Package ‘twang’

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twang-package
twang: Toolkit for Weighting and Analysis of Nonequivalent Groups

Description

Provides functions for propensity score estimating and weighting, nonresponse weighting, and diagnosis of the weights.
Description

A small subset of the data from McCaffrey et al. (2013).

Usage

data(AOD)

Format

A data frame with 600 observations on the following 10 variables.

treat  Treatment that each study subject received. Either community, metcbt5, or scy.
suf12  outcome variable, substance use frequency at 12 month follow-up
illact covariate, illicit activities scale
crimjust covariate, criminal justice involvement
subprob covariate, substance use problem scale
subdep covariate, substance use dependence scale
white  1 if non-Hispanic white, 0 otherwise

References


bal.stat Calculate weighted balance statistics

Description

‘bal.stat’ compares the treatment and control subjects by means, standard deviations, effect size, and KS statistics
Usage

```r
bal.stat(
  data,
  vars = NULL,
  treat.var,
  w.all,
  sampw,
  get.means = TRUE,
  get.ks = TRUE,
  na.action = "level",
  estimand,
  multinom,
  fillNAs = FALSE
)
```

Arguments

data A data frame containing the data

vars A vector of character strings with the names of the variables on which the function will assess the balance

treat.var The name of the treatment variable

w.all Observation weights (e.g. propensity score weights, sampling weights, or both)
sampw Sampling weights. These are passed in addition to ‘w.all’ because the "unweighted" results should be adjusted for sample weights (though not propensity score weights).

get.means logical. If ‘TRUE’ then ‘bal.stat’ will compute means and variances

get.ks logical. If ‘TRUE’ then ‘bal.stat’ will compute KS statistics

na.action A character string indicating how ‘bal.stat’ should handle missing values. Current options are "level", "exclude", or "lowest"

estimand Either "ATT" or "ATE"

multinom logical. ‘TRUE’ if used for multinomial propensity scores.

fillNAs logical. If ‘TRUE’, fills in zeros for missing values.

Details

‘bal.stat’ calls auxiliary functions for each variable and assembles the results in a table.

Value

‘get.means’ and ‘get.ks’ manipulate the inclusion of certain columns in the returned result.

References

bal.table

See Also

The example for [ps] contains an example of the use of [bal.table]

---

**bal.table**

*Compute the balance table.*

---

**Description**

Extract the balance table from ps, dx.wts, and mnps objects

**Usage**

```
bal.table(
  x, 
  digits = 3,
  collapse.to = c("pair", "covariate", "stop.method")[1],
  subset.var = NULL, 
  subset.treat = NULL,
  subset.stop.method = NULL,
  es.cutoff = 0,
  ks.cutoff = 0,
  p.cutoff = 1,
  ks.p.cutoff = 1,
  timePeriods = NULL,
  ...
)
```

**Arguments**

- `x` A ps or dx.wts object.
- `digits` The number of digits that the numerical entries should be rounded to. Default: 3.
- `collapse.to` For mnps ATE objects, the comparisons can be given for all pairs (default), summarized by pre-treatment covariate and stop.method, or as a single summary for each stop.method.
- `subset.var` Eliminate all but a specified subset of covariates.
- `subset.treat` Subset to either all pairs that include a specified treatment or a single pair of treatments.
- `subset.stop.method` Subset to either all pairs that include a specified treatment or a single pair of treatments.
- `es.cutoff` Subsets to comparisons with absolute ES values bigger than `es.cutoff`. Default: 0.
- `ks.cutoff` Subsets to comparisons with KS values bigger than `ks.cutoff`. Default: 0.
p.cutoff  Subsets to comparisons with t- or chi-squared p-values no bigger than p.cutoff.  Default: 1.
ks.p.cutoff Subsets to comparisons with t- or chi-squared p-values no bigger than p.cutoff.  Default: 1.
timePeriods  Used to subset times for iptw fits.

Details

bal.table is a generic function for extracting balance tables from ps and dx.wts objects. These objects usually have several sets of candidate weights, one for an unweighted analysis and perhaps several stop.methods. bal.table will return a table for each set of weights combined into a list. Each list component will be named as given in the x, usually the name of the stop.method. The balance table labeled “unw” indicates the unweighted analysis.

Value

Returns a data frame containing the balance information.

- tx.mn  The mean of the treatment group.
- tx.sd  The standard deviation of the treatment group.
- ct.mn  The mean of the control group.
- ct.sd  The standard deviation of the control group.
- std.eff.sz  The standardized effect size, (tx.mn-ct.mn)/tx.sd. If tx.sd is small or 0, the standardized effect size can be large or INF. Therefore, standardized effect sizes greater than 500 are set to NA.
- stat  The t-statistic for numeric variables and the chi-square statistic for continuous variables.
- p  The p-value for the test associated with stat
- ks  The KS statistic.
- ks.pval  The KS p-value computed using the analytic approximation, which does not necessarily work well with a lot of ties.

Description

This function produces a collection of diagnostic plots for mnps objects.
Usage

## S3 method for class 'mnps'
boxplot(
  x,
  stop.method = NULL,
  color = TRUE,
  figureRows = NULL,
  singlePlot = NULL,
  multiPage = FALSE,
  time = NULL,
  print = TRUE,
  ...
)

Arguments

x         A ‘ps’ object
stop.method Only 1 ‘stop.method’ can be presented at a time for ‘mnps’ objects. Use a
            numeric indicator of which ‘stop.method’ (among those specified when fitting
            the ‘mnps’ object) should be used.
color      If ‘FALSE’, a grayscale figure will be returned.
figureRows The number of rows in the figure. Defaults to the number of panels.
singlePlot If multiple sets of boxplots are produced, ‘singlePlot‘ can be used to select only
            one. For example, ‘singlePlot = 2‘ would return only the second set of boxplots.
multiPage  When multiple frames of a figure are produced, ‘multiPage = TRUE’ will print
            each frame on a different page. This is intended for situations where the graphi-
            cal output is being saved to a file.
time       For use with iptw fits.
print      If ‘FALSE’, the figure is returned but not printed.
...        Additional arguments that are passed to boxplot function, which may be passed
to the underlying ‘lattice’ package plotting functions.

Details

This function produces lattice-style graphics of diagnostic plots.

