

# Package ‘PSweight’

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**Type** Package

**Title** Propensity Score Weighting for Causal Inference

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**Description** Supports propensity score weighting analysis of observational studies and randomized trials. Enables the estimation and inference of average causal effects among target populations with binary and multiple treatments using the methods developed in Li, Morgan and Zaslavsky (2018) <doi:10.1080/01621459.2016.1260466> and Li and Li (2019) <doi:10.1214/19-AOAS1282>.

**Depends** R (>= 3.5.0)

**License** GPL (>= 2)

**URL** <https://github.com/thuizhou/PSweight>

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**Suggests** knitr, rmarkdown

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plot.SumStat	<i>Plot the distribution of propensity scores and balance statistics</i>
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---

### Description

Summarize the SumStat x, generate histogram or density of estimated propensity scores and plot the balance statistics under weighting versus no weighting.

### Usage

```
## S3 method for class 'SumStat'
plot(
  x,
  type = "balance",
  weighted.var = TRUE,
  threshold = 0.1,
  metric = "ASD",
  ...
)
```

### Arguments

x	a SumStat object obtained with <code>SumStat</code> function.
type	a character indicating the type of plot to produce, including histogram of estimated propensity scores ("hist"), density of estimated propensity scores ("density"), and plot of balance statistics ("balance").
weighted.var	logical. Indicating whether weighted variance should be used in calculating the balance statistics. Default is TRUE.
threshold	an optional numeric value indicating the balance threshold for the balance plot. Default is 0.1. Only valid when type = "balance".

metric a character indicating the type of metric used in balance plot. Only "ASD" or "PSD" is allowed. If not specified, the default is "ASD". See [summary.SumStat](#) for additional details on balance metrics.

... further arguments passed to or from other methods.

### Details

For the balance plot, a vertical line at threshold is used to define balance on covariates. The default value is threshold = 0.1 following Austin and Stuart (2015). If more than 2 treatments are considered, only density of the estimated generalized propensity scores will be produced, regardless of whether type = "density" or type = "hist".

### Value

Plot of the indicated type.

### References

Austin, P.C. and Stuart, E.A. (2015). Moving towards best practice when using inverse probability of treatment weighting (IPTW) using the propensity score to estimate causal treatment effects in observational studies. *Statistics in Medicine*, 34(28), 3661-3679.

### Examples

```
data("psdata")
ps.formula<-trt~cov1+cov2+cov3+cov4+cov5+cov6
msstat <- SumStat(ps.formula, trtgrp="2", data=psdata,
  weight=c("ATE", "AT0", "ATT"))

plot(msstat, type="hist")
plot(msstat, type="balance", weighted.var=TRUE, threshold=0.1, metric="ASD")
```

---

print.PSweight      *Print the results of PSweight*

---

### Description

The `print` method for class "PSweight"

### Usage

```
## S3 method for class 'PSweight'
print(x, ...)
```

### Arguments

x an object used to select a method.

... further arguments passed to or from other methods.

**Value**

The output from `print`

---

<code>print.PSweightsum</code>	<i>Print the results of Summary.PSweight</i>
--------------------------------	--

---

**Description**

The `print` method for class "PSweightsum"

**Usage**

```
## S3 method for class 'PSweightsum'  
print(x, ...)
```

**Arguments**

<code>x</code>	an object used to select a method.
<code>...</code>	further arguments passed to or from other methods.

**Value**

The output from `print`

---

<code>print.SumStat</code>	<i>Print the results of SumStat</i>
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---

**Description**

The `print` method for class "SumStat"

**Usage**

```
## S3 method for class 'SumStat'  
print(x, ...)
```

**Arguments**

<code>x</code>	an object used to select a method.
<code>...</code>	further arguments passed to or from other methods.

**Value**

The output from `print`

---

print.SumSumStat	<i>Print the results of Summary.SumStat</i>
------------------	---

---

**Description**

The `print` method for class "SumSumStat"

**Usage**

```
## S3 method for class 'SumSumStat'  
print(x, ...)
```

**Arguments**

x	an object used to select a method.
...	further arguments passed to or from other methods.

