

# Package ‘twang’

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**Title** Toolkit for Weighting and Analysis of Nonequivalent Groups

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**Suggests** knitr

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

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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.

---

`AOD`*Subset of Alcohol and Other Drug treatment data*

---

**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**

McCaffrey, DF, BA Griffin, D Almirall, ME Slaughter, R Ramchand and LF Burgette (2013). A tutorial on propensity score estimation for multiple treatments using generalized boosted models. *Statistics in Medicine*.

---

<code>bal.stat</code>	<i>Calculate weighted balance statistics</i>
-----------------------	--

---

### Description

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

### Usage

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

### Arguments

<code>data</code>	A data frame containing the data
<code>vars</code>	A vector of character strings with the names of the variables on which the function will assess the balance
<code>treat.var</code>	The name of the treatment variable
<code>w.all</code>	Observation weights (e.g. propensity score weights, sampling weights, or both)
<code>sampw</code>	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).
<code>get.means</code>	logical. If 'TRUE' then 'bal.stat' will compute means and variances
<code>get.ks</code>	logical. If 'TRUE' then 'bal.stat' will compute KS statistics
<code>na.action</code>	A character string indicating how 'bal.stat' should handle missing values. Current options are "level", "exclude", or "lowest"
<code>estimand</code>	Either "ATT" or "ATE"
<code>multinom</code>	logical. 'TRUE' if used for multinomial propensity scores.
<code>fillNAs</code>	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**

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

**See Also**

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

---

bal.table	<i>Compute the balance table.</i>
-----------	-----------------------------------

---

**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 <a href="#">ps</a> or <a href="#">dx.wts</a> object.
digits	The number of digits that the numerical entries should be rounded to. Default: 3.
collapse.to	For <a href="#">mnps</a> 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.

<code>subset.treat</code>	Subset to either all pairs that include a specified treatment or a single pair of treatments.
<code>subset.stop.method</code>	Subset to either all pairs that include a specified treatment or a single pair of treatments.
<code>es.cutoff</code>	Subsets to comparisons with absolute ES values bigger than <code>es.cutoff</code> . Default: 0.
<code>ks.cutoff</code>	Subsets to comparisons with KS values bigger than <code>ks.cutoff</code> . Default: 0.
<code>p.cutoff</code>	Subsets to comparisons with t- or chi-squared p-values no bigger than <code>p.cutoff</code> . Default: 1.
<code>ks.p.cutoff</code>	Subsets to comparisons with t- or chi-squared p-values no bigger than <code>p.cutoff</code> . Default: 1.
<code>timePeriods</code>	Used to subset times for iptw fits.
<code>...</code>	Additional arguments.

## 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 graphical 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**

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

**See Also**

[mnps]

---

boxplot.ps

*Boxplot for 'ps' objects*

---

**Description**

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

**Usage**

```
## 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**

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

**See Also**

[ps]

---

desc.wts                      *Diagnosis of weights*

---

## Description

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

## Usage

```
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 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%
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**

<code>ptList</code>	A list of plots to display.
<code>figureRows</code>	The number of rows in the figure.
<code>singlePlot</code>	An integer indicating the index of the plot to display.
<code>multiPage</code>	Whether to display plots on multiple pages.
<code>bxpt</code>	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

```
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](#)

---

egsingle

*US Sustaining Effects study*

---

**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

**Source**

Reproduced from the `lmRev` 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**

Doran, H.C. and J.R. Lockwood (2006). "Fitting value-added models in R," *Journal of Educational and Behavioral Statistics*, 31(1)

---

<code>get.weights</code>	<i>Extract propensity score weights.</i>
--------------------------	--

---

**Description**

Extracts propensity score weights from a `ps` or `mnp` object.

**Usage**

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

**Arguments**

<code>ps1</code>	A <code>ps</code> or <code>mnp</code> object.
<code>stop.method</code>	Indicates which set of weights to retrieve from the <code>ps</code> object.
<code>estimand</code>	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, <code>get.weights</code> will use the estimand used to fit the <code>ps</code> object.
<code>withSampW</code>	Whether to return weights with sample weights multiplied in, if they were provided in the original <code>ps</code> or <code>mnp</code> 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](#), [mnp](#)

---

get.weights.num      *Get numerators to stabilize propensity score weights for 'iptw' fits.*

---

### Description

Forms numerators to stabilize weights for an iptw object.

### Usage