References


See Also

[mnps]
Description

This function produces a collection of diagnostic plots for ps objects.

Usage

```r
## S3 method for class 'ps'
boxplot(x, subset = NULL, color = TRUE, time = NULL, ...)
```

Arguments

- `x`: A `ps` object
- `subset`: If multiple `stop.method` rules were used in the `ps()` call, `subset` restricts the plots of a subset of the stopping rules that were employed. This argument expects a subset of the integers from 1 to k, if k `stop.method` s were used.
- `color`: If `FALSE`, a grayscale figure will be returned.
- `time`: For use with iptw fits.
- `...`: Additional arguments that are passed to boxplot function, which may be passed to the underlying `lattice` package plotting functions.

Details

This function produces lattice-style graphics of diagnostic plots.

References


See Also

[ps]
**Description**

`desc.wts` assesses the quality of a set of weights on balancing a treatment and control group.

**Usage**

```r
desc.wts(data, w, sampw = sampw, vars = NULL, treat.var, tp, na.action = "level", perm.test.iters=0, verbose=TRUE, alerts.stack, estimand, multinom = FALSE, fillNAs = FALSE)
```

**Arguments**

- `data` a data frame containing the dataset
- `w` a vector of weights equal to `nrow(data)`
- `sampw` sampling weights, if provided
- `vars` a vector of variable names corresponding to `data`
- `treat.var` the name of the treatment variable
- `tp` a title for the method "type" used to create the weights, used to label the results
- `na.action` a string indicating the method for handling missing data
- `perm.test.iters` an non-negative integer giving the number of iterations of the permutation test for the KS statistic. If `perm.test.iters=0` then the function returns an analytic approximation to the p-value. This argument is ignored is `x` is a `ps` object. Setting `perm.test.iters=200` will yield precision to within 3% if the true p-value is 0.05. Use `perm.test.iters=500` to be within 2%
- `verbose` if TRUE, lots of information will be printed to monitor the the progress of the fitting
- `alerts.stack` an object for collecting warnings issued during the analyses
- `estimand` the estimand of interest: either "ATT" or "ATE"
- `multinom` Indicator that weights are from a propensity score analysis with 3 or more treatment groups.
- `fillNAs` If TRUE fills NAs with zeros.
Details

desc.wts calls `bal.stat` to assess covariate balance. If `perm.test.iters`>0 it will call `bal.stat` multiple times to compute Monte Carlo p-values for the KS statistics and the maximum KS statistic. It assembles the results into a list object, which usually becomes the `desc` component of `ps` objects that `ps` returns.

Value

See the description of the `desc` component of the `ps` object that `ps` returns

See Also

`ps`

---

displayPlots | Display plots

Description

Display plots

Usage

displayPlots(ptList, figureRows, singlePlot, multiPage, bxpt = FALSE)

Arguments

- `ptList`  A list of plots to display.
- `figureRows`  The number of rows in the figure.
- `singlePlot`  An integer indicating the index of the plot to display.
- `multiPage`  Whether to display plots on multiple pages.
- `bxpt`  Whether to display boxplots. Default: ‘FALSE’.
**dx.wts**  

*Compute diagnostics assessing covariates balance.*

**Description**

`dx.wts` takes a `ps` object or a set of propensity scores and computes diagnostics assessing covariates balance.

**Usage**

```r
dx.wts(
  x, 
  data, 
  estimand, 
  vars = NULL, 
  treat.var, 
  x.as.weights = TRUE, 
  sampw = NULL, 
  perm.test.iters = 0
)
```

**Arguments**

- **x**: A data frame, matrix, or vector of propensity score weights or a `ps` object. `x` can also be a data frame, matrix, or vector of propensity scores if `x.as.weights=FALSE`.
- **data**: A data frame.
- **estimand**: The estimand of interest: either "ATT" or "ATE".
- **vars**: A vector of character strings naming variables in `data` on which to assess balance.
- **treat.var**: A character string indicating which variable in `data` contains the 0/1 treatment group indicator.
- **x.as.weights**: TRUE or FALSE indicating whether `x` specifies propensity score weights or propensity scores. Ignored if `x` is a `ps` object. Default: TRUE.
- **sampw**: Optional sampling weights. If `x` is a `ps` object, then the sampling weights should have been passed to `ps` and not specified here. `dx.wts` will issue a warning if `x` is a `ps` object and `sampw` is also specified.
- **perm.test.iters**: A non-negative integer giving the number of iterations of the permutation test for the KS statistic. If `perm.test.iters`=0, then the function returns an analytic approximation to the p-value. This argument is ignored if `x` is a `ps` object. Setting `perm.test.iters`=200 will yield precision to within 3% if the true p-value is 0.05. Use `perm.test.iters`=500 to be within 2%. 


Details

Creates a balance table that compares unweighted and weighted means and standard deviations, computes effect sizes, and KS statistics to assess the ability of the propensity scores to balance the treatment and control groups.

Value

Returns a list containing

- `treat` The vector of 0/1 treatment assignment indicators.

See Also

`ps`

---

table

Description

A subset of the mathematics scores from the U.S. Sustaining Effects Study. The subset consists of information on 1721 students from 60 schools. This dataset is available in the `mlmRev` package.

Usage

`data(egsingle)`

Format

A data frame with 7230 observations on the following 12 variables.

- `schoolid` a factor of school identifiers
- `childid` a factor of student identifiers
- `year` a numeric vector indicating the year of the test
- `grade` a numeric vector indicating the student’s grade
- `math` a numeric vector of test scores on the IRT scale score metric
- `retained` a factor with levels 0 1 indicating if the student has been retained in a grade.
- `female` a factor with levels Female Male
- `black` a factor with levels 0 1 indicating if the student is Black
- `hispanic` a factor with levels 0 1 indicating if the student is Hispanic
- `size` a numeric vector indicating the number of students enrolled in the school
- `lowinc` a numeric vector giving the percentage of low-income students in the school
- `mobility` a numeric vector
get.weights

Source
Reproduced from the mlmRev package for use in the section on nonresponse weighting in the twang package vignette. These data are distributed with the HLM software package (Bryk, Raudenbush, and Congdon, 1996). Conversion to the R format is described in Doran and Lockwood (2006).

References

get.weights Extract propensity score weights.

Description
Extracts propensity score weights from a ps or mnps object.