**Value**

The output from `print`

---

psdata	<i>Simulated dataset for PSweight</i>
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---

**Description**

This is a simulated observational study with three treatment groups to illustrate the utility of PSweight.

**Usage**

```
data(psdata)
```

**Format**

A data frame with 1500 rows and 8 columns.

**Details**

The simulated dataset includes 1500 rows, with each row representing information recorded from each individual. There are 8 variables (columns). The treatment is the variable `trt`, which has three treatment arms. The outcome of interest is variable `Y`. `cov1-cov6` are pre-treatment covariates among which `cov1-cov5` are continuous, and `cov6` is binary.

**Examples**

```
data("psdata")
```

---

PStrim

*Trim the input data and propensity estimate*


---

### Description

Trim the original data and propensity estimate according to symmetric propensity score trimming rules.

### Usage

```
PStrim(data, ps.formula = NULL, zname = NULL, ps.estimate = NULL, delta = 0)
```

### Arguments

<code>data</code>	an optional data frame containing the variables required by <code>ps.formula</code> .
<code>ps.formula</code>	an object of class <code>formula</code> (or one that can be coerced to that class): a symbolic description of the propensity score model to be fitted. Additional details of model specification are given under ‘Details’. This argument is optional if <code>ps.estimate</code> is not <code>NULL</code> .
<code>zname</code>	an optional character specifying the name of the treatment variable in <code>data</code> .
<code>ps.estimate</code>	an optional matrix or data frame containing estimated (generalized) propensity scores for each observation. Typically, this is an $N$ by $J$ matrix, where $N$ is the number of observations and $J$ is the total number of treatment levels. Preferably, the column name of this matrix should match the name of treatment level, if column name is missing or there is a mismatch, the column names would be assigned according to alphabetic order of the treatment levels. A vector of propensity score estimates is also allowed in <code>ps.estimate</code> , in which case a binary treatment is implied and the input is regarded as the propensity to receive the last category of treatment by alphabetic order, unless otherwise stated by <code>trtgrp</code> .
<code>delta</code>	trimming threshold for estimated (generalized) propensity scores. Should be no larger than $1 / \text{number of treatment groups}$ . Default is 0, corresponding to no trimming.

### Details

A typical form for `ps.formula` is `treatment ~ terms` where `treatment` is the treatment variable (identical to the variable name used to specify `zname`) and `terms` is a series of terms which specifies a linear predictor for treatment. `ps.formula` specifies generalized linear model for estimating the propensity scores, when `ps.estimate` is `NULL`. See `glm` for more details on generalized linear models.

When comparing two treatments, `ps.estimate` can either be a vector or a two-column matrix of estimated propensity scores. If a vector is supplied, it is assumed to be the propensity scores to receive the treatment, and the treatment group corresponds to the last group in the alphabetic order, unless otherwise specified by `trtgrp`. When comparing multiple ( $J \geq 3$ ) treatments, `ps.estimate` needs to be specified as an  $N$  by  $J$  matrix, where  $N$  indicates the number of observations, and  $J$

indicates the total number of treatments. This matrix specifies the estimated generalized propensity scores to receive each of the  $J$  treatments. In general, `ps.estimate` should have column names that indicate the level of the treatment variable, which should match the levels given in `Z`. If column names are empty or there is a mismatch, the column names will be created following the alphabetic order of values in `Z`, and the rightmost column of `ps.estimate` is assumed to be the treatment group, when estimating ATT. `trtgrp` can also be used to specify the treatment group for estimating ATT.

The argument `zname` is required when `ps.estimate` is not `NULL`.

## Value

`PStrim` returns a list of the following values:

`data` a data frame of trimmed data.

`trim_sum` a table summarizing the number of cases by treatment groups before and after trimming.

`ps.estimate` an optional dataframe of propensity estimate after trimming if propensity estimate is imported.

