LUND UNIVERSITY

Matching and synthetic controls

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2021 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:

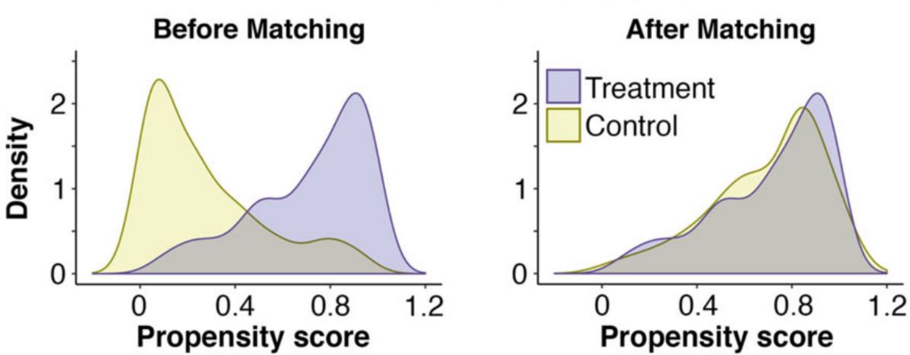

Image source: Schleicher et al. 2020

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> ***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 $\xrightarrow[\text{to Subsample}]{\text{Matching Methods}}$ ***Average Treatment Effect on the Treated + ~~Selection Bias~~***

Image source: Image source: Sizemore and Alkurdi 2019

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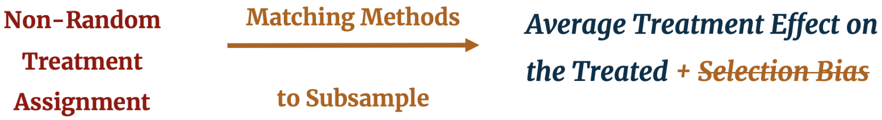

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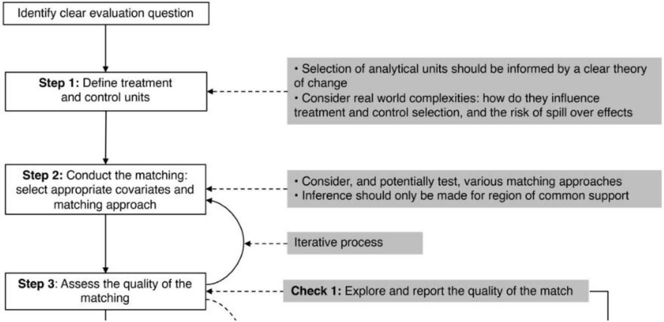
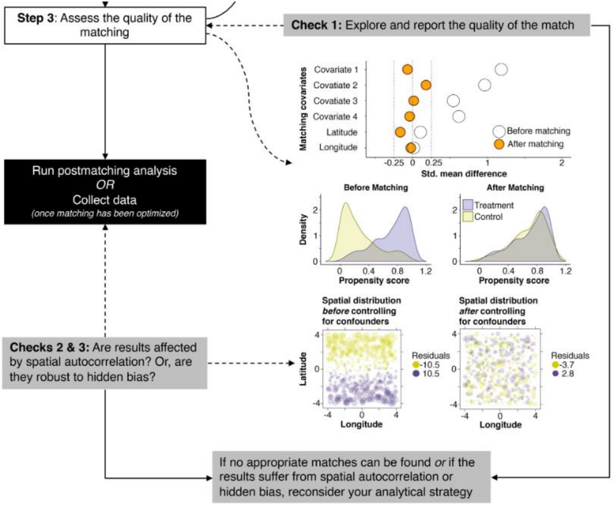
→ matching is a ***pre-analytical procedure***, allowing unbiased inference.