Usage
get.weights(ps1, stop.method = NULL, estimand = NULL, withSampW = TRUE)

Arguments
ps1 A ps or mnps object.
stop.method Indicates which set of weights to retrieve from the ps object.
estimand Indicates whether the weights are for the average treatment effect on the treated (ATT) or the average treatment effect on the population (ATE). By default, get.weights will use the estimand used to fit the ps object.
withSampW Whether to return weights with sample weights multiplied in, if they were provided in the original ps or mnps call. Default: TRUE.

Details
Weights for ATT are 1 for the treatment cases and p/(1-p) for the control cases. Weights for ATE are 1/p for the treatment cases and 1/(1-p) for the control cases.

Value
Returns a vector of weights.

See Also
ps, mnps
**get.weights.num**

*Get numerators to stabilize propensity score weights for ‘iptw’ fits.*

**Description**

Forms numerators to stabilize weights for an iptw object.

**Usage**

```r
get.weights.num(iptw, fitList)
```

**Arguments**

- `iptw`: An ‘iptw’ object.
- `fitList`: A list containing objects with an associated "fitted" function.

**Value**

Returns numerator of stabilized weights to be used in conjunction with 'get.weights.unstab'.

**See Also**

[iptw]

---

**get.weights.unstab**

*Extract unstabilized propensity score weights for ‘iptw’ fits*

**Description**

Extracts propensity score weights from an ‘iptw’ or ‘mniptw’ object.

**Usage**

```r
get.weights.unstab(x, stop.method = NULL, withSampW = TRUE)
```

**Arguments**

- `x`: An ‘iptw’ or ‘mniptw’ object.
- `stop.method`: The twop method used for the fit of interest.
- `withSampW`: Returns weights with sample weights multiplied in, if they were provided in the original ‘iptw’ call. Default: TRUE.

**Details**

Weights are the reciprocal of the product of the probability of receiving the treatment received.
Value

Returns a data.frame of weights.

See Also

[iptw]

Description

iptw calculates propensity scores for sequential treatments using gradient boosted logistic regression and diagnoses the resulting propensity scores using a variety of methods.

Usage

iptw(
  formula,
  data,
  timeInvariant = NULL,
  cumulative = TRUE,
  timeIndicators = NULL,
  ID = NULL,
  priorTreatment = TRUE,
  n.trees = 10000,
  interaction.depth = 3,
  shrinkage = 0.01,
  bag.fraction = 1,
  n.minobsinnode = 10,
  perm.test.iters = 0,
  print.level = 2,
  verbose = TRUE,
  stop.method = c("es.max"),
  sampw = NULL,
  version = "gbm",
  ks.exact = NULL,
  n.keep = 1,
  n.grid = 25,
  ...
)
Arguments

formula Either a single formula (long format) or a list with formulas.
data The dataset, includes treatment assignment as well as covariates.
timeInvariant An optional formula (with no left-hand variable) specifying time-invariant characteristics.
cumulative If TRUE, the time t model includes time-varying characteristics from times 1 through t-1. Default: TRUE.
timeIndicators For long format fits, a vector of times for each observation.
ID For long format fits, a vector of numeric identifiers for unique analytic units.
priorTreatment For long format fits, includes treatment levels from previous times if TRUE. This argument is ignored for wide format fits. Default: TRUE.
n.trees Number of gbm iterations passed on to gbm::gbm().
interaction.depth A positive integer denoting the tree depth used in gradient boosting. Default: 3.
shrinkage A numeric value between 0 and 1 denoting the learning rate. See gbm for more details. Default: 0.01.
bag.fraction A numeric value between 0 and 1 denoting the fraction of the observations randomly selected in each iteration of the gradient boosting algorithm to propose the next tree. See gbm for more details. Default: 1.0.
n.minobsinnode An integer specifying the minimum number of observations in the terminal nodes of the trees used in the gradient boosting. See gbm for more details. Default: 10.
perm.test.iters A non-negative integer giving the number of iterations of the permutation test for the KS statistic. If perm.test.iters=0 then the function returns an analytic approximation to the p-value. Setting perm.test.iters=200 will yield precision to within 3% if the true p-value is 0.05. Use perm.test.iters=500 to be within 2%. Default: 0.
print.level The amount of detail to print to the screen. Default: 2.
verbose If TRUE, lots of information will be printed to monitor the progress of the fitting. Default: TRUE.
stop.method A method or methods of measuring and summarizing balance across pretreatment variables. Current options are ks.mean, ks.max, es.mean, and es.max. ks refers to the Kolmogorov-Smirnov statistic and es refers to standardized effect size. These are summarized across the pretreatment variables by either the maximum (.max) or the mean (.mean). Default: c("es.max").
sampw Optional sampling weights.
version "gbm", "xgboost", or "legacy", indicating which version of the twang package to use.
"gbm" uses gradient boosting from the gbm package.
"xgboost" uses gradient boosting from the xgboost package.
"legacy" uses the prior implementation of the ps function.
Default: "gbm".

ks.exact
NULL or a logical indicating whether the Kolmogorov-Smirnov p-value should be based on an approximation of exact distribution from an unweighted two-sample Kolmogorov-Smirnov test. If NULL, the approximation based on the exact distribution is computed if the product of the effective sample sizes is less than 10,000. Otherwise, an approximation based on the asymptotic distribution is used. **Warning:** setting ks.exact = TRUE will add substantial computation time for larger sample sizes. Default: NULL.

n.keep
A numeric variable indicating the algorithm should only consider every n.keep-th iteration of the propensity score model and optimize balance over this set instead of all iterations. Default: 1.

n.grid
A numeric variable that sets the grid size for an initial search of the region most likely to minimize the stop.method. A value of n.grid=50 uses a 50 point grid from 1:n.trees. It finds the minimum, say at grid point 35. It then looks for the actual minimum between grid points 34 and 36. If specified with n.keep>1, n.grid corresponds to a grid of points on the kept iterations as defined by 'n.keep. Default: 25.

... Additional arguments that are passed to ps function.

Details

For user more comfortable with the options of xgboost::xgboost(), the options for iptw controlling the behavior of the gradient boosting algorithm can be specified using the xgboost naming scheme. This includes nrounds, max_depth, eta, and subsample. In addition, the list of parameters passed to xgboost can be specified with params.

