

Package ‘PSAboot’

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Type Package

Title Bootstrapping for Propensity Score Analysis

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Description It is often advantageous to test a hypothesis more than once in the context of propensity score analysis (Rosenbaum, 2012) <doi:10.1093/biomet/ass032>. The functions in this package facilitate bootstrapping for propensity score analysis (PSA). By default, bootstrapping using two classification tree methods (using 'rpart' and 'ctree' functions), two matching methods (using 'Matching' and 'MatchIt' packages), and stratification with logistic regression. A framework is described for users to implement additional propensity score methods. Visualizations are emphasized for diagnosing balance; exploring the correlation relationships between bootstrap samples and methods; and to summarize results.

License GPL

URL <https://github.com/jbryer/PSAboot>

BugReports <https://github.com/jbryer/PSAboot/issues>

Depends ggplot2, graphics, PSAgraphics, R (>= 3.0)

Imports ggthemes, Matching, MatchIt, modeltools, parallel, party, psych, reshape2, rpart, stats, TriMatch, utils

Suggests knitr, rmarkdown

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Description

Bootstrapping procedures for Propensity Score Analysis.

as.data.frame.PSABootSummary

Convert the results of PSABoot summary to a data frame.

Description

Convert the results of PSABoot summary to a data frame.

Usage

```
## S3 method for class 'PSABootSummary'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

x	results of summary.PSABoot
row.names	row names.
optional	unused.
...	unused.

Value

a data.frame.

balance

Returns a summary of the balance for all bootstrap samples.

Description

This method provides some crude overall measures of balance.

Usage

```
balance(psaboot, na.rm = TRUE, pool.fun = mean)
```

Arguments

psaboot	results from PSABoot .
na.rm	should NAs be removed. NAs generally occur when there is insufficient sample for a particular covariate or an unused level.
pool.fun	a function specifying how the effect sizes across all covariates should be combined. Possible values include mean (default), q25 , q75 , median, max, or any function that takes a vector of numeric values.

Value

a list with three elements:

unadjusted named numeric vector with unadjusted effect size before adjustment for each covariate

complete a matrix with adjusted effect size for each covariate (columns) for each method (rows).

pooled a matrix with mean adjusted effect size for all covariates for each method (columns) and each bootstrap sample (rows).

balances a list with an $M \times n$ covariates matrix for each method.

Examples

```
library(PSAboot)
data(pisa.psa.cols)
data(pisausa)
bm.usa <- PSAboot(Tr = as.integer(pisausa$PUBPRIV) - 1,
  Y = pisausa$Math,
  X = pisausa[,pisa.psa.cols],
  control.ratio = 5, M = 100, seed = 2112)
bm.usa.bal <- balance(bm.usa)
```

balance.matching	<i>Returns balance for each covariate from propensity score matching.</i>
------------------	---

Description

This function is primarily used by [PSAboot::balance()] and probably does not need to be called directly.

Usage

```
balance.matching(index.treated, index.control, covs)
```

Arguments

index.treated a vector with the index of treated rows in covs.

index.control a vector with the index of control rows in covs.

covs data frame or matrix of covariates. Factors should already be recoded. See [cv.trans.psa](#)

Value

a named vector with one element per covariate.

boot.ctree	<i>Stratification using classification trees for bootstrapping.</i>
------------	---

Description

Stratification using classification trees for bootstrapping.

Usage

```
boot.ctree(Tr, Y, X, X.trans, formu, minStrata = 5, ...)
```

Arguments

Tr	vector indicating treatment assignment.
Y	vector of outcome.
X	matrix or data frame of covariates.
X.trans	a data frame of X with factors recoded. See cv.trans.psa
formu	the formula to use to estimate propensity scores. Note that the dependent variable (i.e. treatment variable) name will be updated using the Tr vector.
minStrata	minimum number of treatment or control units within a strata to include that strata.
...	other parameters passed from PSAboot

Value

a list with three elements:

summary a named numeric vector (with at minimum estimate, ci.min, and ci.max but other values allowed)

balance a named numeric vector with one element per covariate listed in X.trans representing a balance statistic (usually standardized effect size after adjustment)

details an arbitrary object that contains the full results of the analysis

boot.matching	<i>Matching package implementation for bootstrapping.</i>
---------------	---

Description

Matching package implementation for bootstrapping.

Usage

