

2018 STATA ECONOMETRICS WINTER SCHOOL

Anabela Carneiro¹ João Cerejeira² Miguel Portela^{2,3} Paulo
Guimarães^{1,4}

¹FEP and CEF.UP – U.Porto

²NIPE – UMinho

³IZA, Bonn

⁴Banco de Portugal

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Propensity score matching (PSM) constructs a statistical comparison group that is based on a model of the probability of participating in the treatment, using observed characteristics and these are believed to affect program participation.

Participants are then matched on the basis of this probability, or propensity score, to nonparticipants.

PSM is a useful approach when only observed characteristics.

The average treatment effect of the program is then calculated as the mean difference in outcomes across these two groups.

Introduction

With matching methods, one tries to develop a counterfactual or control group that is as similar to the treatment group as possible in terms of observed characteristics.

The idea is to find, from a large group of nonparticipants, individuals who are observationally similar to participants in terms of characteristics not affected by the program.

If one assumes that differences in participation are based solely on differences in observed characteristics, and if enough nonparticipants are available to match with participants, the corresponding treatment effect can be measured even if treatment is not random.

In PSM, each participant is matched to a nonparticipant on the basis of a single propensity score, reflecting the probability of participating conditional on their different observed characteristics X_i .

PSM constructs a statistical comparison group that is based on a model of the probability of participating in the treatment T conditional on observed characteristics X , or the propensity score: $P(X) = \Pr(T = 1|X)$.

Rosenbaum and Rubin (1983): under certain assumptions, matching on $P(X)$ is as good as matching on X . Assumptions:

- conditional independence;
- presence of a common support.

Assumption of Conditional Independence

Conditional independence states that given a set of observable covariates X that are not affected by treatment, potential outcomes Y are independent of treatment assignment.

$$(Y_i^T, Y_i^C) \perp T_i | X_i. \quad (1)$$

To estimate the ATT a weaker assumption is needed:

$$Y_i^C \perp T_i | X_i. \quad (2)$$

Assumption of Conditional Independence

Conditional independence is a strong assumption and is not a directly testable criterion; it depends on specific features of the program itself.

If unobserved characteristics determine program participation, conditional independence will be violated, and PSM is not an appropriate method.

Assumption of Common Support

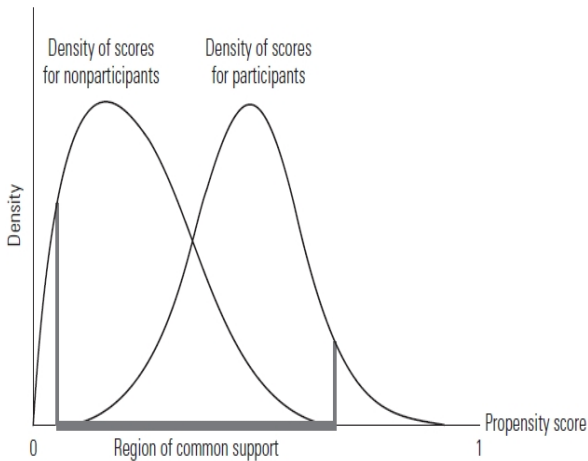
Treatment observations have comparison observations “nearby” in the propensity score distribution.

The effectiveness of PSM also depends on having a large and roughly equal number of participant and nonparticipant observations so that a substantial region of common support can be found.

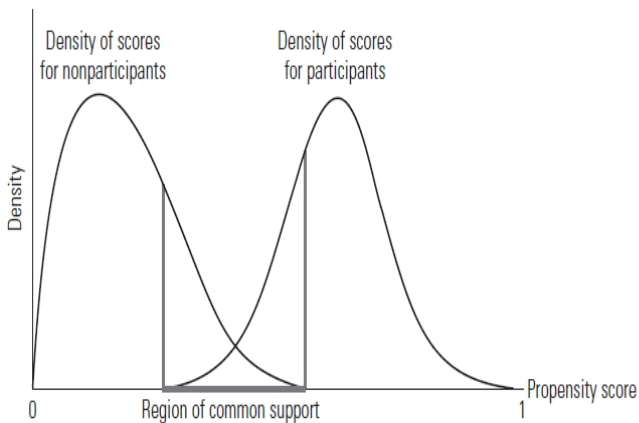
$$0 < P(T_i = 1|X_i) < 1 \quad (3)$$

Treatment units will therefore have to be similar to nontreatment units in terms of observed characteristics unaffected by participation; thus, some nontreatment units may have to be dropped to ensure comparability.

Example of Common Support



Example of Poor Balancing and Weak Common Support



The ATT using PSM

With cross-section data and within the common support, the treatment effect can be written as follows:

$$ATT_{PSM} = E_{P(X)|T=1} \{E[Y^T | T = 1, P(X)] - E[Y^C | T = 0, P(X)]\}. \quad (4)$$

$$ATT_{PSM} = \frac{1}{N} \left[\sum_{i \in T} Y_i^T - \sum_{j \in C} w(i, j) Y_j^C \right]. \quad (5)$$

Application of the PSM Method

Step 1: Estimating a model of program participation

Step 2: Defining the region of common support and balancing tests

Step 3: Matching Participants to Nonparticipants

- Nearest-neighbor matching.
- Caliper or radius matching.
- Stratification or interval matching.
- Kernel and local linear matching.
- Difference-in-difference matching

Step 4: Calculating the Average Treatment Impact