## Examples

```
data("psdata")

# the propensity model
ps.formula<-trt~cov1+cov2+cov3+cov4+cov5+cov6

# trim the original data by setting the threshold of propensity as 0.05
PStrim(data=psdata, ps.formula=ps.formula, delta=0.05)
```

---

PSweight

*Estimate causal effects by propensity score weighting*

---

## Description

The function `PSweight` is used to estimate the average potential outcomes corresponding to each treatment group among the target population. The function currently implements three types of weights: the inverse probability weights (target population is the combined population), ATT weights (target population is the population receiving one treatment) and overlap weights (target population is the overlap population at clinical equipoise). Augmented propensity score weighting estimators are also allowed, with propensity scores and outcome estimates either estimated within the function, or estimated by external routines.

## Usage

```
PSweight(
  ps.formula = NULL,
  ps.estimate = NULL,
```

```

  trtgrp = NULL,
  zname = NULL,
  yname,
  data,
  weight = "ATO",
  delta = 0,
  augmentation = FALSE,
  bootstrap = FALSE,
  R = 200,
  out.formula = NULL,
  out.estimate = NULL,
  family = "gaussian"
)

```

### Arguments

<code>ps.formula</code>	an object of class <code>formula</code> (or one that can be coerced to that class): a symbolic description of the propensity score model to be fitted. Additional details of model specification are given under ‘Details’. This argument is optional if <code>ps.estimate</code> is not <code>NULL</code> .
<code>ps.estimate</code>	an optional matrix or data frame containing estimated (generalized) propensity scores for each observation. Typically, this is an $N$ by $J$ matrix, where $N$ is the number of observations and $J$ is the total number of treatment levels. Preferably, the column name of this matrix should match the name of treatment level, if column name is missing or there is a mismatch, the column names would be assigned according to alphabetic order of the treatment levels. A vector of propensity score estimates is also allowed in <code>ps.estimate</code> , in which case a binary treatment is implied and the input is regarded as the propensity to receive the last category of treatment by alphabetic order, unless otherwise stated by <code>trtgrp</code> .
<code>trtgrp</code>	an optional character defining the "treated" population for estimating the average treatment effect among the treated (ATT). Only necessary if <code>weight = "ATT"</code> . This option can also be used to specify the treatment (in a two-treatment setting) when a vector argument is supplied for <code>ps.estimate</code> . Default value is the last group in the alphabetic order.
<code>zname</code>	an optional character specifying the name of the treatment variable in data.
<code>yname</code>	an optional character specifying the name of the outcome variable in data.
<code>data</code>	an optional data frame containing the variables in the propensity score model and outcome model (if augmented estimator is used). If not found in data, the variables are taken from <code>environment(formula)</code> .
<code>weight</code>	a character or vector of characters including the types of weights to be used. "ATE" specifies the inverse probability weights for estimating the average treatment effect among the combined population. "ATT" specifies the weights for estimating the average treatment effect among the treated. "ATO" specifies the (generalized) overlap weights for estimating the average treatment effect among the overlap population, or population at clinical equipoise. Default is "ATO".



<code>delta</code>	trimming threshold for estimated (generalized) propensity scores. Should be no larger than 1 / number of treatment groups. Default is 0, corresponding to no trimming.
<code>augmentation</code>	logical. Indicate whether augmented weighting estimators should be used. Default is FALSE.
<code>bootstrap</code>	logical. Indicate whether bootstrap is used to estimate the standard error of the point estimates. Default is FALSE.
<code>R</code>	an optional integer indicating number of bootstrap replicates. Default is $R = 200$ .
<code>out.formula</code>	an object of class <code>formula</code> (or one that can be coerced to that class): a symbolic description of the outcome model to be fitted. Additional details of model specification are given under ‘Details’. This argument is optional if <code>out.estimate</code> is not NULL.
<code>out.estimate</code>	an optional matrix or data frame containing estimated potential outcomes for each observation. Typically, this is an N by J matrix, where N is the number of observations and J is the total number of treatment levels. Preferably, the column name of this matrix should match the name of treatment level, if column name is missing or there is a mismatch, the column names would be assigned according to alphabetic order of the treatment levels, with a similar mechanism as in <code>ps.estimate</code> .
<code>family</code>	a description of the error distribution and link function to be used in the outcome model. Only required if <code>out.formula</code> is provided. Supported distributional families include "gaussian" (link = identity), "binomial" (link = logit) and "poisson" (link = log). See <code>family</code> in <code>glm</code> for more details. Default is "gaussian".