```
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

```
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]

---

iptw	<i>Inverse probability of treatment weighting for marginal structural models.</i>
------	---

---

**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**

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

	Default: "gbm".
<code>ks.exact</code>	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. <b>**Warning:**</b> setting <code>ks.exact = TRUE</code> will add substantial computation time for larger sample sizes. Default: NULL.
<code>n.keep</code>	A numeric variable indicating the algorithm should only consider every <code>n.keep</code> -th iteration of the propensity score model and optimize balance over this set instead of all iterations. Default: 1.
<code>n.grid</code>	A numeric variable that sets the grid size for an initial search of the region most likely to minimize the <code>stop.method</code> . A value of <code>n.grid=50</code> uses a 50 point grid from <code>1:n.trees</code> . 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 <code>n.keep&gt;1</code> , <code>n.grid</code> corresponds to a grid of points on the kept iterations as defined by <code>'n.keep</code> . Default: 25.
<code>...</code>	Additional arguments that are passed to <code>ps</code> 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.

---

lalonde

*Lalonde's National Supported Work Demonstration data*

---

### 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

<http://www.columbia.edu/~rd247/nswdata.html> <http://cran.r-project.org/src/contrib/Descriptions/MatchIt.html>

### References

Lalonde, R. (1986). Evaluating the econometric evaluations of training programs with experimental data. *American Economic Review* 76: 604-620.

Dehejia, R.H. and Wahba, S. (1999). Causal Effects in Nonexperimental Studies: Re-Evaluating the Evaluation of Training Programs. *Journal of the American Statistical Association* 94: 1053-1062.

lindner

*Lindner Center data on 996 PCI patients analyzed by Kereiakes et al. (2000)*

### 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.

**sixMonthSurvive** Survival at six months — a recoded version of lifepres.

### References

Kereiakes DJ, Obenchain RL, Barber BL, et al. Abciximab provides cost effective survival advantage in high volume interventional practice. *Am Heart J* 2000; **140**: 603-610.

Obenchain RL. (2009) **USPSinR.pdf** ../R\_HOME/library/USPS 40 pages.

---

means.table	<i>Extract table of means from an 'mnps' object</i>
-------------	---

---

**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]

---

mnIptwExLong	<i>Example data for iptw function (long version, more than two treatments).</i>
--------------	---

---

**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.

---

mnIptwExWide

*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).

**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.

mnps

*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**

```
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 <a href="#">gbm</a> : <code>gbm()</code> . 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 <a href="#">gbm</a> 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 <a href="#">gbm</a> for more details. Default: 1.0.

<code>n.minobsinnode</code>	An integer specifying the minimum number of observations in the terminal nodes of the trees used in the gradient boosting. See <a href="#">gbm</a> for more details. Default: 10.
<code>perm.test.iters</code>	A non-negative integer giving the number of iterations of the permutation test for the KS statistic. If <code>perm.test.iters=0</code> then the function returns an analytic approximation to the p-value. Setting <code>perm.test.iters=200</code> will yield precision to within 3% if the true p-value is 0.05. Use <code>perm.test.iters=500</code> to be within 2%. Default: 0.
<code>print.level</code>	The amount of detail to print to the screen. Default: 2.
<code>verbose</code>	If TRUE, lots of information will be printed to monitor the the progress of the fitting. Default: TRUE.
<code>estimand</code>	"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".
<code>stop.method</code>	A method or methods of measuring and summarizing balance across pretreatment variables. Current options are <code>ks.mean</code> , <code>ks.max</code> , <code>es.mean</code> , and <code>es.max</code> . <code>ks</code> refers to the Kolmogorov-Smirnov statistic and <code>es</code> refers to standardized effect size. These are summarized across the pretreatment variables by either the maximum ( <code>.max</code> ) or the mean ( <code>.mean</code> ). Default: <code>c("es.mean")</code> .
<code>sampw</code>	Optional sampling weights.
<code>version</code>	"gbm", "xgboost", or "legacy", indicating which version of the twang package to use. "gbm" uses gradient boosting from the <a href="#">gbm</a> package. "xgboost" uses gradient boosting from the <a href="#">xgboost</a> package. "legacy" uses the prior implementation of the <a href="#">ps</a> function. Default: "gbm".
<code>ks.exact</code>	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. <b>**Warning:**</b> setting <code>ks.exact = TRUE</code> will add substantial computation time for larger sample sizes. Default: NULL.
<code>n.keep</code>	A numeric variable indicating the algorithm should only consider every <code>n.keep</code> -th iteration of the propensity score model and optimize balance over this set instead of all iterations. Default: 1.
<code>n.grid</code>	A numeric variable that sets the grid size for an initial search of the region most likely to minimize the <code>stop.method</code> . A value of <code>n.grid=50</code> uses a 50 point grid from <code>1:n.trees</code> . 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 <code>n.keep&gt;1</code> , <code>n.grid</code> corresponds to a grid of points on the kept iterations as defined by <code>n.keep</code> . Default: 25.

treatATT	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 <a href="#">ps</a> 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.

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

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### References

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

### See Also

[ps](#), [gbm](#), [xgboost](#), [plot](#), [bal.table](#)

---

plot.dxwts	<i>Plot dxwts</i>
------------	-------------------

---

**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 <ul style="list-style-type: none"> <li>• "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.</li> <li>• "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases</li> <li>• "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing</li> <li>• "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.</li> <li>• "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.</li> </ul>
...	Additional arguments.

