Australian National University

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OLS and Matching

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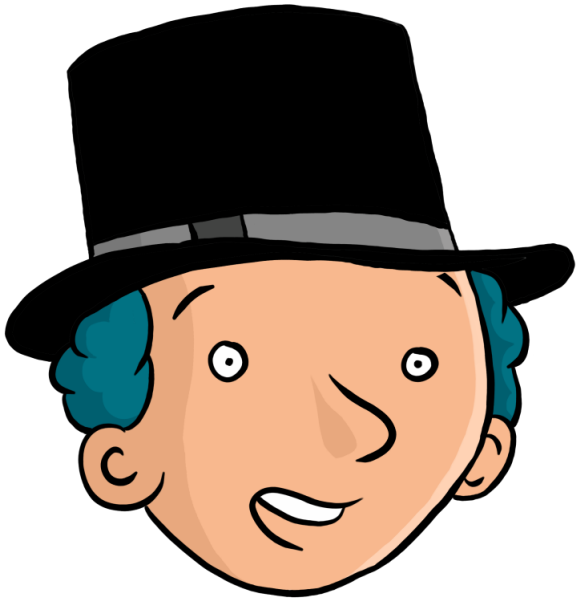
The intuition

- Assumption for both OLS and Matching:
  - Everything that determines program allocation is observed
- Then after controlling for observed variables, the assignment into treatment and control is random
- OLS compares the averages of all treated with average of all untreated
- Matching calculates the average of the difference between each treated and its chosen comparison in untreated

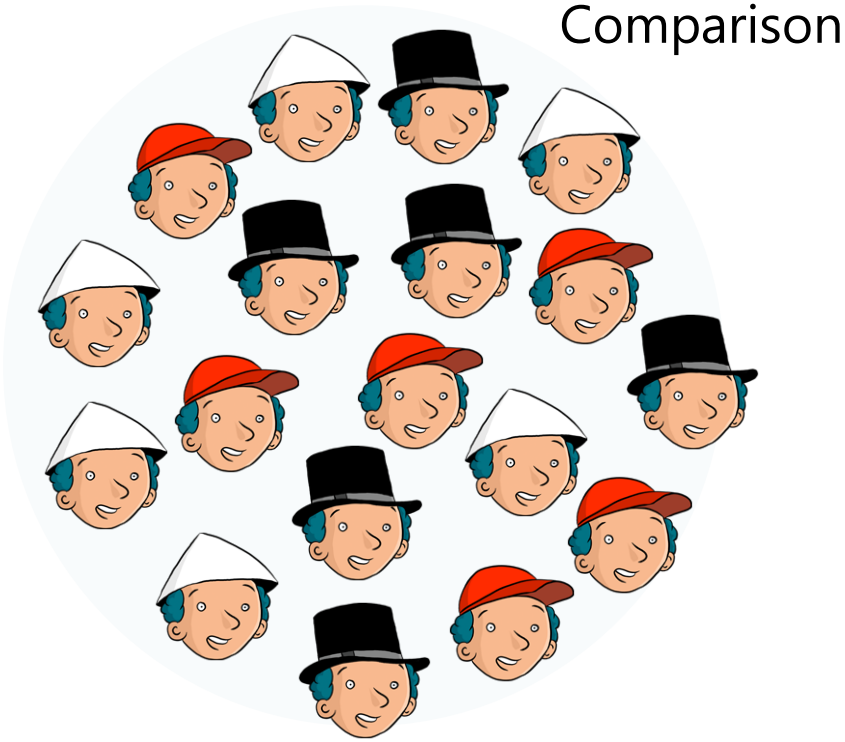
Intuition of Matching: The Perfect Clone

Beneficiary

Clone



Intuition of Matching: The Perfect Clone



- Matching identifies a control group that is as similar as possible to the treatment group!

