Package ‘twangContinuous’

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**License** GPL (>= 2)

**Encoding** UTF-8

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**VignetteBuilder** knitr

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**Suggests** knitr, rmarkdown

**RoxygenNote** 7.1.1

**NeedsCompilation** no

**Author** Donna Coffman [aut, cre] (<https://orcid.org/0000-0001-6305-6579>), Brian Vegetabile [ctb]

**Maintainer** Donna Coffman <donna.coffman@gmail.com>

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**R topics documented:**

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bal.table

Compute the balance table.

Description

‘bal.table’ is a generic function for extracting balance tables from ‘ps.cont’ objects, one for an unweighted analysis and one for the weighted analysis.

Usage

bal.table(x, digits = 3, ...)

Arguments

x A ‘ps.cont’ object
digits Number of digits to round to. Default: 3
... Additional arguments.

Value

Returns a data frame containing the balance information. * ‘unw’ The unweighted correlation between the exposure and each covariate. * ‘wcor’ The weighted correlation between the exposure and each covariate.

See Also

[ps.cont]

Examples

## Not run: bal.table(test.mod)
A synthetic data set that was derived from a large scale observational study on youth in substance use treatment.

Description

A subset of measures from the Global Appraisal of Individual Needs biopsychosocial assessment instrument (GAIN) (Dennis, Titus et al. 2003) from sites that administered two different types of substance use disorder treatments (treatment “A” and treatment “B”). The Center for Substance Abuse Treatment (CSAT) funded the sites that administered these two SUD treatments. This dataset consists of 4,000 adolescents, 2,000 in each treatment group. The dataset includes substance use and mental health variables.

Usage

data("dat")

Format

A data frame with 4000 observations on the following 29 variables.

- `treat` a factor with levels A B
- `tss_0` a numeric vector
- `tss_3` a numeric vector
- `tss_6` a numeric vector
- `sfs8p_0` a numeric vector
- `sfs8p_3` a numeric vector
- `sfs8p_6` a numeric vector
- `eps7p_0` a numeric vector
- `eps7p_3` a numeric vector
- `eps7p_6` a numeric vector
- `ias5p_0` a numeric vector
- `dss9_0` a numeric vector
- `nhrt_0` a numeric vector
- `sati_0` a numeric vector
- `sp_sm_0` a numeric vector
- `sp_sm_3` a numeric vector
- `sp_sm_6` a numeric vector
- `gvs` a numeric vector
- `ers21_0` a numeric vector
- `nproc` a numeric vector
dat

ada_0  a numeric vector
ada_3  a numeric vector
ada_6  a numeric vector
recov_0  a numeric vector
recov_3  a numeric vector
recov_6  a numeric vector
subgrps_n  a numeric vector
sncnt  a numeric vector
engage  a numeric vector

details

tss_0  Traumatic Stress Scale - Baseline
tss_3  Traumatic Stress Scale - 3 months
tss_6  Traumatic Stress Scale - 6 months
sfs8p_0  Substance Frequency Scale - Baseline
sfs8p_3  Substance Frequency Scale - 3 months
sfs8p_6  Substance Frequency Scale - 6 months
eps7p_0  Emotional Problems Scale - Baseline
eps7p_3  Emotional Problems Scale - 3 months
eps7p_6  Emotional Problems Scale - 6 months
ias5p_0  Illegal Activities Scale - baseline
dss9_0  depressive symptom scale - baseline
mhtrt_0  mental health treatment in the past 90 days - baseline
sati_0  substance abuse treatment index - baseline
sp_sm_0  substance problem scale (past month) - baseline
sp_sm_3  substance problem scale (past month) - 3 months
sp_sm_6  substance problem scale (past month) - 6 months
gvs  General Victimization Scale
ers21_0  Environmental Risk Scale - baseline
ada_0  adjusted days abstinent (any in past 90) - baseline
ada_3  adjusted days abstinent (any in past 90) - 3 months
ada_6  adjusted days abstinent (any in past 90) - 6 months
recov_0  in recovery - baseline
recov_3  in recovery - 3 months
recov_6  in recovery - 6 months
subgrps_n  primarily opioid using youth vs alcohol/marijuana using youth vs other


Source

References

Examples

data(dat)
## maybe str(dat) ; plot(dat) ...

get.weights

Extract propensity score weights

Description
Extracts propensity score weights from a ps.cont object.