Value

Returns an object of class iptw, a list containing

psList A list of ps objects with length equal to the number of time periods.
estimand The specified estimand.
stop.methods The stopping rules used to optimize iptw balance.
nFits The number of ps objects (i.e., the number of distinct time points).
uniqueTimes The unique times in the specified model.

See Also

ps, mnps, gbm, xgboost, plot, bal.table
**iptwExLong**

*Example data for iptw function (long version)*

**Description**

These data are simulated to demonstrate the iptw function in the "long" data format.

**Usage**

data(lindner)

**Format**

A list with a covariate matrix and outcomes.

- **covariates** Time-invariant covariates are gender and age. The time-varying covariate is use. The treatment indicator is given by tx. An individual level identifier is given in ID, and the time period is time.
- **outcome** Vector of post-treatment outcomes.

**iptwExWide**

*Example data for iptw function (wide version)*

**Description**

These data are simulated to demonstrate the iptw function in the "wide" data format.

**Usage**

data(lindner)

**Format**

A list with a covariate matrix and outcomes.

- **gender** Gender.
- **age** Age.
- **use0** Baseline substance use.
- **use1** Use following first time period treatment.
- **use2** Use following second time period treatment.
- **tx1** Treatment indicator (first time period).
- **tx2** Treatment indicator (second time period).
- **tx3** Treatment indicator (third time period).
- **covariates** Time-invariant covariates are gender and age. The time-varying covariate is use. The treatment indicator is given by tx. An individual level identifier is given in ID, and the time period is time.
- **outcome** Post-treatment outcomes.
Description

One of the datasets used by Dehejia and Wahba in their paper "Causal Effects in Non-Experimental Studies: Reevaluating the Evaluation of Training Programs." Also used as an example dataset in the MatchIt package.

Usage

data(lalonde)

Format

A data frame with 614 observations on the following 10 variables.

treat 1 if treated in the National Supported Work Demonstration, 0 if from the Current Population Survey
age age
educ years of education
black 1 if black, 0 otherwise
hispan 1 if Hispanic, 0 otherwise
married 1 if married, 0 otherwise
nodegree 1 if no degree, 0 otherwise
re74 earnings in 1974 (pretreatment)
re75 earnings in 1975 (pretreatment)
re78 earnings in 1978 (outcome)

Source


References


**Description**

These data are adapted from the `lindner` dataset in the `USPS` package. The description comes from that package, except for the variable `sixMonthSurvive`, which is a recode of `lifepres`.

Data from an observational study of 996 patients receiving an initial Percutaneous Coronary Intervention (PCI) at Ohio Heart Health, Christ Hospital, Cincinnati in 1997 and followed for at least 6 months by the staff of the Lindner Center. The patients thought to be more severely diseased were assigned to treatment with abciximab (an expensive, high-molecular-weight IIb/IIIa cascade blocker); in fact, only 298 (29.9 percent) of patients received usual-care-alone with their initial PCI.

**Usage**

data(lindner)

**Format**

A data frame of 10 variables collected on 996 patients; no NAs.

- **lifepres** Mean life years preserved due to survival for at least 6 months following PCI; numeric value of either 11.4 or 0.
- **cardbill** Cardiac related costs incurred within 6 months of patient’s initial PCI; numeric value in 1998 dollars; costs were truncated by death for the 26 patients with `lifepres` == 0.
- **abcix** Numeric treatment selection indicator; 0 implies usual PCI care alone; 1 implies usual PCI care deliberately augmented by either planned or rescue treatment with abciximab.
- **stent** Coronary stent deployment; numeric, with 1 meaning YES and 0 meaning NO.
- **height** Height in centimeters; numeric integer from 108 to 196.
- **female** Female gender; numeric, with 1 meaning YES and 0 meaning NO.
- **diabetic** Diabetes mellitus diagnosis; numeric, with 1 meaning YES and 0 meaning NO.
- **acutemi** Acute myocardial infarction within the previous 7 days; numeric, with 1 meaning YES and 0 meaning NO.
- **ejecfrac** Left ejection fraction; numeric value from 0 percent to 90 percent.
- **ves1proc** Number of vessels involved in the patient’s initial PCI procedure; numeric integer from 0 to 5.

**References**


means.table

Extract table of means from an 'mnps' object

Description

Extracts table of means from an mnps object.

Usage

means.table(mnps, stop.method = 1, includeSD = FALSE, digits = NULL)

Arguments

mnps
An 'mnps' object.

stop.method
Indicates which set of weights to retrieve from the 'ps' object. Either the name of the stop.method used, or a natural number with 1, for example, . indicating the first stop.method specified.

includeSD
Indicates whether standard deviations as well as means are to be displayed. By default, they are not displayed.

digits
If not 'NULL', results will be rounded to the specified number of digits.

Details

Displays a table with weighted and unweighted means and standardized effect sizes, and – if requested – standard deviations.

Value

'A table of means, standardized effect sizes, and perhaps standard deviations, by treatment group.

See Also

[mnps]

Example data for iptw function (long version, more than two treatments).

Description

These data are simulated to demonstrate the iptw function in the "long" data format.

Usage

data(lindner)
Format

A list with a covariate matrix and outcomes.

covariates  Time-invariant covariates are gender and age. The time-varying covariate is use. The treatment indicator is given by tx. An individual level identifier is given in ID, and the time period is time.

outcome  Vector of post-treatment outcomes.

Example data for iptw function (wide version, more than two treatments)

Description

These data are simulated to demonstrate the iptw function in the "wide" data format.

Usage

data(lindner)

Format

A list with a covariate matrix and outcomes.

gender  Gender.
age  Age.
use0  Baseline substance use.
use1  Use following first time period treatment.
use2  Use following second time period treatment.
tx1  Treatment indicator (first time period).
tx2  Treatment indicator (second time period).
tx3  Treatment indicator (third time period).

Time-invariant covariates are gender and age. The time-varying covariate is use. The treatment indicator is given by tx. An individual level identifier is given in ID, and the time period is time.

outcome  Post-treatment outcomes.
Propensity score estimation for multiple treatments

Description

`mnps` calculates propensity scores for more than two treatment groups using gradient boosted logistic regression, and diagnoses the resulting propensity scores using a variety of methods.