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
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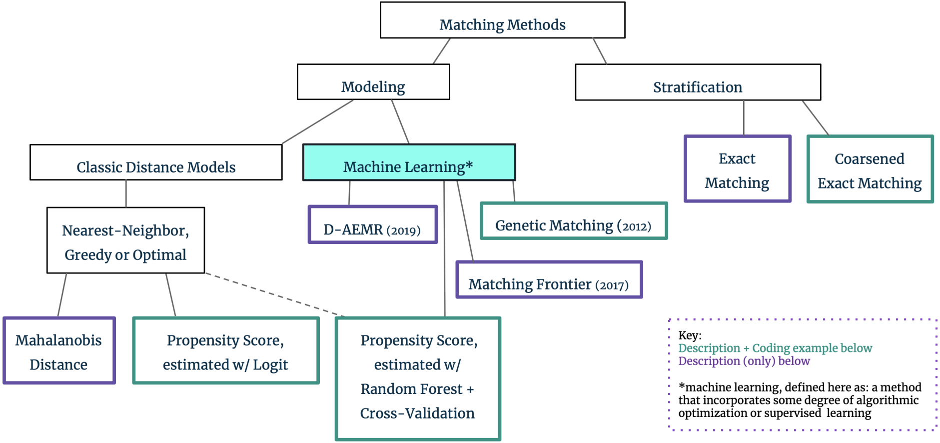
$\rightarrow \pi(X_i) = Pr(D_i = 1|X_i)$ or *propensity score* can be used for matching
$\rightarrow$ but should maybe not (King and R. Nielsen 2019), we will see alternatives

Overview

Here is a general overview of possible matching methods



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

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

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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)

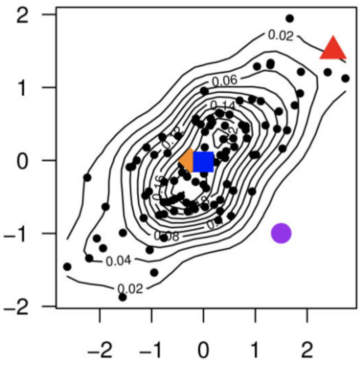
For coarsened exact matching we approximate

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

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]

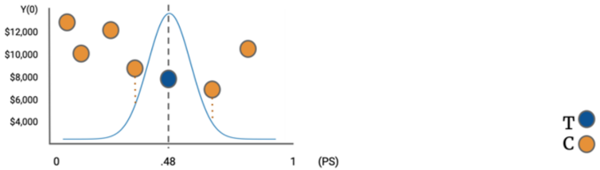
(Left) A contour plot is overlaid on a Mahalanobis distance scatter plot of 100 observations randomly drawn from a bivariate normal distribution. The centroid, in blue, is the reference point for distance between two points.

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

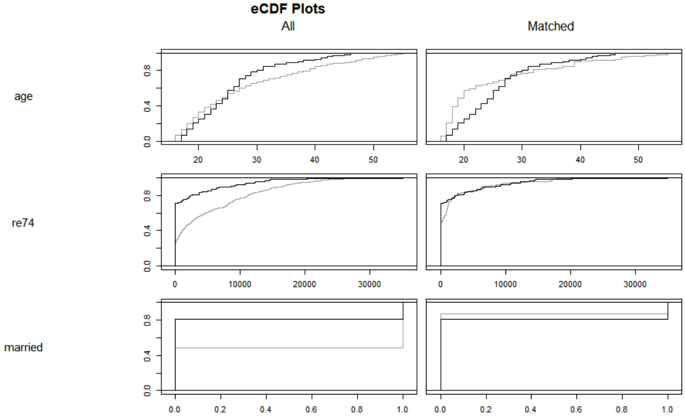

```
library(tidyverse)
library(MatchIt)

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")
```