```
boot.matching(Tr, Y, X, X.trans, formu, estimand = "ATE", ...)
```

Arguments

Tr	vector indicating treatment assignment.
Y	vector of outcome.
X	matrix or data frame of covariates.
X.trans	a data frame of X with factors recoded. See cv.trans.psa
formu	the formula to use to estimate propensity scores. Note that the dependent variable (i.e. treatment variable) name will be updated using the Tr vector.
estimand	character string for estimand, either ATE, ATT, or ATC. See Match for more details.
...	other parameters passed to Match .

Value

a list with three elements:

summary a named numeric vector (with at minimum estimate, ci.min, and ci.max but other values allowed)

balance a named numeric vector with one element per covariate listed in X.trans representing a balance statistic (usually standardized effect size after adjustment)

details an arbitrary object that contains the full results of the analysis

boot.matchit	<i>MatchIt package implementation for bootstrapping.</i>
--------------	--

Description

MatchIt package implementation for bootstrapping.

Usage

```
boot.matchit(Tr, Y, X, X.trans, formu, ...)
```

Arguments

Tr	vector indicating treatment assignment.
Y	vector of outcome.
X	matrix or data frame of covariates.
X.trans	a data frame of X with factors recoded. See cv.trans.psa
formu	the formula to use to estimate propensity scores. Note that the dependent variable (i.e. treatment variable) name will be updated using the Tr vector.
...	other parameters passed from PSAboot

Value

a list with three elements:

`summary` a named numeric vector (with at minimum `estimate`, `ci.min`, and `ci.max` but other values allowed)

`balance` a named numeric vector with one element per covariate listed in `X.trans` representing a balance statistic (usually standardized effect size after adjustment)

`details` an arbitrary object that contains the full results of the analysis

`boot.rpart`

Stratification using classification trees for bootstrapping.

Description

Stratification using classification trees for bootstrapping.

Usage

```
boot.rpart(Tr, Y, X, X.trans, formu, minStrata = 5, ...)
```

Arguments

`Tr` vector indicating treatment assignment.

`Y` vector of outcome.

`X` matrix or data frame of covariates.

`X.trans` a data frame of `X` with factors recoded. See [cv.trans.psa](#)

`formu` the formula to use to estimate propensity scores. Note that the dependent variable (i.e. treatment variable) name will be updated using the `Tr` vector.

`minStrata` minimum number of treatment or control units within a strata to include that strata.

`...` other parameters passed from [PSAboot](#)

Value

a list with three elements:

`summary` a named numeric vector (with at minimum `estimate`, `ci.min`, and `ci.max` but other values allowed)

`balance` a named numeric vector with one element per covariate listed in `X.trans` representing a balance statistic (usually standardized effect size after adjustment)

`details` an arbitrary object that contains the full results of the analysis

boot.strata	<i>Stratification implementation for bootstrapping.</i>
-------------	---

Description

Stratification implementation for bootstrapping.

Usage

```
boot.strata(Tr, Y, X, X.trans, formu, nstrata = 5, ...)
```

Arguments

Tr	vector indicating treatment assignment.
Y	vector of outcome.
X	matrix or data frame of covariates.
X.trans	a data frame of X with factors recoded. See cv.trans.psa
formu	the formula to use to estimate propensity scores. Note that the dependent variable (i.e. treatment variable) name will be updated using the Tr vector.
nstrata	number of strata to divide the propensity scores.
...	other parameters passed from PSAboot

Value

a list with three elements:

- summary a named numeric vector (with at minimum estimate, ci.min, and ci.max but other values allowed)
- balance a named numeric vector with one element per covariate listed in X.trans representing a balance statistic (usually standardized effect size after adjustment)
- details an arbitrary object that contains the full results of the analysis

boot.weighting	<i>Propensity score weighting implementation for bootstrapping.</i>
----------------	---

Description

Propensity score weighting implementation for bootstrapping.

Usage

```
boot.weighting(Tr, Y, X, X.trans, formu, estimand = "ATE", ...)
```

Arguments

Tr	vector indicating treatment assignment.
Y	vector of outcome.
X	matrix or data frame of covariates.
X.trans	a data frame of X with factors recoded. See cv.trans.psa
formu	the formula to use to estimate propensity scores. Note that the dependent variable (i.e. treatment variable) name will be updated using the Tr vector.
estimand	which treatment effect to estimate. Values can be ATE, ATT, ATC, or ATM.
...	other parameters passed from PSAboot

Value

a list with three elements:

- summary a named numeric vector (with at minimum estimate, ci.min, and ci.max but other values allowed)
- balance a named numeric vector with one element per covariate listed in X.trans representing a balance statistic (usually standardized effect size after adjustment)
- details an arbitrary object that contains the full results of the analysis

boxplot.PSAboot	<i>Boxplot of PSA bootstrap results.</i>
-----------------	--

Description

Boxplot of PSA bootstrap results.

Usage