---

plot.iptw	<i>Plots for iptw objects</i>
-----------	-------------------------------

---

**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,
```

```

    timePeriods = NULL,
    multiPage = FALSE,
    figureRows = 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 <ul style="list-style-type: none"> <li>• "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.</li> <li>• "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases</li> <li>• "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing</li> <li>• "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.</li> <li>• "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.</li> </ul>
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 <a href="#">displayPlots</a> . Default: NULL.
hline	Arguments passed to panel.abline.
...	Additional arguments.

## Details

This function produces lattice-style graphics of diagnostic plots.

## References

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

**See Also**[iptw](#)


---

plot.mnptw	<i>Plot mnptw</i>
------------	-------------------

---

**Description**

Plot mnptw

**Usage**

```
## S3 method for class 'mnptw'
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 <ul style="list-style-type: none"> <li>• "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.</li> <li>• "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases</li> <li>• "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing</li> <li>• "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.</li> <li>• "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.</li> </ul>
pairwiseMax	If FALSE, the plots for the underlying ps fits will be returned. Otherwise, pairwise maxima will be returned.

figureRows	The figure rows, passed to <code>displayPlots</code> . Default: NULL.
color	If <code>color = FALSE</code> , figures will be gray scale. Default: TRUE.
subset	Used to restrict which of the <code>stop.methods</code> will be used in the figure. For example <code>subset = c(1,3)</code> would indicate that the first and third <code>stop.methods</code> (in alphabetical order of those specified in the original call to <code>iptw</code> ) should be included in the figure.
treatments	Only applicable when <code>pairwiseMax</code> 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 <code>singlePlot</code> will return only the corresponding plot. E.g., specifying <code>singlePlot = 2</code> will return the second plot.
multiPage	When multiple frames of a figure are produced, <code>multiPage = TRUE</code> 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.
timePeriods	The number of distinct time points. If NULL, this is assumed to be the number of <code>ps</code> objects (i.e., the number of distinct time points).
hline	Arguments passed to <code>panel.abline</code> .
...	Additional arguments.

---

plot.mnps

*Plots for mnps objects*


---

## Description

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

## Usage

```
## 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 mnps object.
plots	An indicator of which type of plot is desired. The options are <ul style="list-style-type: none"> <li>• "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.</li> <li>• "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases</li> <li>• "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing</li> <li>• "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.</li> <li>• "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.</li> </ul>
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 mnps) 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**

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

**See Also**

[mnps](#)

---

plot.ps	<i>Plots for ps objects</i>
---------	-----------------------------

---

**Description**

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

**Usage**

```
## 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 <ul style="list-style-type: none"> <li>• "optimize" or 1 A plot of the balance criteria as a function of the GBM iteration.</li> <li>• "boxplot" or 2 Boxplots of the propensity scores for the treatment and control cases</li> <li>• "es" or 3 Plots of the standardized effect size of the pre-treatment variables before and after reweighing</li> <li>• "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.</li> <li>• "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.</li> </ul>
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**

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

**See Also**

[ps](#)

---

print.dxwts	<i>Default print statement for dxwts class</i>
-------------	--

---

**Description**

Default print statement for dxwts class

**Usage**

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

**Arguments**

x	A dxwts object
...	Additional arguments.

---

print.iptw	<i>Default print statement for iptw class</i>
------------	---

---

**Description**

Default print statement for iptw class

**Usage**

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

**Arguments**

x	A iptw object
...	Additional arguments.

---

print.mnptw	<i>Default print statement for mnptw class</i>
-------------	--

---

**Description**

Default print statement for mnptw class

**Usage**

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

**Arguments**

x	A mnptw object
...	Additional arguments.

---

print.mnps	<i>Default print statement for mnps class</i>
------------	---

---

**Description**

Default print statement for mnps class

**Usage**

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

**Arguments**

x	A mnps object
...	Additional arguments.

---

print.ps	<i>Default print statement for ps class</i>
----------	---

---

**Description**

Default print statement for ps class

**Usage**

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

**Arguments**

x	An ps object
...	Additional arguments.

---

print.summary.iptw	<i>Produces a summary table for iptw object</i>
--------------------	---

---

**Description**

Produces a summary table for iptw object

**Usage**

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

**Arguments**

x	An iptw object
...	Additional arguments.

---

`print.summary.mnptw` *Produces a summary table for mnptw object*

---

**Description**

Produces a summary table for mnptw object

**Usage**

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

**Arguments**

x            An mnptw object  
...          Additional arguments.

---

`print.summary.mnps` *Produces a summary table for mnps object*

---

**Description**

Produces a summary table for mnps object

**Usage**

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

**Arguments**

x            An mnps object  
...          Additional arguments.

---

<code>print.summary.ps</code>	<i>Produces a summary table for ps object</i>
-------------------------------	---

---

**Description**

Produces a summary table for ps object

**Usage**

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

**Arguments**

<code>x</code>	An ps object
<code>...</code>	Additional arguments.

---

<code>ps</code>	<i>Gradient boosted propensity score estimation</i>
-----------------	---

---

**Description**

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

**Usage**