Principle of matching

Indiv 1:

X_1

Given that $T = 1$

Indiv 2:

X_2

Given that $T = 1$

…

Indiv N_T:

X_{N_T}

Given that $T = 1$

Match for Indiv 1:

X_{M1}

Given that $T = 0$

Match for Indiv 2

X_{M2}

Given that $T = 0$

…

Match for Indiv N_T:

X_{MN_T}

Given that $T = 0$

Matching treated to controls

- If we know the selection criteria (X), then we know who is eligible
- If X consists of discrete variables we can match treated and non-treated with similar eligibility (according to X):
  1. Assign (or *match*) observations into cells with similar X,
  2. drop the cells where we have only treated or controls,
  3. and simply do a non-parametric difference in each cell
  4. to retrieve ATE for respective cells
- However, matching suffers from the ***curse of dimensionality***!
  - If selection criteria X includes 1 or two 2 variables: no problem
  - But as the dimensions of selection increase → matching becomes impossible very quickly

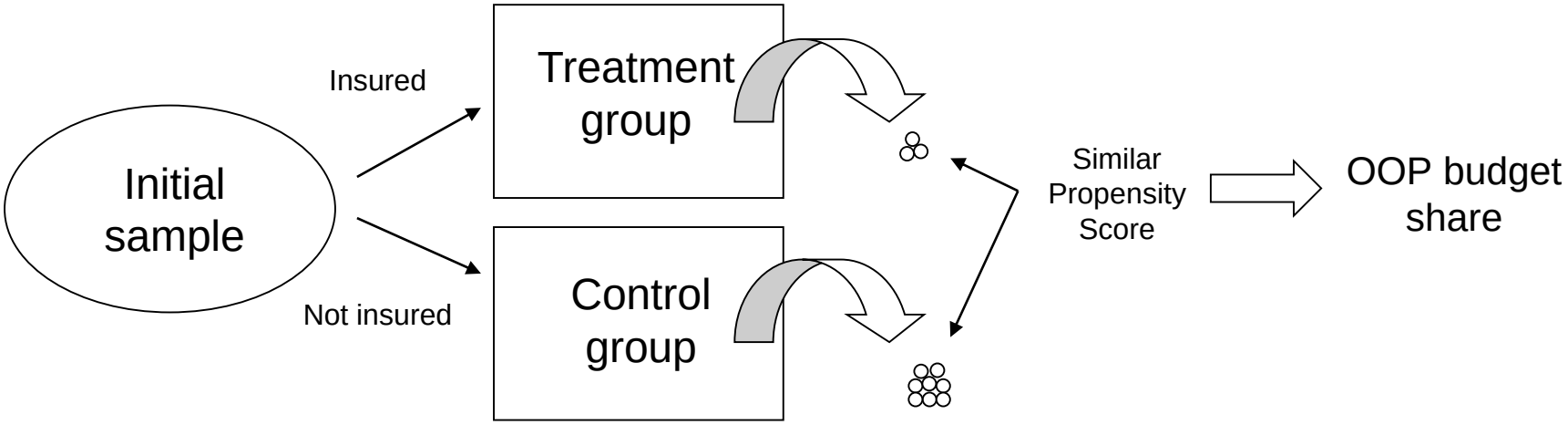
Propensity score matching (1)

- An alternative approach: do not match on observed characteristics, but on the **probability of being treated**.
- Propensity score matching (PSM) is a method that summarizes X to a single indicator: the probability of selection as a function of X

$$p(X) = \Pr(T = 1|X) = F(\hat{\beta}X)$$

- This is the ***propensity score***: the conditional probability of receiving treatment given X
- This greatly reduces dimensionality: now only match on 1 variable!