Usage
get.weights(ps1, stop.method = "wcor", withSampW = TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ps1</td>
<td>a ps.cont object</td>
</tr>
<tr>
<td>stop.method</td>
<td>indicates which set of weights to retrieve from the ps.cont object</td>
</tr>
<tr>
<td>withSampW</td>
<td>Returns weights with sample weights multiplied in, if they were provided in the original ps.cont call.</td>
</tr>
</tbody>
</table>

Value
a vector of weights

Author(s)
Donna L. Coffman

See Also
ps.cont
Plot the ‘ps.cont’ object.

Description

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

Usage

## S3 method for class 'ps.cont'
plot(x, plots = "optimize", subset = NULL, ...)

Arguments

x
‘ps.cont’ object

plots
An indicator of which type of plot is desired. The options are * "optimize": A plot of the balance criteria as a function of the GBM iteration. * "es": Plots of the standardized effect size of the pre-treatment variables before and after weighting

subset
Used to restrict which of the ‘stop.method’s will be used in the figure.

... Additional arguments.

Value

Returns diagnostic plots for ‘ps.cont’ objects.

See Also

[ps.cont]

Examples

## Not run: plot(test.mod)
Usage

```r
ps.cont(
  formula,
  data,
  n.trees = 10000,
  interaction.depth = 3,
  shrinkage = 0.01,
  bag.fraction = 1,
  sampw = NULL,
  print.level = 2,
  verbose = FALSE,
  stop.method = "wcor",
  treat.as.cont = FALSE,
  ...
)
```

Arguments

- `formula`: An object of class `[formula]`: a symbolic description of the propensity score model to be fit with the treatment variable on the left side of the formula and the potential confounding variables on the right side.
- `data`: A dataset that includes the treatment 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.
- `sampw`: Optional sampling weights.
- `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: ‘FALSE’.
- `treat.as.cont`: Used as a check on whether the exposure has greater than five levels. If it does not and treat.as.cont=FALSE, an error will be produced. Default: FALSE
- `...`: Additional arguments that are passed to `ps` function.

Value

Returns an object of class ‘ps.cont’, a list containing
* `gbm.obj` The returned [gbm] object.
* `treat` 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.
  - `n` The number of subjects.
  - `max.wcor` The largest weighted correlation across the covariates.
  - `mean.wcor` The average weighted correlation across the covariates.
  - `rms.wcor` The root mean square of the absolute weighted correlations across the covariates.
  - `bal.tab` a (potentially large) table summarizing the quality of the weights for balancing the distribution of the pretreatment covariates. This table is best extracted using the [bal.table] method. See the help for [bal.table] for details.
  - `n.trees` The estimated optimal number of [gbm] iterations to optimize the loss function.
* `ps.den` Denominator values for the propensity score weights.
* `ps.num` Numerator values for the propensity score weights.
* `w` The propensity score weights. If sampling weights are given then these are incorporated into these weights.
* `datestamp` Records the date of the analysis.
* `parameters` Saves the `ps.cont` 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.
* `sampw` The sampling weights as specified in the `sampw` argument.
* `preds` Predicted values based on the propensity score model.
* `covariates` Data frame containing the covariates used in the propensity score model.
* `n.trees` Maximum number of trees considered in GBM fit.
* `data` Data as specified in the `data` argument.

References


See Also

[gbm], [plot.ps.cont], [bal.table], [summary.ps.cont]
Examples

```r
## Not run: test.mod <- ps.cont(tss_0 ~ sfs8p_0 + sati_0 + sp_sm_0
+ recov_0 + subsgrps_n + treat, data=dat
## End(Not run)
```

summary.ps.cont

Displays a useful description of a 'ps.cont' object.

Description

Computes a short summary table describing the size of the dataset and the quality of the propensity score weights about a stored 'ps.cont' object.

Usage

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

Arguments

- `object`: A 'ps.cont' object
- `...`: Additional arguments.

Value

- `'n'`: The number of subjects.
- `'ess'`: The effective sample size.
- `'max.wcor'`: The largest weighted correlation across the covariates.
- `'mean.wcor'`: The average weighted correlation across the covariates.
- `'rms.wcor'`: The root mean square of the absolute weighted correlations across the covariates.
- `'iter'`: The estimated optimal number of [gbm] iterations to optimize the loss function.

See Also

- [ps.cont]

Examples

```r
## Not run: summary(test.mod)
```
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