Package 'twang'

March 30, 2021

Version 2.0

Date 2021-03-22

Title Toolkit for Weighting and Analysis of Nonequivalent Groups

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Depends R (>= 2.10)

Imports gbm (>= 1.5-3), survey, xtable, lattice, latticeExtra, MatrixModels, data.table, ggplot2, xgboost

Suggests knitr

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

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Encoding UTF-8

NeedsCompilation yes

Repository CRAN

VignetteBuilder knitr

RoxygenNote 7.1.1

Date/Publication 2021-03-30 06:50:02 UTC

R topics documented:

`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.

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

```
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	Oobservation 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 shoud 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

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` *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.
...	Additional arugments.

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.

---

boxplot.mnps *Boxplot for 'mnps' objects*

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 bepassed 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 bepassed 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 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 propsensity 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

```
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 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%.

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 themlmRev 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)

`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

```
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` *Inverse probability of treatment weighting for marginal structural models.*

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 charar-acteristics.
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.
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.
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], 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 reatment 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 reatment 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 *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]

mnIptwExLong *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 reatment 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 reatment 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 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("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.
- `"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.

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 ps function.

Details

For user more comfortable with the options of 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

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 *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 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.
...	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,
```

```
  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 • "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

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.mniptw` *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.

figureRows	The figure rows, passed to displayPlots. Default: NULL.
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 iptw) 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. Default: FALSE.
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).
hline	Arguments passed to panel.abline.
...	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 • "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 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` *Plots for* `ps` *objects*

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 • "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

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` *Default print statement for* `dxwts` *class*

Description

Default print statement for `dxwts` class

Usage

```
## 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

```
## 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
...	Additional 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
...	Additional arguments.

print.summary.mniptw *Produces a summary table for* mniptw *object*

Description

Produces a summary table for mniptw object

Usage

```
## 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

```
## 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

```
## 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

```
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. 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 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.

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, 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).

- 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 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` 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

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` *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

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` *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.

`summary.iptw` *Summarize a* `iptw` *object*

Description

Computes summary information about a stored `iptw` object

Usage

```
## 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 mniptw object

Usage

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

Arguments

object	A mniptw object.
...	Additional arguments.

summary.mnps *Summarize a* mnps *object*

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

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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