Package ‘twang’
October 25, 2021

Version 2.5
Date 2021-10-20
Title Toolkit for Weighting and Analysis of Nonequivalent Groups
Author Matthew Cefalu, Greg Ridgeway, Dan McCaffrey, Andrew Morral, Beth Ann Griffin, and Lane Burgette
Maintainer Matthew Cefalu
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.
License GPL-3 | file LICENSE
Encoding UTF-8
NeedsCompilation yes
Repository CRAN
VignetteBuilder knitr
RoxygenNote 7.1.1
Date/Publication 2021-10-25 12:50:02 UTC

R topics documented:

  twang-package ..................................................... 2
  AOD .................................................................. 3
  bal.stat ............................................................. 3
  bal.table .......................................................... 5
  boxplot.mnps ....................................................... 6
  boxplot.ps .......................................................... 8
  desc.wts ............................................................ 9
  displayPlots ......................................................... 10
twang-package

dx.wts ................................................................. 11
egsingle .............................................................. 12
get.weights ......................................................... 13
get.weights.num .................................................. 14
get.weights.unstab ............................................... 14
iptw ................................................................. 15
iptwExLong ....................................................... 18
iptwExWide ....................................................... 18
lalonde ............................................................. 19
lindner .............................................................. 20
means.table ......................................................... 21
mnIptwExLong .................................................... 21
mnIptwExWide .................................................... 22
mnps ................................................................. 23
plot.dxwts .......................................................... 26
plot.iptw ............................................................ 26
plot.mniptw ........................................................ 28
plot.mnps ........................................................... 29
plot.ps ............................................................... 31
print.dxwts ........................................................ 32
print.iptw ........................................................... 32
print.mniptw ....................................................... 33
print.mnps ........................................................ 33
print.ps .............................................................. 34
print.summary.iptw ............................................... 34
print.summary.mniptw .......................................... 35
print.summary.mnps ............................................. 35
print.summary.ps ................................................ 36
ps ................................................................. 36
raceprofiling ....................................................... 40
sensitivity .......................................................... 41
stop.methods ....................................................... 41
summary.iptw ...................................................... 42
summary.mniptw .................................................. 43
summary.mnps ..................................................... 43
summary.ps ......................................................... 44

Index 45

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.
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


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 Observation weights (e.g. propensity score weights, sampling weights, or both)
sampw Sampling weights. These are passed in addition to ‘w.all’ because the "unweighted" results should be adjusted for sample weights (though not propensity score weights).
get.means logical. If ‘TRUE’ then ‘bal.stat’ will compute means and variances
get.ks logical. If ‘TRUE’ then ‘bal.stat’ will compute KS statistics
na.action A character string indicating how ‘bal.stat’ should handle missing values. Current options are "level", "exclude", or "lowest"
estimand Either "ATT" or "ATE"
multinom logical. ‘TRUE’ if used for multinomial propensity scores.
fillNAs logical. If ‘TRUE’, fills in zeros for missing values.

Details

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

Value

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

References

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.
The `p.cutoff` argument is used to subset comparisons with t- or chi-squared p-values no bigger than `p.cutoff`. Default: 1.

The `ks.p.cutoff` argument is used to subset comparisons with t- or chi-squared p-values no bigger than `p.cutoff`. Default: 1.

The `timePeriods` argument is used to subset times for IPTW fits.