## Details

A typical form for `ps.formula` is `treatment ~ terms` where `treatment` is the treatment variable (identical to the variable name used to specify `zname`) and `terms` is a series of terms which specifies a linear predictor for treatment. Similarly, a typical form for `out.formula` is `outcome ~ terms` where `outcome` is the outcome variable (identical to the variable name used to specify `yname`) and `terms` is a series of terms which specifies a linear predictor for outcome. Both `ps.formula` and `out.formula` specify generalized linear models when `ps.estimate` and/or `out.estimate` is NULL. See `glm` for more details on generalized linear models.

When comparing two treatments, `ps.estimate` can either be a vector or a two-column matrix of estimated propensity scores. If a vector is supplied, it is assumed to be the propensity scores to receive the treatment, and the treatment group corresponds to the last group in the alphabetic order, unless otherwise specified by `trtgrp`. When comparing multiple ( $J \geq 3$ ) treatments, `ps.estimate` needs to be specified as an N by J matrix, where N indicates the number of observations, and J indicates the total number of treatments. This matrix specifies the estimated generalized propensity scores to receive each of the J treatments. In general, `ps.estimate` should have column names that indicate the level of the treatment variable, which should match the levels given in Z. If column names are empty or there is a mismatch, the column names will be created following the alphabetic order of values in Z, and the rightmost column of `ps.estimate` is assumed to be the treatment group, when estimating ATT. `trtgrp` can also be used to specify the treatment group for estimating ATT. The same mechanism applies to `out.estimate`, except that the input for `out.estimate` must be

an N by J matrix, where each row corresponds to the estimated potential outcomes (corresponding to each treatment) for each observation.

The argument `zname` and/or `yname` is required when `ps.estimate` and/or `out.estimate` is not NULL.

Current version of PSweight allows for three types of propensity score weights used to estimate ATE, ATT and ATO. These weights are members of larger class of balancing weights defined in Li, Morgan, and Zaslavsky (2018). When there is a practical violation of the positivity assumption, `delta` defines the symmetric propensity score trimming rule following Crump et al. (2009). With multiple treatments, `delta` defines the multinomial trimming rule introduced in Yoshida et al. (2019). The overlap weights can also be considered as a data-driven continuous trimming strategy without specifying trimming rules, see Li, Thomas and Li (2019). Additional details on balancing weights and generalized overlap weights for multiple treatment groups are provided in Li and Li (2019).

If `augmentation = TRUE`, an augmented weighting estimator will be implemented. For binary treatments, the augmented weighting estimator is presented in Mao, Li and Greene (2018). For multiple treatments, the augmented weighting estimator is mentioned in Li and Li (2019), and additional details will appear in our ongoing work (Zhou et al. 2020+). When `weight = "ATE"`, the augmented estimator is also referred to as a doubly-robust (DR) estimator.

When `bootstrap = TRUE`, the variance will be calculated by nonparametric bootstrap, with R bootstrap replications. The default of R is 200. Otherwise, the variance will be calculated using the sandwich variance formula obtained in the M-estimation framework.

## Value

PSweight returns a PSweight object containing a list of the following values: estimated propensity scores, average potential outcomes corresponding to each treatment, variance-covariance matrix of the point estimates, the label for each treatment group, and estimates in each bootstrap replicate if `bootstrap = TRUE`. A summary of PSweight can be obtained with `summary.PSweight`.

`trtgrp` a character indicating the treatment group.

`propensity` a data frame of estimated propensity scores.

`muhat` average potential outcomes by treatment groups, with reference to specific target populations.

`covmu` variance-covariance matrix of `muhat`.

`muboot` an optional list of point estimates in each bootstrap replicate `bootstrap = TRUE`.

`group` a table of treatment group labels corresponding to the output point estimates `muhat`.