Usage

```r
mnps(
  formula,
  data,
  n.trees = 10000,
  interaction.depth = 3,
  shrinkage = 0.01,
  bag.fraction = 1,
  n.minobsinnode = 10,
  perm.test.iters = 0,
  print.level = 2,
  verbose = TRUE,
  estimand = "ATE",
  stop.method = c("es.max"),
  sampw = NULL,
  version = "gbm",
  ks.exact = NULL,
  n.keep = 1,
  n.grid = 25,
  treatATT = NULL,
  ...
)
```

Arguments

- **formula**: A formula for the propensity score model with the treatment indicator on the left side of the formula and the potential confounding variables on the right side.
- **data**: The dataset, includes treatment assignment as well as covariates.
- **n.trees**: Number of gbm iterations passed on to `gbm::gbm()`. Default: 10000.
- **interaction.depth**: A positive integer denoting the tree depth used in gradient boosting. Default: 3.
- **shrinkage**: A numeric value between 0 and 1 denoting the learning rate. See `gbm` for more details. Default: 0.01.
- **bag.fraction**: A numeric value between 0 and 1 denoting the fraction of the observations randomly selected in each iteration of the gradient boosting algorithm to propose the next tree. See `gbm` for more details. Default: 1.0.
n.minobsinnode: An integer specifying the minimum number of observations in the terminal nodes of the trees used in the gradient boosting. See \texttt{gbm} for more details. Default: 10.

\texttt{perm.test.iters}: A non-negative integer giving the number of iterations of the permutation test for the KS statistic. If \texttt{perm.test.iters=0} then the function returns an analytic approximation to the p-value. Setting \texttt{perm.test.iters=200} will yield precision to within 3\% if the true p-value is 0.05. Use \texttt{perm.test.iters=500} to be within 2\%. Default: 0.

\texttt{print.level}: The amount of detail to print to the screen. Default: 2.

\texttt{verbose}: If \texttt{TRUE}, lots of information will be printed to monitor the progress of the fitting. Default: \texttt{TRUE}.

\texttt{estimand}: "ATE" (average treatment effect) or "ATT" (average treatment effect on the treated) : the causal effect of interest. ATE estimates the change in the outcome if the treatment were applied to the entire population versus if the control were applied to the entire population. ATT estimates the analogous effect, averaging only over the treated population. Default: "ATE".

\texttt{stop.method}: A method or methods of measuring and summarizing balance across pre-treatment variables. Current options are \texttt{ks.mean}, \texttt{ks.max}, \texttt{es.mean}, and \texttt{es.max}. \texttt{ks} refers to the Kolmogorov-Smirnov statistic and \texttt{es} refers to standardized effect size. These are summarized across the pre-treatment variables by either the maximum (\texttt{.max}) or the mean (\texttt{.mean}). Default: \texttt{c("es.mean")}.

\texttt{sampw}: Optional sampling weights.

\texttt{version}: "gbm", "xgboost", or "legacy", indicating which version of the \texttt{twang} package to use.

- "gbm" uses gradient boosting from the \texttt{gbm} package.
- "xgboost" uses gradient boosting from the \texttt{xgboost} package.
- "legacy" uses the prior implementation of the \texttt{ps} function.

Default: "\texttt{gbm}".

\texttt{ks.exact}: NULL or a logical indicating whether the Kolmogorov-Smirnov p-value should be based on an approximation of exact distribution from an unweighted two-sample Kolmogorov-Smirnov test. If NULL, the approximation based on the exact distribution is computed if the product of the effective sample sizes is less than 10,000. Otherwise, an approximation based on the asymptotic distribution is used. **Warning:** setting \texttt{ks.exact = TRUE} will add substantial computation time for larger sample sizes. Default: NULL.

\texttt{n.keep}: A numeric variable indicating the algorithm should only consider every \texttt{n.keep}-th iteration of the propensity score model and optimize balance over this set instead of all iterations. Default: 1.

\texttt{n.grid}: A numeric variable that sets the grid size for an initial search of the region most likely to minimize the \texttt{stop.method}. A value of \texttt{n.grid=50} uses a 50 point grid from 1:\texttt{n.trees}. It finds the minimum, say at grid point 35. It then looks for the actual minimum between grid points 34 and 36. If specified with \texttt{n.keep>1}, \texttt{n.grid} corresponds to a grid of points on the kept iterations as defined by \texttt{n.keep}. Default: 25.
If the estimand is specified to be ATT, this argument is used to specify which treatment condition is considered 'the treated'. It must be one of the levels of the treatment variable. It is ignored for ATE analyses.

Additional arguments that are passed to ps function.

Details

For user more comfortable with the options of xgboost::xgboost(), the options for mnps controlling the behavior of the gradient boosting algorithm can be specified using the xgboost naming scheme. This includes nrounds, max_depth, eta, and subsample. In addition, the list of parameters passed to xgboost can be specified with params.

Note that unlike earlier versions of twang, the plotting functions are no longer included in the mnps function. See plot for details of the plots.

Value

Returns an object of class mnps, which consists of the following.

- psList A list of ps objects with length equal to the number of time periods.
- nFits The number of ps objects (i.e., the number of distinct time points).
- estimand The specified estimand.
- treatATT For ATT fits, the treatment category that is considered "the treated".
- treatLev The levels of the treatment variable.
- levExceptTreatAtt The levels of the treatment variable, excluding the treatATT level.
- data The data used to fit the model.
- treatVar The vector of treatment indicators.
- stopMethods The stopping rules specified in the call to mnps.
- sampw Sampling weights provided to mnps, if any.

Author(s)

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References


See Also

ps, gbm, xgboost.plot, bal.table
plot.dxwts

Description

Plot dxwts

Usage

## S3 method for class 'dxwts'
plot(x, plots = "es", ...)

Arguments

x
An dxwts object.

plots
An indicator of which type of plot is desired. The options are
• "optimize" or 1: A plot of the balance criteria as a function of the GBM iteration.
• "boxplot" or 2: Boxplots of the propensity scores for the treatment and control cases
• "es" or 3: Plots of the standardized effect size of the pretreatment variables before and after reweighing
• "t" or 4: Plots of the p-values from t-statistics comparing means of treated and control subjects for pretreatment variables, before and after weighting.
• "ks" or 5: Plots of the p-values from Kolmogorov-Smirnov statistics comparing distributions of pretreatment variables of treated and control subjects, before and after weighting.