Example: effect of health insurance on health spending



Propensity score matching: overview

Indiv 1:

$\Pr(T = 1|X_1) = p_1$

Given that $T = 1$

Indiv 2:

$\Pr(T = 1|X_2) = p_2$

Given that $T = 1$

$\cdots$

Indiv N:

$\Pr(T = 1|X_N) = p_N$

Given that $T = 1$

Match for Indiv 1:

$\Pr(T = 1|X_{M1}) \approx p_1$

Given that $T = 0$

Match for Indiv 2:

$\Pr(T = 1|X_{M2}) \approx p_2$

Given that $T = 0$

$\cdots$

Match for Indiv N:

$\Pr(T = 1|X_{MN}) \approx p_N$

Given that $T = 0$

$Difference\ in\ outcome$ $\quad$ $Difference\ in\ outcome$ $\quad$ $Difference\ in\ outcome$ $\xrightarrow{\text{average}}$ ATT

Estimating the propensity score

- Estimate $p(X)$ by means of logit or probit estimation and then predicting the probability of selection

$$p(X) = \Pr(T = 1|X) = F(\hat{\beta}X)$$

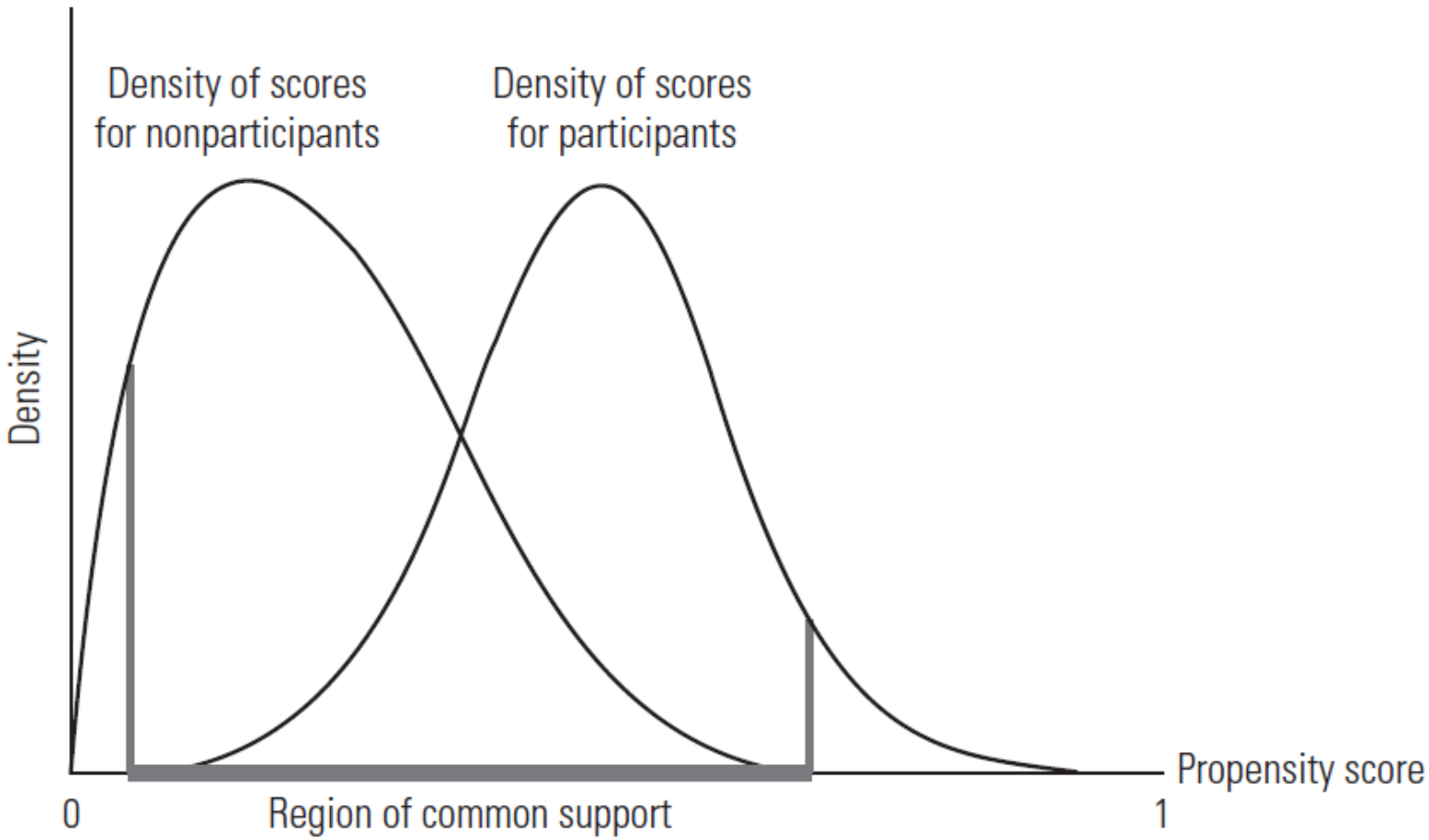
- Choice of X:
  - Covariates must include determinants of participation
  - Exogenous data
    - Measured prior to program exposure
    - Unaffected by the program
  - Include trends prior to program exposure if possible
  - Knowledge about the program, setting and selection process
    - Qualitative field work