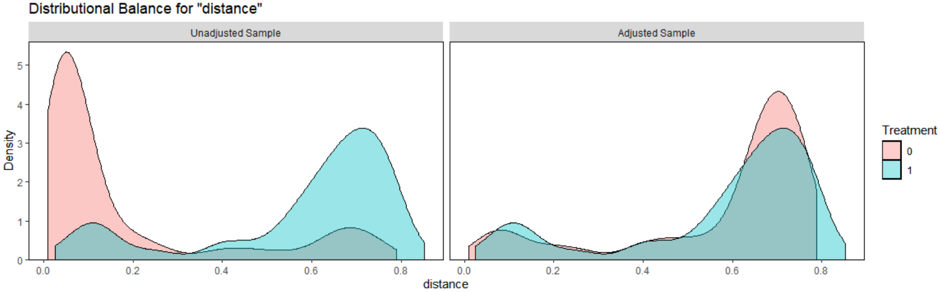
Code source: Greifer 2020

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

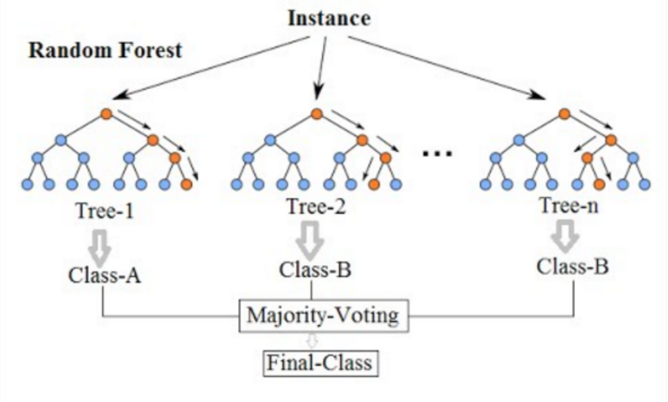
Intermediate discussion

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

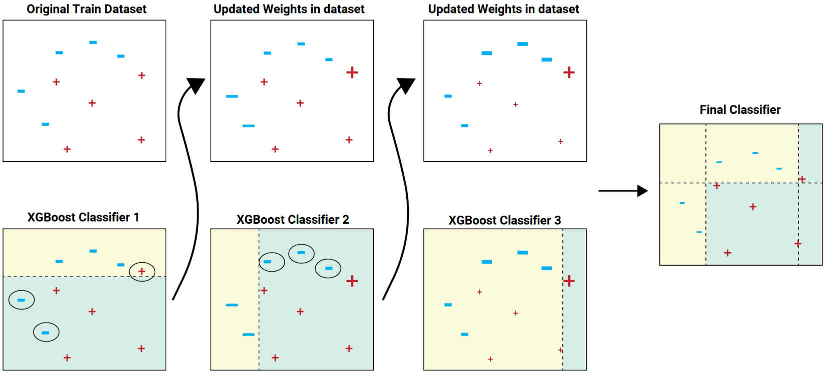


Code source: [Wikipedia]

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

eXtreme Gradient Boosting (XGBoost)

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



Code source: Quant Insti

→ predict treatment (aka propensity scores)

Genetic matching

Genetic Matching combines PSM and MDM

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

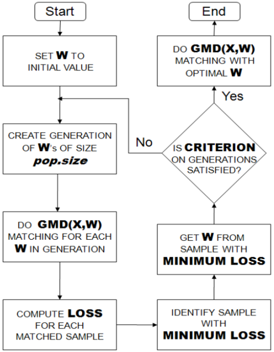
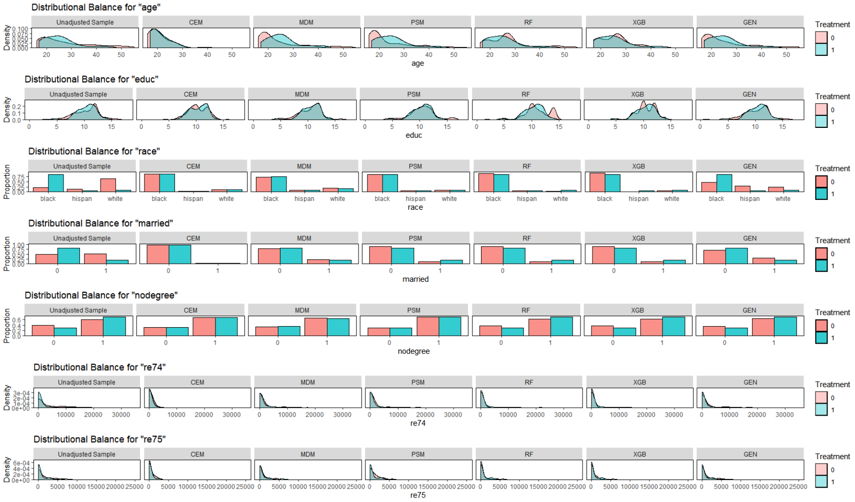