...
Additional arguments.

plot.iptw

Plots for iptw objects

Description

This function produces a collection of diagnostic plots for iptw objects.

Usage

## S3 method for class 'iptw'
plot(
  x,
  plots = "optimize",
  subset = NULL,
  color = TRUE,
)
Arguments

x  An iptw object.
plots  An indicator of which type of plot is desired. The options are
  • "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.
  • "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases
  • "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing
  • "t" or 4 Plots of the p-values from t-statistics comparing means of treated and control subjects for pretreatment variables, before and after weighting.
  • "ks" or 5 Plots of the p-values from Kolmogorov-Smirnov statistics comparing distributions of pretreatment variables of treated and control subjects, before and after weighting.
subset  Used to restrict which of the stop.methods will be used in the figure. For example subset = c(1,3) would indicate that the first and third stop.methods (in alphabetical order of those specified in the original call to iptw) should be included in the figure.
color  If color = FALSE, figures will be gray scale. Default: TRUE.
timePeriods  The number of distinct time points. If NULL, this is assumed to be the number of ps objects (i.e., the number of distinct time points).
multiPage  When multiple frames of a figure are produced, multiPage = TRUE will print each frame on a different page. This is intended for situations where the graphical output is being saved to a file. Default: FALSE.
figureRows  The figure rows, passed to displayPlots. Default: NULL.
hline  Arguments passed to panel.abline.
...  Additional arguments.

Details

This function produces lattice-style graphics of diagnostic plots.

References

See Also

iptw

plot.mniptw

Description

Plot mniptw

Usage

## S3 method for class 'mniptw'
plot(
  x,
  plots = "optimize",
  pairwiseMax = TRUE,
  figureRows = NULL,
  color = TRUE,
  subset = NULL,
  treatments = NULL,
  singlePlot = NULL,
  multiPage = FALSE,
  timePeriods = NULL,
  hline = c(0.1, 0.5, 0.8),
  ...
)

Arguments

x
An iptw object.

plots
An indicator of which type of plot is desired. The options are

- "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.
- "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases
- "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing
- "t" or 4 Plots of the p-values from t-statistics comparing means of treated and control subjects for pretreatment variables, before and after weighting.
- "ks" or 5 Plots of the p-values from Kolmogorov-Smirnov statistics comparing distributions of pretreatment variables of treated and control subjects, before and after weighting.

pairwiseMax
If FALSE, the plots for the underlying ps fits will be returned. Otherwise, pairwise maxima will be returned.
The figure rows, passed to displayPlots. Default: NULL.

If color = FALSE, figures will be gray scale. Default: TRUE.

Used to restrict which of the stop.methods will be used in the figure. For example subset = c(1,3) would indicate that the first and third stop.methods (in alphabetical order of those specified in the original call to iptw) should be included in the figure.

Only applicable when pairwiseMax is FALSE and plots 3, 4, and 5. If left at NULL, panels for all treatment pairs are created. If one level of the treatment variable is specified, plots comparing that treatment to all others are produced. If two levels are specified, a comparison for that single pair is produced.

For Plot calls that produce multiple plots, specifying an integer value of singlePlot will return only the corresponding plot. E.g., specifying singlePlot = 2 will return the second plot.

When multiple frames of a figure are produced, multiPage = TRUE will print each frame on a different page. This is intended for situations where the graphical output is being saved to a file. Default: FALSE.

The number of distinct time points. If NULL, this is assumed to be the number of ps objects (i.e., the number of distinct time points).

Arguments passed to panel.abline.

Additional arguments.

This function produces a collection of diagnostic plots for mnps objects.

## S3 method for class 'mnps'
plot(
  x,
  plots = "optimize",
  pairwiseMax = TRUE,
  figureRows = NULL,
  color = TRUE,
  subset = NULL,
  treatments = NULL,
  singlePlot = NULL,
  multiPage = FALSE,
  time = NULL,
  print = TRUE,
  hline = c(0.1, 0.5, 0.8),
  ...
)
Arguments

x
An mmps object.

plots
An indicator of which type of plot is desired. The options are
- "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.
- "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases
- "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing
- "t" or 4 Plots of the p-values from t-statistics comparing means of treated and control subjects for pretreatment variables, before and after weighting.
- "ks" or 5 Plots of the p-values from Kolmogorov-Smirnov statistics comparing distributions of pretreatment variables of treated and control subjects, before and after weighting.

pairwiseMax
If FALSE, the plots for the underlying ps fits will be returned. Otherwise, pairwise maxima will be returned.

figureRows
The number of rows of figures that should be used. If left as NULL, twang tries to find a reasonable value.

color
If color = FALSE, figures will be gray scale. Default: TRUE.

subset
Used to restrict which of the stop.methods will be used in the figure. For example subset = c(1,3) would indicate that the first and third stop.methods (in alphabetical order of those specified in the original call to mmps) should be included in the figure.

treatments
Only applicable when pairwiseMax is FALSE and plots 3, 4, and 5. If left at NULL, panels for all treatment pairs are created. If one level of the treatment variable is specified, plots comparing that treatment to all others are produced. If two levels are specified, a comparison for that single pair is produced.

singlePlot
For Plot calls that produce multiple plots, specifying an integer value of singlePlot will return only the corresponding plot. E.g., specifying singlePlot = 2 will return the second plot.

multiPage
When multiple frames of a figure are produced, multiPage = TRUE will print each frame on a different page. This is intended for situations where the graphical output is being saved to a file.

time
For use with iptw.

print
If FALSE, the figure is returned but not printed. Default: TRUE.

hline
Arguments passed to panel.abline.

...
Additional arguments.

Details

This function produces lattice-style graphics of diagnostic plots.
References


See Also

mnps

---

### Description

This function produces a collection of diagnostic plots for ps objects.

#### Usage

```r
## S3 method for class 'ps'
plot(x, plots = "optimize", subset = NULL, color = TRUE, ...)
```

#### Arguments

- `x` A ps object.
- `plots` An indicator of which type of plot is desired. The options are
  - "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.
  - "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases
  - "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing
  - "t" or 4 Plots of the p-values from t-statistics comparing means of treated and control subjects for pretreatment variables, before and after weighting.
  - "ks" or 5 Plots of the p-values from Kolmogorov-Smirnov statistics comparing distributions of pretreatment variables of treated and control subjects, before and after weighting.
- `subset` If multiple stop.method rules were used in the ps() call, subset restricts the plots of a subset of the stopping rules that were employed. This argument expects a subset of the integers from 1 to k, if k stop.methods were used.
- `color` If color = FALSE, figures will be gray scale. Default: TRUE.
- `...` Additional arguments.