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 `mmps` objects.
Usage

```r
## 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


See Also

[mnps]
**Boxplot for 'ps' objects**

**Description**

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

**Usage**

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

**Arguments**

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

**Details**

This function produces lattice-style graphics of diagnostic plots.

**References**


**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**

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

**Arguments**

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

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

Display plots

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 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
get.weights

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

References

get.weights  
Extract propensity score weights.

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

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

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

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

Value
Returns a vector of weights.

See Also
ps, mnps
get.weights.num

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

Description

Forms numerators to stabilize weights for an iptw object.

Usage

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]

generate.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 characteristics.
cumulative If TRUE, the time t model includes time-varying characteristics from times 1 through t-1. Default: TRUE.
timeIndicators For long format fits, a vector of times for each observation.
ID For long format fits, a vector of numeric identifiers for unique analytic units.
priorTreatment For long format fits, includes treatment levels from previous times if TRUE. This argument is ignored for wide format fits. Default: TRUE.
n.trees Number of gbm iterations passed on to gbm.
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.
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.

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`
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.

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’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


References


Description

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

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

Usage

data(lindner)

Format

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

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

References


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, 1 indicating the first stop.method specified.
includeSD Indicates whether standard deviations as well as means are to be displayed. By default, they are not displayed.
digits If not ‘NULL’, results will be rounded to the specified number of digits.

Details

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

Value

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

See Also

[mnps]

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

Description

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

Usage

data(lindner)
Format

A list with a covariate matrix and outcomes.

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

outcome  Vector of post-treatment outcomes.

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

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

Arguments

- **formula**
  A formula for the propensity score model with the treatment indicator on the left side of the formula and the potential confounding variables on the right side.

- **data**
  The dataset, includes treatment assignment as well as covariates.

- **n.trees**
  Number of gbm iterations passed on to `gbm`. Default: 10000.

- **interaction.depth**
  A positive integer denoting the tree depth used in gradient boosting. Default: 3.

- **shrinkage**
  A numeric value between 0 and 1 denoting the learning rate. See `gbm` for more details. Default: 0.01.

- **bag.fraction**
  A numeric value between 0 and 1 denoting the fraction of the observations randomly selected in each iteration of the gradient boosting algorithm to propose the next tree. See `gbm` for more details. Default: 1.0.
n.minobsinnode  An integer specifying the minimum number of observations in the terminal nodes of the trees used in the gradient boosting. See \texttt{gbm} for more details. Default: 10.

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

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

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

\textbf{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".

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

\textbf{sampw}  
Optional sampling weights.

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

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

Default: "gbm".

\textbf{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 \texttt{NULL}, the approximation based on the exact distribution is computed if the product of the effective sample sizes is less than 10,000. Otherwise, an approximation based on the asymptotic distribution is used. **Warning:** setting \texttt{ks.exact = TRUE} will add substantial computation time for larger sample sizes. Default: \texttt{NULL}.

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

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

Additional arguments that are passed to ps function.

Details

For user more comfortable with the options of xgboost, 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)

Lane Burgette `<burgette@rand.org>', Beth Ann Griffin `<bethg@rand.org>', Dan McCaffrey `<danielm@rand.org>'

References


See Also

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

Description
Plot dxwts

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

Arguments
- **x**: An dxwts object.
- **plots**: An indicator of which type of plot is desired. The options are
  - "optimize" or 1: A plot of the balance criteria as a function of the GBM iteration.
  - "boxplot" or 2: Boxplots of the propensity scores for the treatment and control cases.
  - "es" or 3: Plots of the standardized effect size of the 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,
)
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.

Details

This function produces lattice-style graphics of diagnostic plots.

References

See Also

iptw

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.
plot.mnps

Plots for mnps objects

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

Usage

```r
## 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),
  ...
)
```

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.
Arguments

- **x**
  - An `mnp` 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 mnp) should be included in the figure.

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

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

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

- **time**
  - For use with iptw.

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

- **hline**
  - Arguments passed to panel.abline.

- **...**
  - Additional arguments.

Details

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


See Also

mnps

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

See Also
ps

---

print.dwxts

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
...


---

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
...

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**

```r
## 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**

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

**Arguments**

- `x`  
  An iptw object
- `...`  
  Additional arguments.
print.summary.mniptw

Produces a summary table for \texttt{mniptw} object

Description

Produces a summary table for \texttt{mniptw} object

Usage

\begin{verbatim}
## S3 method for class 'summary.mniptw'
print(x, ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{x} \hspace{1cm} An \texttt{mniptw} object
  \item \texttt{...} \hspace{1cm} Additional arguments.
\end{itemize}

print.summary.mnps

Produces a summary table for \texttt{mnps} object

Description

Produces a summary table for \texttt{mnps} object

Usage

\begin{verbatim}
## S3 method for class 'summary.mnps'
print(x, ...)
\end{verbatim}

Arguments

\begin{itemize}
  \item \texttt{x} \hspace{1cm} An \texttt{mnps} object
  \item \texttt{...} \hspace{1cm} Additional arguments.
\end{itemize}
print.summary.ps  

Produces a summary table for ps object

Description

Produces a summary table for ps object

Usage

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

Arguments

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

ps

Gradient boosted propensity score estimation

Description

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

Usage

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

Arguments

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

data A dataset that includes the treatment indicator as well as the potential confounding variables.
n.trees Number of gbm iterations passed on to gbm. 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 \texttt{xgboost} package, and
• "legacy" uses the prior implementation of the \texttt{ps} function.