## References

- Crump, R. K., Hotz, V. J., Imbens, G. W., Mitnik, O. A. (2009). Dealing with limited overlap in estimation of average treatment effects. *Biometrika*, 96(1), 187-199.
- Li, F., Morgan, K. L., Zaslavsky, A. M. (2018). Balancing covariates via propensity score weighting. *Journal of the American Statistical Association*, 113(521), 390-400.
- Mao, H., Li, L., Greene, T. (2019). Propensity score weighting analysis and treatment effect discovery. *Statistical Methods in Medical Research*, 28(8), 2439-2454.

Li, F., Thomas, L. E., Li, F. (2019). Addressing extreme propensity scores via the overlap weights. *American Journal of Epidemiology*, 188(1), 250-257.

Yoshida, K., Solomon, D.H., Haneuse, S., Kim, S.C., Patorno, E., Tedeschi, S.K., Lyu, H., Franklin, J.M., Stürmer, T., Hernández-Díaz, S. and Glynn, R.J. (2019). Multinomial extension of propensity score trimming methods: A simulation study. *American Journal of Epidemiology*, 188(3), 609-616.

Li, F., Li, F. (2019). Propensity score weighting for causal inference with multiple treatments. *The Annals of Applied Statistics*, 13(4), 2389-2415.

## Examples

```
data("psdata")
# the propensity and outcome models
ps.formula<-trt~cov1+cov2+cov3+cov4+cov5+cov6
out.formula<-Y~cov1+cov2+cov3+cov4+cov5+cov6

# without augmentation
ato1<-PSweight(ps.formula = ps.formula, yname = 'Y', data = psdata, weight = 'AT0')
summary(ato1)

# augmented weighting estimator
ato2<-PSweight(ps.formula = ps.formula, yname = 'Y', data = psdata,
               augmentation = TRUE, out.formula = out.formula, family = 'gaussian', weight = 'AT0')
summary(ato2)
```

---

summary.PSweight	<i>Summarize a PSweight object</i>
------------------	------------------------------------

---

## Description

summary.PSweight is used to summarize the results from [PSweight](#). The output contains the average causal effects defined by specific contrasts, as well as their standard error estimates.

## Usage

```
## S3 method for class 'PSweight'
summary(object, contrast = NULL, type = "DIF", ...)
```

## Arguments

object	a PSweight object obtained from the <a href="#">PSweight</a> function.
contrast	a vector or matrix specifying the causal contrast of interest. The average causal effects will be defined by such contrasts. For multiple treatments, the contrast parameters are explained in Li and Li (2019) for estimating general causal effects. Default is all pairwise contrasts between any two treatment groups.

`type` a character specifying the target estimand. The most commonly seen additive estimand is specified by `type = "DIF"`, abbreviated for weighted difference-in-means. This is the usual pairwise average treatment effects as those defined in Li, Morgan, and Zaslavsky (2018) and Li and Li (2019). For binary (or count outcomes), we also allow two ratio estimands: causal relative risk (`type = "RR"`) and causal odds ratio (`type = "OR"`). Estimates for these two ratio estimands will be reported on the log scale (log relative risk and log odds ratio) to improve the approximate for asymptotic normality. With binary outcomes, "DIF" is the same as the average causal risk difference. Default is "DIF" if left empty.

`...` further arguments passed to or from other methods.

### Details

For the `contrast` argument, one specifies the contrast of interest and thus defines the target estimand for comparing treatments. For example, if there are three treatment levels: A, B, and C, the contrast A-C (i.e.,  $E[Y(A)] - E[Y(C)]$ ) can be specified by `c(1, 0, -1)`. The contrasts of A-C and B-C can be jointly specified by `rbind(c(1, 0, -1), c(0, 1, -1))`.

For estimating the causal relative risk (`type = "RR"`), the contrast is specified at the log scale. For example, the contrast A-C (specified by `c(1, 0, -1)`) implies the estimation of  $\log\{E[Y(A)]\} - \log\{E[Y(C)]\}$ . For estimating the causal odds ratio, the contrast is specified at the log odds scale. For example, the contrast A-C (specified by `c(1, 0, -1)`) implies the estimation of  $\log\{E[Y(A)]/E[1-Y(A)]\} - \log\{E[Y(C)]/E[1-Y(C)]\}$ .