```
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

<code>formula</code>	An object of class <code>formula</code> : 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.
<code>data</code>	A dataset that includes the treatment indicator as well as the potential confounding variables.
<code>n.trees</code>	Number of <code>gbm</code> iterations passed on to <code>gbm::gbm()</code> . Default: 10000.
<code>interaction.depth</code>	A positive integer denoting the tree depth used in gradient boosting. Default: 3.
<code>shrinkage</code>	A numeric value between 0 and 1 denoting the learning rate. See <code>gbm</code> for more details. Default: 0.01.
<code>bag.fraction</code>	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 <code>gbm</code> for more details. Default: 1.0.
<code>n.minobsinnode</code>	An integer specifying the minimum number of observations in the terminal nodes of the trees used in the gradient boosting. See <code>gbm</code> for more details. Default: 10.
<code>perm.test.iters</code>	A non-negative integer giving the number of iterations of the permutation test for the KS statistic. If <code>perm.test.iters=0</code> then the function returns an analytic approximation to the p-value. Setting <code>perm.test.iters=200</code> will yield precision to within 3% if the true p-value is 0.05. Use <code>perm.test.iters=500</code> to be within 2%. Default: 0.
<code>print.level</code>	The amount of detail to print to the screen. Default: 2.
<code>verbose</code>	If TRUE, lots of information will be printed to monitor the the progress of the fitting. Default: TRUE.
<code>estimand</code>	"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".
<code>stop.method</code>	A method or methods of measuring and summarizing balance across pretreatment variables. Current options are <code>ks.mean</code> , <code>ks.max</code> , <code>es.mean</code> , and <code>es.max</code> . <code>ks</code> refers to the Kolmogorov-Smirnov statistic and <code>es</code> refers to standardized effect size. These are summarized across the pretreatment variables by either the maximum ( <code>.max</code> ) or the mean ( <code>.mean</code> ). Default: <code>c("ks.mean", "es.mean")</code> .
<code>sampw</code>	Optional sampling weights.
<code>version</code>	"gbm", "xgboost", or "legacy", indicating which version of the <code>twang</code> package to use. "gbm" uses gradient boosting from the <code>gbm</code> 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 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. <b>**Warning:**</b> 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.
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 component for the unweighted analysis names "unw". Each desc component includes a list with the following components

`ess` 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).  
`timestamp` 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 column 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

Dan McCaffrey, G. Ridgeway, Andrew Morral (2004). "Propensity Score Estimation with Boosted Regression for Evaluating Adolescent Substance Abuse Treatment", *Psychological Methods* 9(4):403-425.

## See Also

`gbm`, `xgboost`, `plot`, `bal.table`

---

raceprofiling

*Traffic stop data*

---

### 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` an 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

G. Ridgeway (2006). "Assessing the effect of race bias in post-traffic stop outcomes using propensity scores," *Journal of Quantitative Criminology* 22(1).

### Examples

```
data(raceprofiling)
```

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

---

sensitivity	<i>Function to run sensitivity analysis described in Ridgeway's paper; currently works only for ATT.</i>
-------------	--

---

**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**

Ridgeway, G. (2006). "The effect of race bias in post-traffic stop outcomes using propensity scores", *Journal of Quantitative Criminology*\* 22(1):1-29.

---

stop.methods	<i>Stop methods (e.g. "es.mean", "ks.mean", etc.) object, used only for backward compatibility</i>
--------------	--

---

**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.

---

`summary.iptw`*Summarize a iptw object*

---

**Description**

Computes summary information about a stored `iptw` object

**Usage**

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

**Arguments**

<code>object</code>	An <code>iptw</code> object.
<code>...</code>	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.mnptw	<i>Summarize a mnptw object</i>
---------------	---------------------------------

---

**Description**

Summarize a mnptw object

**Usage**

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

**Arguments**

object	A mnptw object.
...	Additional arguments.

---

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

---

**Description**

Computes summary information about a stored mnps object

**Usage**

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

**Arguments**

object	An mnps object.
...	Additional arguments.

**Details**

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

**Value**

See [mnps](#) for details on the returned table.

**See Also**

[mnps](#)

---

`summary.ps`*Summarize a ps object*

---

**Description**

Computes summary information about a stored ps object

**Usage**

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

**Arguments**

<code>object</code>	An ps object.
<code>...</code>	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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