```
## S3 method for class 'PSAboot'
boxplot(
  x,
  bootstrap.mean.color = "blue",
  bootstrap.ci.color = "green",
  bootstrap.ci.width = 0.5,
  bootstrap.ci.size = 3,
  overall.mean.color = "red",
  tufte = FALSE,
  coord.flip = TRUE,
  ...
)
```

Arguments

<code>x</code>	result of <code>PSAbboot</code> .
<code>bootstrap.mean.color</code>	the color of the point for the bootstrap mean, or NA to omit.
<code>bootstrap.ci.color</code>	the color of the confidence intervals of the bootstrap samples, or NA to omit.
<code>bootstrap.ci.width</code>	the width of the confidence interval lines at the end.
<code>bootstrap.ci.size</code>	the size of the confidence interval lines.
<code>overall.mean.color</code>	the color of the point for the overall (before bootstrapping) mean, or NA to omit.
<code>tufte</code>	use Tufte's boxplot style. Requires the <code>ggthemes</code> package.
<code>coord.flip</code>	Whether to flip the coordinates.
<code>...</code>	unused

Value

a `ggplot2` expression.

`boxplot.PSAbboot.balance`

Boxplot of the balance statistics for bootstrapped samples.

Description

Boxplot of the balance statistics for bootstrapped samples.

Usage

```
## S3 method for class 'PSAbboot.balance'
boxplot(
  x,
  unadjusted.color = "red",
  pooled.color = "blue",
  point.size = 3,
  point.alpha = 0.5,
  ...
)
```

Arguments

x	results of balance
unadjusted.color	the color used for the unadjusted effect size.
pooled.color	the color used for the mean bootstrap effect size.
point.size	the size of the points.
point.alpha	the transparency level for the points.
...	other parameters passed to facet_wrap

Value

a ggplot2 expression.

Examples

```
library(PSAboot)
data(pisa.psa.cols)
data(pisausa)
bm.usa <- PSAboot(Tr = as.integer(pisausa$PUBPRIV) - 1,
  Y = pisausa$Math,
  X = pisausa[,pisa.psa.cols],
  control.ratio = 5, M = 100, seed = 2112)
bm.usa.bal <- balance(bm.usa)
boxplot(bm.usa.bal, nrow = 1)
```

calculate_ps_weights *Calculates propensity score weights.*

Description

Calculates propensity score weights.

Usage

```
calculate_ps_weights(treatment, ps, estimand = "ATE")
```

Arguments

treatment	a logical vector for treatment status.
ps	numeric vector of propensity scores
estimand	character string indicating which estimand to be used. Possible values are ATE (average treatment effect), ATT (average treatment effect for the treated), ATC (average treatment effect for the controls), ATM (Average Treatment Effect Among the Evenly Matchable), ATO (Average Treatment Effect Among the Overlap Populatio)

getPSAbootMethods	Returns a vector with the default methods used by PSAboot .
-------------------	---

Description

The current default methods are:

Stratification [boot.strata](#)

ctree [boot.ctree](#)

rpart [boot.rpart](#)

Matching [boot.matching](#)

MatchIt [boot.matchit](#)

Usage

```
getPSAbootMethods()
```

Details

The default methods can be changed by setting the `PSAboot.methods` option using `options('PSAboot.methods'=c(...))` where `...` is a named list of functions.

Value

a vector of methods for use by [PSAboot](#)

hist.PSAboot	Histogram of PSA bootstrap results
--------------	------------------------------------

Description

Histogram of PSA bootstrap results

Usage

```
## S3 method for class 'PSAboot'
hist(x, ...)
```

Arguments

<code>x</code>	result of PSAboot .
<code>...</code>	other parameters passed to geom_histogram

Value

a `ggplot2` expression.

matrixplot	<i>Matrix Plot of Bootstrapped Propensity Score Analysis</i>
------------	--

Description

Matrix Plot of Bootstrapped Propensity Score Analysis

Usage