The variance of the contrasts will be estimated by the delta method (if `sandwich` variance is used, or `bootstrap = FALSE`), or nonparametric bootstrap (if `bootstrap = TRUE`). Details will be given in Zhou et al. (2020+).

The argument `type` takes one of three options: "DIF", "RR", or "OR", with "DIF" as the default option. Typically, "RR" is relevant for binary or count outcomes, and "OR" is relevant only for binary outcomes. "DIF" applies to all types of outcomes.

### Value

A list of following values:

`trtgrp` a character indicating the treatment group, or target population under ATT weights.

`estimates` a matrix of point estimates, standard errors and 95 for contrasts of interest.

`bootestimates` a list of data frames containing estimated contrasts in each bootstrap replicate, if bootstrap is used to estimate standard errors.

`contrast` a table listing the specified contrasts of interest.

`group` a table of treatment group labels corresponding to the output point estimates, provided in results obtained from [PSweight](#).

### References

Li, F., Morgan, K. L., Zaslavsky, A. M. (2018). Balancing covariates via propensity score weighting. *Journal of the American Statistical Association*, 113(521), 390-400.

Li, F., Li, F. (2019). Propensity score weighting for causal inference with multiple treatments. *The Annals of Applied Statistics*, 13(4), 2389-2415.

**Examples**

```
## For examples, run: example(PSweight).
```

---

```
summary.SumStat      Summarize a SumStat object.
```

---

**Description**

summary.SumStat is used to summarize results obtained from function [SumStat](#). The output includes effective sample sizes and tables for balance statistics.

**Usage**

```
## S3 method for class 'SumStat'
summary(object, weighted.var = TRUE, metric = "ASD", ...)
```

**Arguments**

object	a SumStat object obtained with the <a href="#">SumStat</a> function.
weighted.var	logical. Indicate whether the propensity score weighted variance should be used in calculating the balance metrics. Default is TRUE.
metric	a character indicating the type of balance metrics. "ASD" refers to the pairwise absolute standardized difference and "PSD" refers to the population standardized difference. Default is "ASD".
...	further arguments passed to or from other methods.

**Details**

For metric, the two options "ASD" and "PSD" are defined in Li and Li (2019) for the general family of balancing weights. Similar definitions are also given in McCaffrey et al. (2013) for inverse probability weighting. weighted.var specifies whether weighted or unweighted variance should be used in calculating ASD or PSD. An example of weighted variance with two treatment groups is given in Austin and Stuart (2015). For more than two treatment groups, the maximum of ASD (across all pairs of treatments) and maximum of PSD (across all treatments) are calculated, as explained in Li and Li (2019).

**Value**

A list of tables containing effective sample sizes and balance statistics on covariates for specified propensity score weighting schemes.

effective.sample.size a table of effective sample sizes. This serves as a conservative measure to characterize the variance inflation or precision loss due to weighting, see Li and Li (2019).

unweighted A table summarizing mean, variance by treatment groups, and standardized mean difference.

ATE If "ATE" is specified, this is a data table summarizing mean, variance by treatment groups, and standardized mean difference under inverse probability weighting.

ATT If "ATT" is specified, this is a data table summarizing mean, variance by treatment groups, and standardized mean difference under the ATT weights.

ATO If "ATO" is specified, this is a data table summarizing mean, variance by treatment groups, and standardized mean difference under the (generalized) overlap weights.

## References

McCaffrey, D. F., Griffin, B. A., Almirall, D., Slaughter, M. E., Ramchand, R. and Burgette, L. F. (2013). A tutorial on propensity score estimation for multiple treatments using generalized boosted models. *Statistics in Medicine*, 32(19), 3388-3414.

Austin, P.C. and Stuart, E.A. (2015). Moving towards best practice when using inverse probability of treatment weighting (IPTW) using the propensity score to estimate causal treatment effects in observational studies. *Statistics in Medicine*, 34(28), 3661-3679.