Default: "gbm".

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

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

\texttt{n.grid} \ A numeric variable that sets the grid size for an initial search of the region most likely to minimize the \texttt{stop.method}. A value of \texttt{n.grid=50} uses a 50 point grid from \texttt{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 \texttt{n.keep>1}, \texttt{n.grid} corresponds to a grid of points on the kept iterations as defined by \texttt{n.keep}. Default: 25.

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

\ldots \ Additional arguments that are passed to \texttt{ps} function.

\textbf{Details}

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

Note that unlike earlier versions of ‘twang’, the plotting functions are no longer included in the \texttt{ps} function. See \texttt{plot} for details of the plots.

\textbf{Value}

Returns an object of class \texttt{ps}, a list containing

• \texttt{gbm.obj} \ The returned \texttt{gbm} or \texttt{xgboost} object.
• \texttt{treat} \ The vector of treatment indicators.
• \texttt{treat.var} \ The treatment variable.
• \texttt{desc} \ A list containing balance tables for each method selected in \texttt{stop.methods}. Includes a component for the unweighted analysis names “unw”. Each \texttt{desc} component includes a list with the following components
  – \texttt{ess} \ The effective sample size of the control group.
  – \texttt{n.treat} \ The number of subjects in the treatment group.
  – \texttt{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).

**References**


**See Also**

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

Simulated example data for assessing race bias in traffic stop outcomes

Usage

data(raceprofiling)

Format

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

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

Source

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

References


Examples

data(raceprofiling)

# the first five lines of the dataset
raceprofiling[1:5,]
Function to run sensitivity analysis described in Ridgeway's paper; currently works only for ATT.

Description

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

Usage

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

Arguments

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

Value

Returns the following * 'tx' Summary for treated observations. * 'ctrl' Summary for control observations.

References


Stop methods (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

### S3 method for class 'iptw'

```r
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**

```r
## 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**

```r
## 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**

```r
## 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`
Index

* datasets
  AOD, 3
  egsingle, 12
  iptwExLong, 18
  iptwExWide, 18
  lalonde, 19
  lindner, 20
  mnIptwExLong, 21
  mnIptwExWide, 22
  raceprofiling, 40
  stop.methods, 41
* models
  desc.wts, 9
  ps, 36
  summary.iptw, 42
  summary.mnps, 43
  summary.ps, 44
* multivariate
  bal.stat, 3
  boxplot.mnps, 6
  boxplot.ps, 8
  ps, 36
* propensity
  twang-package, 2
* score
  twang-package, 2

AOD, 3
bal.stat, 3, 10
bal.table, 5, 17, 25, 39
boxplot.mnps, 6
boxplot.ps, 8
desc.wts, 9
displayPlots, 10, 27, 29
dx.wts, 5, 6, 11
egsingle, 12
formula, 37

gbm, 16, 17, 23–25, 37–39
get.weights, 13
get.weights.num, 14
get.weights.unstab, 14
iptw, 15, 28, 42
iptwExLong, 18
iptwExWide, 18
lalonde, 19
lindner, 20
means.table, 21
mnIptwExLong, 21
mnIptwExWide, 22
mnps, 5, 13, 17, 23, 31, 43
plot, 17, 25, 38, 39
plot.dxwts, 26
plot.iptw, 26
plot.mniptw, 28
plot.mnps, 29
plot.ps, 31
print.dxwts, 32
print.iptw, 32
print.mniptw, 33
print.mnps, 33
print.ps, 34
print.summary.iptw, 34
print.summary.mniptw, 35
print.summary.mnps, 35
print.summary.ps, 36
ps, 5, 6, 10–13, 16, 17, 24, 25, 32, 36, 44
raceprofiling, 40
sensitivity, 41
stop.methods, 41
summary.iptw, 42
summary.mniptw, 43
summary.mnps, 43

45
summary.ps, 44

twang (twang-package), 2
twang-package, 2

xgboost, 16, 17, 24, 25, 38, 39