```
matrixplot(bm)
```

Arguments

bm result from [PSAboot](#).

Value

Nothing returned. Creates a plot using the `[graphics::pairs()]` function.

pisa.psa.cols	<i>Character vector representing the list of covariates used for estimating propensity scores.</i>
---------------	--

Description

Character vector representing the list of covariates used for estimating propensity scores.

Format

a character vector with covariate names for estimating propensity scores.

pisalux	<i>Programme of International Student Assessment (PISA) results from the Luxembourg in 2009.</i>
---------	--

Description

Student results from the 2009 Programme of International Student Assessment (PISA) as provided by the Organization for Economic Co-operation and Development (OECD). See <https://www.oecd.org/pisa/> for more information including the code book.

Format

a data frame with 4,622 rows and 65 columns.

CNT Country

SCHOOLID SchoolID

ST01Q01 Grade

ST04Q01 Sex

ST05Q01 Attend

ST06Q01 Age

ST07Q01 Repeat

ST08Q01 At home mother

ST08Q02 At home father

ST08Q03 At home brothers

ST08Q04 At home sisters

ST08Q05 At home grandparents

ST08Q06 At home others

ST10Q01 Mother highest schooling

ST12Q01 Mother current job status

ST14Q01 Father highest schooling

ST16Q01 Father current job status

ST19Q01 Language at home

ST20Q01 Desk

ST20Q02 Own room

ST20Q03 Study place

ST20Q04 Computer

ST20Q05 Software

ST20Q06 Internet

ST20Q07 Literature

ST20Q08 Poetry

ST20Q09 Art

ST20Q10 Textbooks

ST20Q12 Dictionary

ST20Q13 Dishwasher

ST20Q14 DVD

ST21Q01 How many cellphones

ST21Q02 How many TVs

ST21Q03 How many computers

ST21Q04 How many cars

ST21Q05 How many rooms bath or shower
 ST22Q01 How many books
 ST23Q01 Reading enjoyment time
 ST31Q01 Enrich in test language
 ST31Q02 Enrich in mathematics
 ST31Q03 Enrich in science
 ST31Q05 Remedial in test language
 ST31Q06 Remedial in mathematics
 ST31Q07 Remedial in science
 ST32Q01 Out of school lessons in test language
 ST32Q02 Out of school lessons maths
 ST32Q03 Out of school lessons in science
 PUBPRIV Public or private school
 STRATIO Student to teacher ratio in school

Details

Note that missing values have been imputed using the mice package. Details on the specific procedure are in the `pisa.impute` function in the [pisa package](#).

References

Organisation for Economic Co-operation and Development (2009). Programme for International Student Assessment (PISA).

pisausa	<i>Programme of International Student Assessment (PISA) results from the United States in 2009.</i>
---------	---

Description

Student results from the 2009 Programme of International Student Assessment (PISA) as provided by the Organization for Economic Co-operation and Development (OECD). See www.oecd.org/pisa/ for more information including the code book.

Format

a data frame with 5,233 rows and 65 columns.

CNT Country

SCHOOLID SchoolID

ST01Q01 Grade

ST04Q01 Sex

ST05Q01 Attend
ST06Q01 Age
ST07Q01 Repeat
ST08Q01 At home mother
ST08Q02 At home father
ST08Q03 At home brothers
ST08Q04 At home sisters
ST08Q05 At home grandparents
ST08Q06 At home others
ST10Q01 Mother highest schooling
ST12Q01 Mother current job status
ST14Q01 Father highest schooling
ST16Q01 Father current job status
ST19Q01 Language at home
ST20Q01 Desk
ST20Q02 Own room
ST20Q03 Study place
ST20Q04 Computer
ST20Q05 Software
ST20Q06 Internet
ST20Q07 Literature
ST20Q08 Poetry
ST20Q09 Art
ST20Q10 Textbooks
ST20Q12 Dictionary
ST20Q13 Dishwasher
ST20Q14 DVD
ST21Q01 How many cellphones
ST21Q02 How many TVs
ST21Q03 How many computers
ST21Q04 How many cars
ST21Q05 How many rooms bath or shower
ST22Q01 How many books
ST23Q01 Reading enjoyment time
ST31Q01 Enrich in test language
ST31Q02 Enrich in mathematics
ST31Q03 Enrich in science

ST31Q05 Remedial in test language
 ST31Q06 Remedial in mathematics
 ST31Q07 Remedial in science
 ST32Q01 Out of school lessons in test language
 ST32Q02 Out of school lessons maths
 ST32Q03 Out of school lessons in science
 PUBPRIV Public or private school
 STRATIO Student to teacher ratio in school

Details

Note that missing values have been imputed using the mice package. Details on the specific procedure are in the `pisa.impute` function in the [pisa package](#).

References

Organisation for Economic Co-operation and Development (2009). Programme for International Student Assessment (PISA).

plot.PSAbboot	<i>Plot the results of PSAbboot</i>
---------------	-------------------------------------

Description

Plot the results of PSAbboot

Usage