Li, F., Li, F. (2019). Propensity score weighting for causal inference with multiple treatments. *The Annals of Applied Statistics*, 13(4), 2389-2415.

## Examples

```
## For examples, run: example(SumStat).
```

---

SumStat

*Calculate summary statistics for propensity score weighting*

---

## Description

SumStat is used to generate distributional plots of the estimated propensity scores and balance diagnostics after propensity score weighting.

## Usage

```
SumStat(
  ps.formula,
  ps.estimate = NULL,
  trtgrp = NULL,
  Z = NULL,
  covM = NULL,
  zname = NULL,
  xname = NULL,
  data = NULL,
  weight = "ATO",
  delta = 0
)
```

**Arguments**

<code>ps.formula</code>	an object of class <code>formula</code> (or one that can be coerced to that class): a symbolic description of the propensity score model to be fitted. Additional details of model specification are given under 'Details'. This argument is optional if <code>ps.estimate</code> is not NULL.
<code>ps.estimate</code>	an optional matrix or data frame containing estimated (generalized) propensity scores for each observation. Typically, this is an N by J matrix, where N is the number of observations and J is the total number of treatment levels. Preferably, the column names of this matrix should match the names of treatment level, if column names are missing or there is a mismatch, the column names would be assigned according to the alphabetic order of treatment levels. A vector of propensity score estimates is also allowed in <code>ps.estimate</code> , in which case a binary treatment is implied and the input is regarded as the propensity to receive the last category of treatment by alphabetic order, unless otherwise stated by <code>trtgrp</code> .
<code>trtgrp</code>	an optional character defining the "treated" population for estimating the average treatment effect among the treated (ATT). Only necessary if <code>weight = "ATT"</code> . This option can also be used to specify the treatment (in a two-treatment setting) when a vector argument is supplied for <code>ps.estimate</code> . Default value is the last group in the alphabetic order.
<code>Z</code>	an optional vector specifying the values of treatment, only necessary when the covariate matrix <code>covM</code> is provided instead of <code>data</code> .
<code>covM</code>	an optional covariate matrix or data frame including covariates, their interactions and higher-order terms. When the covariate matrix <code>covM</code> is provided, the balance statistics are generated according to each column of this matrix.
<code>zname</code>	an optional character specifying the name of the treatment variable in <code>data</code> .
<code>xname</code>	an optional vector of characters including the names of covariates in <code>data</code> .
<code>data</code>	an optional data frame containing the variables in the propensity score model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> .
<code>weight</code>	a character or vector of characters including the types of weights to be used. "ATE" specifies the inverse probability weights for estimating the average treatment effect among the combined population. "ATT" specifies the weights for estimating the average treatment effect among the treated. "ATO" specifies the (generalized) overlap weights for estimating the average treatment effect among the overlap population, or population at clinical equipoise. Default is "ATO".
<code>delta</code>	trimming threshold for estimated (generalized) propensity scores. Should be no larger than 1 / number of treatment groups. Default is 0, corresponding to no trimming.

**Details**

A typical form for `ps.formula` is `treatment ~ terms` where `treatment` is the treatment variable (identical to the variable name used to specify `zname`) and `terms` is a series of terms which specifies a linear predictor for `treatment`. `ps.formula` specifies logistic or multinomial logistic models for estimating the propensity scores, when `ps.estimate` is NULL.

When comparing two treatments, `ps.estimate` can either be a vector or a two-column matrix of estimated propensity scores. If a vector is supplied, it is assumed to be the propensity scores to receive the treatment, and the treatment group corresponds to the last group in the alphabetic order, unless otherwise specified by `trtgrp`. When comparing multiple ( $J \geq 3$ ) treatments, `ps.estimate` needs to be specified as an  $N$  by  $J$  matrix, where  $N$  indicates the number of observations, and  $J$  indicates the total number of treatments. This matrix specifies the estimated generalized propensity scores to receive each of the  $J$  treatments. In general, `ps.estimate` should have column names that indicate the level of the treatment variable, which should match the levels given in  $Z$ . If column names are empty or there is a mismatch, the column names will be created following the alphabetic order of treatment levels. The rightmost column of `ps.estimate` is then assumed to be the treatment group when estimating ATT. `trtgrp` can also be used to specify the treatment group for estimating ATT.