#### Details

This function produces lattice-style graphics of diagnostic plots.
References


See Also

ps

---

### print.dxwts

**Default print statement for dxwts class**

**Description**

Default print statement for dxwts class

**Usage**

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

**Arguments**

- `x` A dxwts object
- `...` Additional arguments.

---

### print.iptw

**Default print statement for iptw class**

**Description**

Default print statement for iptw class

**Usage**

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

**Arguments**

- `x` A iptw object
- `...` Additional arguments.
print.mniptw

Default print statement for mniptw class

Description

Default print statement for mniptw class

Usage

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

Arguments

x A mniptw object

... Additional arguments.

print.mnps

Default print statement for mnps class

Description

Default print statement for mnps class

Usage

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

Arguments

x A mnps object

... Additional arguments.
print.ps  

Default print statement for ps class

Description

Default print statement for ps class

Usage

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

Arguments

x  An ps object
...

Arguments

print.summary.iptw  

Produces a summary table for iptw object

Description

Produces a summary table for iptw object

Usage

## S3 method for class 'summary.iptw'
print(x, ...)

Arguments

x  An iptw object
...

Arguments
**print.summary.mniptw**

Produces a summary table for mniptw object

**Description**

Produces a summary table for mniptw object

**Usage**

```r
## S3 method for class 'summary.mniptw'
print(x, ...)
```

**Arguments**

- `x` : An mniptw object
- `...` : Additional arguments.

---

**print.summary.mnps**

*Produces a summary table for mnps object*

**Description**

Produces a summary table for mnps object

**Usage**

```r
## S3 method for class 'summary.mnps'
print(x, ...)
```

**Arguments**

- `x` : An mnps object
- `...` : Additional arguments.
print.summary.ps  
Produces a summary table for ps object

Description

Produces a summary table for ps object

Usage

```r
## S3 method for class 'summary.ps'
print(x, ...)  
```

Arguments

- `x`  
  An ps object
- `...`  
  Additional arguments.

ps  
Gradient boosted propensity score estimation

Description

ps calculates propensity scores using gradient boosted logistic regression and diagnoses the resulting propensity scores using a variety of methods

Usage

```r
ps(
  formula = formula(data),
  data,
  n.trees = 10000,
  interaction.depth = 3,
  shrinkage = 0.01,
  bag.fraction = 1,
  n.minobsinnode = 10,
  perm.test.iters = 0,
  print.level = 2,
  verbose = TRUE,
  estimand = "ATE",
  stop.method = c("ks.mean", "es.mean"),
  sampw = NULL,
  version = "gbm",
  ks.exact = NULL,
  n.keep = 1,
  n.grid = 25,
```
keep.data = TRUE,
... )

Arguments

formula An object of class `formula`: a symbolic description of the propensity score model to be fit with the treatment indicator on the left side of the formula and the potential confounding variables on the right side.

data A dataset that includes the treatment indicator as well as the potential confounding variables.
n.trees Number of gbm iterations passed on to `gbm::gbm()`. Default: 10000.
interaction.depth A positive integer denoting the tree depth used in gradient boosting. Default: 3.
shrinkage A numeric value between 0 and 1 denoting the learning rate. See `gbm` for more details. Default: 0.01.
bag.fraction A numeric value between 0 and 1 denoting the fraction of the observations randomly selected in each iteration of the gradient boosting algorithm to propose the next tree. See `gbm` for more details. Default: 1.0.
n.minobsinnode An integer specifying the minimum number of observations in the terminal nodes of the trees used in the gradient boosting. See `gbm` for more details. Default: 10.
perm.test.iters A non-negative integer giving the number of iterations of the permutation test for the KS statistic. If `perm.test.iters=0` then the function returns an analytic approximation to the p-value. Setting `perm.test.iters=200` will yield precision to within 3% if the true p-value is 0.05. Use `perm.test.iters=500` to be within 2%. Default: 0.
print.level The amount of detail to print to the screen. Default: 2.
verbose If TRUE, lots of information will be printed to monitor the the progress of the fitting. Default: TRUE.
estimand "ATE" (average treatment effect) or "ATT" (average treatment effect on the treated): the causal effect of interest. ATE estimates the change in the outcome if the treatment were applied to the entire population versus if the control were applied to the entire population. ATT estimates the analogous effect, averaging only over the treated population. Default: "ATE".
stop.method A method or methods of measuring and summarizing balance across pretreatment variables. Current options are `ks.mean`, `ks.max`, `es.mean`, and `es.max`. `ks` refers to the Kolmogorov-Smirnov statistic and `es` refers to standardized effect size. These are summarized across the pretreatment variables by either the maximum (.max) or the mean (.mean). Default: c("ks.mean", "es.mean").
sampw Optional sampling weights.
version "gbm", "xgboost", or "legacy", indicating which version of the twang package to use.
"gbm" uses gradient boosting from the `gbm` package,
"xgboost" uses gradient boosting from the xgboost package, and
"legacy" uses the prior implementation of the ps function.
Default: "gbm".

ks.exact NULL or a logical indicating whether the Kolmogorov-Smirnov p-value should be
based on an approximation of exact distribution from an unweighted two-sample
Kolmogorov-Smirnov test. If NULL, the approximation based on the exact dis-
tribution is computed if the product of the effective sample sizes is less than
10,000. Otherwise, an approximation based on the asymptotic distribution is
used. **Warning:** setting ks.exact = TRUE will add substantial computation
time for larger sample sizes. Default: NULL.

n.keep A numeric variable indicating the algorithm should only consider every n.keep-
th iteration of the propensity score model and optimize balance over this set
instead of all iterations. Default: 1.

n.grid A numeric variable that sets the grid size for an initial search of the region
most likely to minimize the stop.method. A value of n.grid=50 uses a 50
point grid from 1:n.trees. It finds the minimum, say at grid point 35. It then
looks for the actual minimum between grid points 34 and 36. If specified with
n.keep>1, n.grid corresponds to a grid of points on the kept iterations as de-
defined by n.keep. Default: 25.

keep.data A logical variable indicating whether or not the data is saved in the resulting
ps object. Default: TRUE.