```
## S3 method for class 'PSAbboot'
plot(
  x,
  sort = "all",
  ci.sig.color = "red",
  plot.overall = FALSE,
  plot.bootstrap = TRUE,
  ...
)
```

Arguments

<code>x</code>	result of PSAbboot .
<code>sort</code>	how the sort the rows by mean difference. Options are to sort using the mean difference from matching, stratification, both individually, or no sorting.
<code>ci.sig.color</code>	the color used for confidence intervals that do not span zero.

plot.overall	whether to plot vertical lines for the overall (non-bootstrapped) estimate and confidence interval.
plot.bootstrap	whether to plot vertical lines for the bootstrap pooled estimate and confidence interval.
...	currently unused.

Value

a ggplot2 expression.

plot.PSAbboot.balance	<i>Plot method for balance.</i>
-----------------------	---------------------------------

Description

Plot method for balance.

Usage

```
## S3 method for class 'PSAbboot.balance'
plot(
  x,
  unadjusted.color = "red",
  complete.color = "blue",
  pooled.color = "black",
  ...
)
```

Arguments

x	results from balance
unadjusted.color	color of the vertical line representing the mean unadjusted effect size for all covariates.
complete.color	color of the vertical line representing the mean adjusted effect size for all covariates using the complete dataset.
pooled.color	color of the vertical line representing the mean adjusted effect size for all covariates across all bootstrapped samples.
...	currently unused.

Value

a ggplot2 expression.

Examples

```
library(PSAbboot)
data(pisa.psa.cols)
data(pisausa)
bm.usa <- PSAbboot(Tr = as.integer(pisausa$PUBPRIV) - 1,
  Y = pisausa$Math,
  X = pisausa[,pisa.psa.cols],
  control.ratio = 5, M = 100, seed = 2112)
bm.usa.bal <- balance(bm.usa)
plot(bm.usa.bal)
```

print.PSAbboot	<i>Print results of PSAbboot</i>
----------------	----------------------------------

Description

Print results of PSAbboot

Usage

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

Arguments

x	result of PSAbboot .
...	currently unused.

Value

Nothing returned. S3 generic function that calls the [PSAbboot::summary()] function.

print.PSAbboot.balance	<i>Print method for balance.</i>
------------------------	----------------------------------

Description

This is a crude measure of overall balance. Absolute value of the standardized effect sizes are calculated for each covariate. Overall balance statistics are the mean of those effect sizes after adjustment for each method across all bootstrap samples.

Usage

```
## S3 method for class 'PSAbboot.balance'
print(x, na.rm = TRUE, ...)
```

Arguments

x	results from balance .
na.rm	whether NA balance statistics should be removed before averaging them.
...	currently unused.

Value

No valued returned.

```
print.PSAbbootSummary
```

Print method for PSAbboot Summary.

Description

Print method for PSAbboot Summary.

Usage

```
## S3 method for class 'PSAbbootSummary'
print(x, digits = 3, ...)
```

Arguments

x	result of summary.PSAbboot
digits	desired number of digits after the decimal point.
...	unused.

Value

Nothing returned.

```
psa.strata
```

Propensity Score Analysis using Stratification

Description

Propensity Score Analysis using Stratification

Usage

```
psa.strata(Y, Tr, strata, trim = 0, minStrata = 5)
```

Arguments

Y	response variable.
Tr	treatment variable.
strata	strata identifier.
trim	allows for a trimmed mean as outcome measure, where trim is from 0 to .5 (.5 implying median).
minStrata	minimum number of treatment or control units within a strata to include that strata.

Value

a character vector containing summary.strata, ATE, se.wtd, approx.t, df, and CI.95.

PSAboot

*Bootstrapping for propensity score analysis***Description**

Bootstrapping has become a popular resampling method for estimating sampling distributions. And propensity score analysis (PSA) has become popular for estimating causal effects in observational studies. This function implements bootstrapping specifically for PSA. Like typical bootstrapping methods, this function estimates treatment effects for M random samples. However, unlike typical bootstrap methods, this function allows for separate sample sizes for treatment and control units. That is, under certain circumstances (e.g. when the ratio of treatment-to-control units is large) bootstrapping only the control units may be desirable. Additionally, this function provides a framework to use multiple PSA methods for each bootstrap sample.

Usage