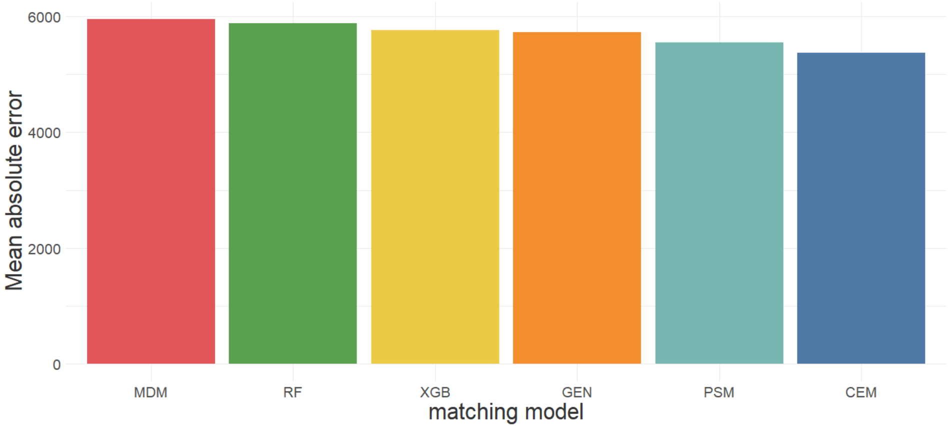
Image source: Sizemore and Alkurdi 2019

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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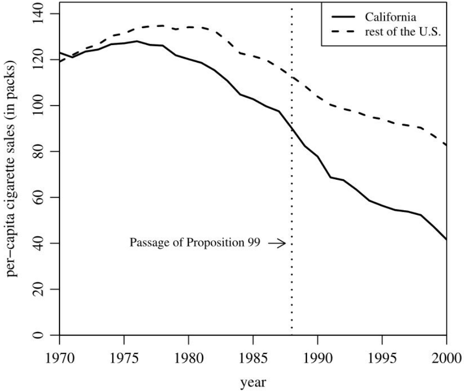
- for the debate around propensity score matching (King and R. Nielsen 2019), see also Hünermund, (2019)

a case

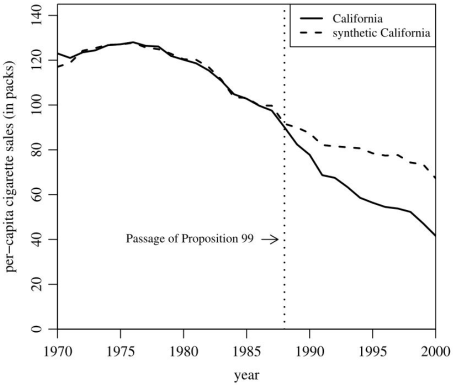
What if we do only have one treated unit?



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

and an idea

How about we compare to a weighted average of untreated?



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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 2016

the process

We compare the treated to the non-treated

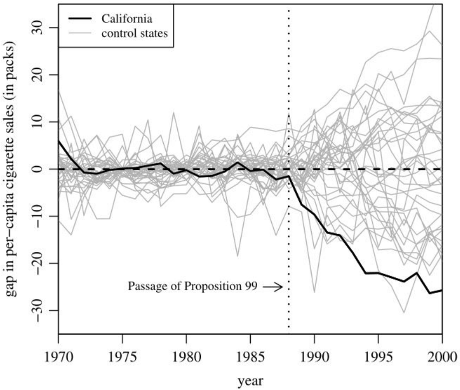

Figure 5. Per-capita cigarette sales gaps in California and placebo gaps in 34 control states (discards states with pre-Proposition 99 MSPE twenty times higher than California's).

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

the process

And compute a synthetic control out of a weighted set of the untreated

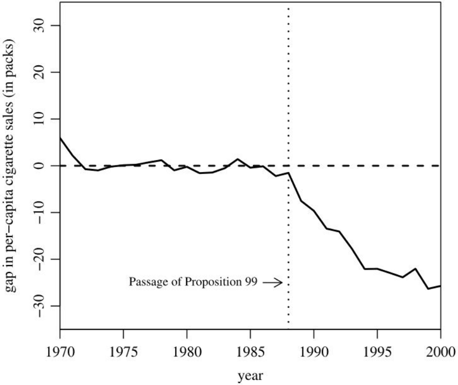

Figure 3. Per-capita cigarette sales gap between California and synthetic California.

California vs SynthCal, cf. Abadie et al. 2010

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