... Additional arguments that are passed to ps function.

Details
For user more comfortable with the options of xgboost::xgboost(), the options for ps controlling
the behavior of the gradient boosting algorithm can be specified using the xgboost naming scheme.
This includes nrounds, max_depth, eta, and subsample. In addition, the list of parameters passed
to xgboost can be specified with params.

Note that unlike earlier versions of 'twang', the plotting functions are no longer included in the ps
function. See plot for details of the plots.

Value
Returns an object of class ps, a list containing
gbm.obj The returned gbm or xgboost object.
treat The vector of treatment indicators.
treat.var The treatment variable.
desc A list containing balance tables for each method selected in stop.methods. Includes a com-
ponent for the unweighted analysis names "unw". Each desc component includes a list with
the following components
esst The effective sample size of the control group.
n.treat The number of subjects in the treatment group.
n.ctrl The number of subjects in the control group.
max.es The largest effect size across the covariates.
mean.es The mean absolute effect size.
max.ks The largest KS statistic across the covariates.
mean.ks The average KS statistic across the covariates.
bal.tab a (potentially large) table summarizing the quality of the weights for equalizing
the distribution of features across the two groups. This table is best extracted using the
bal.table method. See the help for bal.table for details on the table’s contents.
n.trees The estimated optimal number of gradient boosted iterations to optimize the loss
function for the associated stop.methods.
ps a data frame containing the estimated propensity scores. Each column is associated with
one of the methods selected in stop.methods.
w a data frame containing the propensity score weights. Each column is associated with one
of the methods selected in stop.methods. If sampling weights are given then these are
incorporated into these weights.
estimand The estimand of interest (ATT or ATE).
datestamp Records the date of the analysis.
parameters Saves the ps call.
alerts Text containing any warnings accumulated during the estimation.
iters A sequence of iterations used in the GBM fits used by plot function.
balance The balance measures for the pretreatment covariates used in plotting, with a column for
each stop.method.
balance.ks The KS balance measures for the pretreatment covariates used in plotting, with a
column for each covariate.
balance.es The standard differences for the pretreatment covariates used in plotting, with a col-
umn for each covariate.
ks The KS balance measures for the pretreatment covariates on a finer grid, with a column for each
covariate.
es The standard differences for the pretreatment covariates on a finer grid, with a column for each
covariate.
n.trees Maximum number of trees considered in GBM fit.
data Data as specified in the data argument.

References

Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-
425.

See Also

gbm, xgboost, plot, bal.table
Description

Simulated example data for assessing race bias in traffic stop outcomes

Usage

data(raceprofiling)

Format

A data frame with 5000 observations on the following 10 variables.

- id: an ID for each traffic stop
- nhood: a factor indicating the neighborhood in which the stop occurred.
- reason: The reason for the stop, mechanical/registration violations, dangerous moving violation, non-dangerous moving violation
- resident: an indicator whether the driver is a resident of the city
- age: driver's age
- male: an indicator whether the driver was male
- race: the race of the driver, with levels A, B, H, W
- hour: the hour of the stop (24-hour clock)
- month: and ordered factor indicating in which month the stop took place
- citation: an indicator of whether the driver received a citation

Source

This is simulated data to demonstrate how to use twang to adjust estimates of racial bias for important factors. This dataset does not represent real data from any real law enforcement agency.

References


Examples

data(raceprofiling)

# the first five lines of the dataset
raceprofiling[1:5,]
sensitivity

Function to run sensitivity analysis described in Ridgeway’s paper; currently works only for ATT.

Description

Performs the sensitivity analyses described in Ridgeway (2006). This is a beta version of this functionality. Please let the developers know if you have problems with it.

Usage

sensitivity(ps1, data, outcome, order.by.importance = TRUE, verbose = TRUE)

Arguments

ps1
A ‘ps’ object.
data
The dataset including the outcomes
outcome
The outcome of interest.
order.by.importance
Orders the output by relative importance of covariates.
verbose
If ‘TRUE’, extra information will be printed.

Value

Returns the following:
* ‘tx’ Summary for treated observations.
* ‘ctrl’ Summary for control observations.

References


stop.methods

Stop methods (e.g. "es.mean", "ks.mean", etc.) object, used only for backward compatibility

Description

In older versions of twang, the ‘ps’ function specified the ‘stop.method’ in a different manner. This ‘stop.methods’ object is used to ensure backward compatibility; new twang users should not make use of it.

Usage

stop.methods
Format

An object of class matrix (inherits from array) with 1 rows and 6 columns.

Details

This is merely a vector with the names of the stopping rules.

## S3 method for class 'iptw'

summary(object, ...)

Arguments

- **object**  
  An iptw object.

- **...**  
  Additional arguments.

Details

Compresses the information in the desc component of the iptw object into a short summary table describing the size of the dataset and the quality of the propensity score weights.

Value

See iptw for details on the returned table.

See Also

iptw
### summary.mniptw

**Summarize a mniptw object**

**Description**

Summarize a \texttt{mniptw} object

**Usage**

```r
## S3 method for class 'mniptw'
summary(object, ...)
```

**Arguments**

- `object`: A \texttt{mniptw} object.
- `...`: Additional arguments.

### summary.mnps

**Summarize a mnps object**

**Description**

Computes summary information about a stored \texttt{mnps} object

**Usage**

```r
## S3 method for class 'mnps'
summary(object, ...)
```

**Arguments**

- `object`: An \texttt{mnps} object.
- `...`: Additional arguments.

**Details**

Compresses the information in the desc component of the \texttt{mnps} object into a short summary table describing the size of the dataset and the quality of the propensity score weights.

**Value**

See \texttt{mnps} for details on the returned table.

**See Also**

\texttt{mnps}
Summary a ps object

Description
Computes summary information about a stored ps object

Usage
## S3 method for class 'ps'
summary(object, ...)

Arguments
object
An ps object.
...
Additional arguments.

Details
Compresses the information in the desc component of the ps object into a short summary table describing the size of the dataset and the quality of the propensity score weights.

Value
See ps for details on the returned table.

See Also
ps
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