```
PSAboot(
  Tr,
  Y,
  X,
  M = 100,
  formu = as.formula(paste0("treat ~ ", paste0(names(X), collapse = " + "))),
  control.ratio = 5,
  control.sample.size = min(control.ratio * min(table(Tr)), max(table(Tr))),
  control.replace = TRUE,
  treated.sample.size = min(table(Tr)),
  treated.replace = TRUE,
  methods = getPSAbootMethods(),
  parallel = TRUE,
  seed = NULL,
  ...
)
```

Arguments

<code>Tr</code>	numeric (0 or 1) or logical vector of treatment indicators.
<code>Y</code>	vector of outcome variable
<code>X</code>	matrix or data frame of covariates used to estimate the propensity scores.
<code>M</code>	number of bootstrap samples to generate.
<code>formu</code>	formula used for estimating propensity scores. The default is to use all covariates in <code>X</code> .
<code>control.ratio</code>	the ratio of control units to sample relative to the treatment units.
<code>control.sample.size</code>	the size of each bootstrap sample of control units.
<code>control.replace</code>	whether to use replacement when sampling from control units.
<code>treated.sample.size</code>	the size of each bootstrap sample of treatment units. The default uses all treatment units for each bootstrap sample.
<code>treated.replace</code>	whether to use replacement when sampling from treated units.
<code>methods</code>	a named vector of functions for each PSA method to use.
<code>parallel</code>	whether to run the bootstrap samples in parallel.
<code>seed</code>	random seed. Each iteration, <code>i</code> , will use a seed of <code>seed + i</code> .
<code>...</code>	other parameters passed to Match and psa.strata

Value

a list with following elements:

overall.summary Data frame with the results using the complete dataset (i.e. unbootstrapped results).

overall.details Objects returned from each method for complete dataset.

pooled.summary Data frame with results of each bootstrap sample.

pooled.details List of objects returned from each method for each bootstrap sample.

control.sample.size sample size used for control units.

treated.sample.size sample size used for treated units.

control.replace whether control units were sampled with replacement.

treated.replace whether treated units were sampled with replacement.

Tr vector of treatment assignment.

Y vector out outcome.

X matrix or data frame of covariates.

M number of bootstrap samples.

See Also

[getPSAbootMethods](#)

Examples

```
library(PSAboot)
data(pisa.psa.cols)
data(pisausa)
bm.usa <- PSAboot(Tr = as.integer(pisausa$PUBPRIV) - 1,
  Y = pisausa$Math,
  X = pisausa[,pisa.psa.cols],
  control.ratio = 5, M = 100, seed = 2112)
```

q25	<i>Return the 25th percentile.</i>
-----	------------------------------------

Description

Return the 25th percentile.

Usage

```
q25(x, na.rm = FALSE, ...)
```

Arguments

x	numeric vector.
na.rm	logical; if true, any NA and NaN's are removed from x before the quantiles are computed
...	other parameters passed to quantile .

Value

the 25th percentile.

q75	<i>Returns the 75th percentile.</i>
-----	-------------------------------------

Description

Returns the 75th percentile.

Usage

```
q75(x, na.rm = FALSE, ...)
```

Arguments

<code>x</code>	numeric vector.
<code>na.rm</code>	logical; if true, any NA and NaN's are removed from <code>x</code> before the quantiles are computed
<code>...</code>	other parameters passed to quantile .

Value

the 75th percentile.

<code>summary.PSAbboot</code>	<i>Summary of pooled results from PSAbboot</i>
-------------------------------	--

Description

Summary of pooled results from PSAbboot

Usage

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

Arguments

<code>object</code>	result of PSAbboot .
<code>...</code>	currently unused.

Value

a list with pooled summary statistics.

a list with the results from each PSA method. For each method a list contains the following elements:

sig.tot.per Percentage of bootstrap samples where the confidence interval does not span zero.

bootstrap.mean Weighted mean difference across all bootstrap samples.

bootstrap.ci Overall confidence interval across all bootstrap samples.

bootstrap.weighted.mean Overall weighted bootstrap mean.

percent.sig Contingency table of the number of bootstrap samples that don't span zero.

complete Results of the summary of the PSA method.

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