The argument `zname` is required when `ps.estimate` is not `NULL`.

To generate balance statistics, one can directly specify  $Z$  and `covM` to indicate the treatment levels and covariate matrix. Alternatively, one can supply `data`, `zname`, and `xname` to indicate the same information. When both are specified, the function will prioritize inputs from  $Z$  and `covM`.

Current version of `PSweight` allows for three types of propensity score weights used to estimate ATE, ATT and ATO. These weights are members of a larger class of balancing weights defined in Li, Morgan, and Zaslavsky (2018). When there is a practical violation of the positivity assumption, `delta` defines the symmetric propensity score trimming rule following Crump et al. (2009). With multiple treatments, `delta` defines the multinomial trimming rule introduced in Yoshida et al. (2019). The overlap weights can also be considered as a data-driven continuous trimming strategy without specifying trimming rules, see Li, Thomas and Li (2019). Additional details on balancing weights and generalized overlap weights for multiple treatment groups are provided in Li and Li (2019).

## Value

`SumStat` returns a `SumStat` object including a list of the following value: treatment group, propensity scores, propensity score weights, effective sample sizes, and balance statistics. A summary of `SumStat` can be obtained with `summary.SumStat`.

`trtgrp` a character indicating the treatment group.

`propensity` a data frame of estimated propensity scores.

`ps.weights` a data frame of propensity score weights.

`ess` a table of effective sample sizes. This serves as a conservative measure to characterize the variance inflation or precision loss due to weighting, see Li and Li (2019).

`unweighted.sumstat` A list of tables including covariate means and variances by treatment group and standardized mean differences.

`ATE.sumstat` If "ATE" is included in `weight`, this is a list of summary statistics using inverse probability weighting.

`ATT.sumstat` If "ATT" is included in `weight`, this is a list of summary statistics using the ATT weights.

`ATO.sumstat` If "ATO" is included in `weight`, this is a list of summary statistics using the overlap weights.

`trim` If `delta > 0`, this is a table summarizing the number of observations before and after trimming.



## References

- Crump, R. K., Hotz, V. J., Imbens, G. W., Mitnik, O. A. (2009). Dealing with limited overlap in estimation of average treatment effects. *Biometrika*, 96(1), 187-199.
- Li, F., Morgan, K. L., Zaslavsky, A. M. (2018). Balancing covariates via propensity score weighting. *Journal of the American Statistical Association*, 113(521), 390-400.
- Li, F., Thomas, L. E., Li, F. (2019). Addressing extreme propensity scores via the overlap weights. *American Journal of Epidemiology*, 188(1), 250-257.
- Yoshida, K., Solomon, D.H., Haneuse, S., Kim, S.C., Paterno, E., Tedeschi, S.K., Lyu, H., Franklin, J.M., Stürmer, T., Hernández-Díaz, S. and Glynn, R.J. (2019). Multinomial extension of propensity score trimming methods: A simulation study. *American Journal of Epidemiology*, 188(3), 609-616.
- Li, F., Li, F. (2019). Propensity score weighting for causal inference with multiple treatments. *The Annals of Applied Statistics*, 13(4), 2389-2415.

## Examples

```
data("psdata")
# the propensity model
ps.formula<-trt~cov1+cov2+cov3+cov4+cov5+cov6

# using SumStat to estimate propensity scores
msstat <- SumStat(ps.formula, trtgrp="2", data=psdata,
  weight=c("ATE","AT0","ATT"))
summary(msstat)

# importing user-supplied propensity scores "e.h"
fit <- nnet::multinom(formula=ps.formula, data=psdata, maxit=500, trace=FALSE)
e.h <- fit$fitted.values
varname <- c("cov1","cov2","cov3","cov4","cov5","cov6")
msstat0 <- SumStat(zname="trt", xname=varname, data=psdata, ps.estimate=e.h,
  trtgrp="2", weight=c("ATE","ATT","AT0"))
summary(msstat0)
```

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