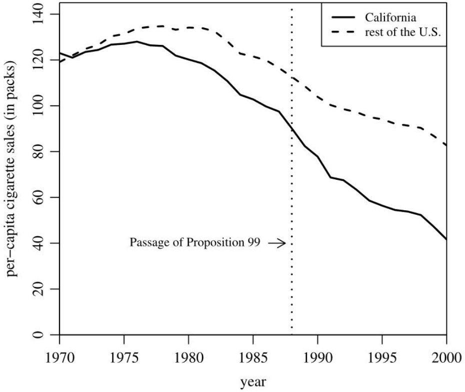
Ferraro and Hanauer (2014) use matching approach (MDM) to assess the effect of protected areas on poverty reduction



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

Synthetic Controls

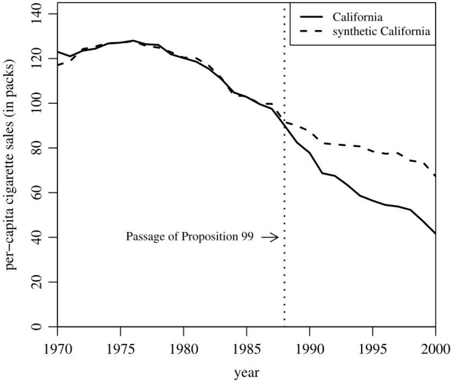
What if we do only have *one* treated unit?



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

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

and a notation

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

"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

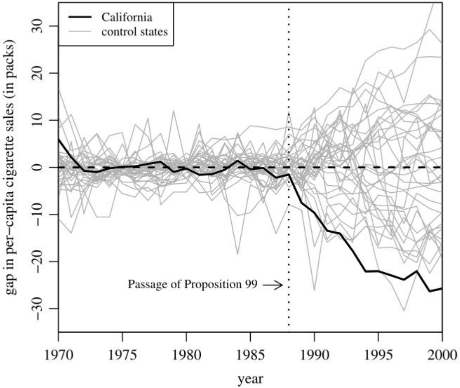


Figure 5. Per-capita cigarette sales gaps in California and placebo gaps in 34 control states (discards states with pre-Proposition 99 MSPE twenty times higher than California's).

A noisy control group, cf. Abadie et al. 2010

the process

and compute the difference to a counterfactual weighted set of untreated

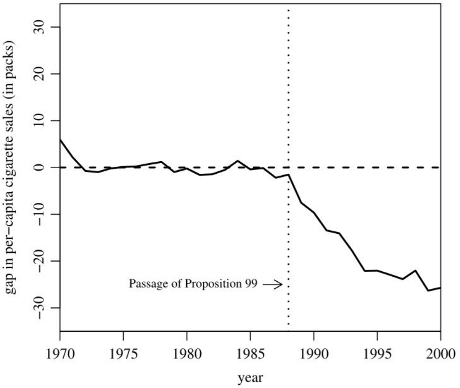
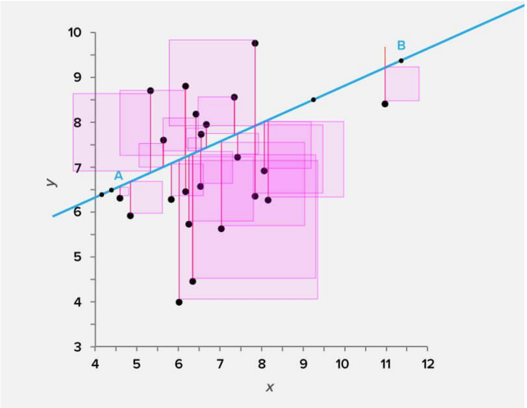


Figure 3. Per-capita cigarette sales gap between California and synthetic California.

California vs SynthCal, cf. Abadie et al. 2010

estimation

Recall the ordinary least square estimate (OLS)



OLS, img source: Gavrilova, 2020

estimation

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)

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

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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)

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

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

estimation

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This matching 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 (á 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.

current development

Arkhangelsky et al. 2021 suggest a synthetic diff-in-diff approach, where W denotes binary treatment, and

SynthControl:

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

DiD:

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

SynthDiD:

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

intermediate summary

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 et al. 2020)
- I think it is so far underestimated (i.e. by applied researchers)

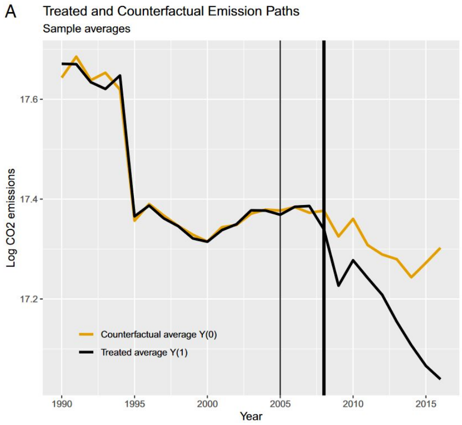
software

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 CO_2 emissions



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

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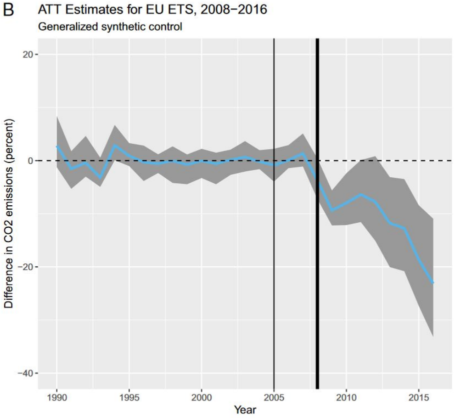

Effect of the EU ETS over time, source: Bayer and Aklin 2020

References I

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Abadie, Alberto et al. (2020). 'Sampling-Based versus Design-Based Uncertainty in Regression Analysis'. In: *Econometrica* 88.1, pp. 265–296. ISSN: 0012-9682. DOI: 10.3982/ecta12675.

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Arkhangelsky, Dmitry et al. (2021). 'Synthetic Difference-in-Differences'. In: *American Economic Review* 111.12, pp. 4088–4118. ISSN: 0002-8282. DOI: 10.1257/aer.20190159. URL: https://doi.org/10.1257/aer.20190159https://github.com/synth-inference/synthdid.Theassociatedvignetteisathttps://synth-inference.github.io/synthdid/.Gotohttps://doi.org/10.1257/aer..

Bayer, Patrick and Michaël Aklin (2020). 'The European Union Emissions Trading System reduced CO2 emissions despite low prices'. In: *Proceedings of the National Academy of Sciences of the United States of America* 117.16, pp. 8804–8812. DOI: 10.1073/pnas.1918128117.

Colson, K. Ellicott et al. (2016). 'Optimizing matching and analysis combinations for estimating causal effects'. In: *Scientific Reports* 6.March, pp. 1–11. DOI: 10.1038/srep23222. URL: http://dx.doi.org/10.1038/srep23222.

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