Range of common support

- Common support:
  - The distribution of $p(X)$ may differ for treated and controls
  - Especially for controls it can be hard to find high values of $p(X)$
  - Matching is only possible if there is a similar range of $p(X)$ for both treated and control units!

  $\rightarrow$ Restrict the match to the ***range of common support***!
- Look where distributions of the propensity score overlap
- Plot $p(X)$ for the treated and non-treated
- Drop non-treated who fall outside of the region of common support

Range of common support



Source: Khandker et al. (2010)

Matching methods

- Once we have estimated $p(X)$ there are several methods for propensity score matching
  1. Nearest neighbour matching
  2. Calliper matching
  3. Kernel matching
     - Weighting by the propensity score

- Basically, these propensity score matching methods aim to recreate an experimental design *ex-post*, by re-weighting the data based on $p(X)$

Summarize: how to do PSM

1. Find data with observed T_i, Y_i and X_i for treated and non-treated
2. Understand the selection process
3. Estimate propensity score $p(X) = \Pr(T = 1 \mid X)$
4. Check the range of common support
5. Choose matching method
6. Match units within range of common support
7. Check balancing properties $T \perp X \mid p(X)$
8. Estimate treatment effects for matched sample

Comparing PSM and OLS

- Identifying assumption
  - Both methods assume that T is exogenous to Y, conditional on X
- Functional form
  - PSM does not impose functional form (semi-parametric estimation)
  - OLS typically imposes a linear specification and assumes constant treatment effects
- Sample
  - PSM only considers observations within range of common support
  - OLS typically uses full sample
- Use of control variables
  - PSM only considers determinants of the selection process (T)
  - OLS should control for determinants of the outcome (Y)

Exercise: Askeskin
using Matching.dta

Sparrow, Suryahadi and Widyanti (2013) “Social health insurance for the poor: Targeting and impact of Indonesia’s Askeskin programme” Social Science & Medicine 96, pp. 264-271

Outcome variables

- Total outpatient utilization (outpat)
- Total outpatient utilization by public provider (outpu)
- Total outpatient utilization by private provider (outpr)
- Out-of-pocket health spending per capita (pcexph)
- Household budget share (oop)
- Incidence of catastrophic health spending (chs10, chs15)

Which control variables?

- Consider selection process and targeting variables:
  - Household size and composition
  - Education of the head of households
  - Participation in other insurance schemes
  - Housing conditions (size, quality and ownership of house)
  - Access to piped water
  - Regional targeting is captured by districts coverage
  - Province effects
- Health: illness of household last month?

Useful Stata commands

- Naïve comparison
  - summarize, table, ttest
- OLS, logit, probit regressions
- Propensity score matching
  - Will use user written ado files: psmatch2, pstest, psgraph
  - May search in the web using Stata interface (type net search psmatch2)
  - Follow the instructions on screen to install

Exercise

1. Estimate the PS: Select the covariates and a specification
2. Choose a matching procedure
3. Are covariates balanced for matched treated & controls?
4. Assess the range of common support
5. Estimate the impact of Askeskin on the outcome variables
6. Does the choice of matching procedures affect impact estimates?