Package ‘twangContinuous’

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Title Toolkit for Weighting and Analysis of Nonequivalent Groups - Continuous Exposures

Version 1.0.0

Description Provides functions for propensity score estimation and weighting for continuous exposures as described in Zhu, Y., Coffman, D. L., & Ghosh, D. (2015). A boosting algorithm for estimating generalized propensity scores with continuous treatments. Journal of Causal Inference, 3(1), 25-40. <doi:10.1515/jci-2014-0022>.

License GPL (>= 2)

Encoding UTF-8

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VignetteBuilder knitr

Imports Rcpp (>= 0.12.19), lattice (>= 0.20-35), gbm (>= 2.1.3), survey, xtable

Suggests knitr, rmarkdown

RoxygenNote 7.1.1

NeedsCompilation no

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Depends R (>= 3.5.0)

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Contents

`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)
```

`dat` *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

`mhtrt_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

`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

`subsgrps_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

`subsgrps_n` primarily opioid using youth vs alcohol/marijuana using youth vs other

Source

Diamond, G., Godley, S. H., Liddle, H. A., Sampl, S., Webb, C., Tims, F. M., & Meyers, R. (2002). Five outpatient treatment models for adolescent marijuana use: a description of the Cannabis Youth Treatment Interventions. Addiction, 97, 70-83.

References

Diamond, G., Godley, S. H., Liddle, H. A., Sampl, S., Webb, C., Tims, F. M., & Meyers, R. (2002). Five outpatient treatment models for adolescent marijuana use: a description of the Cannabis Youth Treatment Interventions. Addiction, 97, 70-83.

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

`ps1`	a `ps.cont` object
`stop.method`	indicates which set of weights to retrieve from the `ps.cont` object
`withSampW`	Returns weights with sample weights multiplied in, if they were provided in the original `ps.cont` call.

Value

a vector of weights

Author(s)

Donna L. Coffman

See Also

`ps.cont`

`plot.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)
```

`ps.cont` *Gradient boosted propensity score estimation for continuous exposures*

Description

‘ps.cont‘ calculates propensity scores using gradient boosted regression and provides diagnostics of the resulting propensity scores.

Usage

```
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‘.
`stop.method`	A method or methods of measuring and summarizing balance across pretreatment variables. Current options are ‘wcor‘, the weighted Pearson correlation, summarized by using the mean across the pretreatment variables. Default: ‘wcor‘.
`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

Zhu, Y., Coffman, D. L., & Ghosh, D. (2015). A boosting algorithm for estimating generalized propensity scores with continuous treatments. *Journal of Causal Inference*, 3(1), 25-40. doi: 10.1515/jci20140022

See Also

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

Examples

```
  ## 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

```
## 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

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

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