

The PSMATCH procedure

The PSMATCH procedure provides a variety of tools for performing propensity score analysis. The PSMATCH procedure reduces the effects of confounding in nonrandomized trials or observational studies where the subjects are not randomly assigned to the treatment and control groups.

The PSMATCH procedure computes propensity scores, which estimate the probability that a subject is assigned to treatment given a set of pretreatments (baseline) covariates. The following methods for using the propensity scores to adjust the data for valid estimation of treatment effect are available:

- Inverse probability of treatment weighting and weighting by the odds.
- Stratification of observations that have similar propensity scores. In a subsequent outcome analysis, the treatment effect can be estimated within each stratum, and the estimates can be combined across strata to compute an average treatment effect.
- Matching treated unit with one or more control units that have a similar value of the propensity score.

Methods of matching include:

- fixed ratio matching
- variable ratio matching
- full matching

Provides various plots for assessing balance. Included plots are:

- cloud plots, which are scatter plots in which the points are jittered to prevent overplotting
- box plots for continuous variables
- bar charts for classification variables
- a standardized differences plot that summarizes differences between the treated and control groups

The PSMATCH procedures saves propensity scores and weights in an output data set that contains a sample that has been adjusted either by weighting, stratification, or matching. If the sample is stratified, you can save the strata identification in the output data set. If the sample is matched, you can save the matching identification in the output data set.

Re-write

SAS provides multiple tools to perform propensity score analysis via SAS STAT procedure called PSMATCH. PSMATCH helps reduce the effects of confounding in studies without random assignment to

control and treatment groups. This procedure computes the propensity score, which estimate the probability of assignment to treatment based on set of baseline covariates. Using methods listed further below, data could be adjusted for valid treatment effect. Some methods are:

- Matching treated unit with one or more control units with same propensity score
- Stratification of observations that have like propensity scores.
- Inverse probability of treatment weighting and weighting by the odds.

Matching methods are:

1. Full matching
2. Fixed ratio matching, and
3. Variable ratio matching

PSMATCH provides plots for finding balance:

Plot	Description
Cloud	Prevents over plotting by spreading points (scatter plot)
Box	Continuous Variables
Bar	Variables classification
Standard Difference	Differences between control & treated groups are summarized.

Results from PSMATCH procedure are in an output sas data set format. Depending on the sample; matched or stratified, strata or match identification is saved.

SAS/IML® or SAS/OR® is needed to use an optimal matching method in PROC PSMATCH such as METHOD=FULL, METHOD=OPTIMAL, or METHOD=VARRATIO.