

Package ‘hbal’

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Type Package

Title Hierarchically Regularized Entropy Balancing

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Description Implements hierarchically regularized entropy balancing proposed by Xu and Yang (2022) <[doi:10.1017/pan.2022.12](https://doi.org/10.1017/pan.2022.12)>. The method adjusts the covariate distributions of the control group to match those of the treatment group. 'hbal' automatically expands the covariate space to include higher order terms and uses cross-validation to select variable penalties for the balancing conditions.

URL <https://yiqingxu.org/packages/hbal/>

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Depends R (>= 3.6.0)

Imports Rcpp (>= 1.0.1), estimatr, glmnet, gtable, gridExtra, ggplot2, stringr, nloptr, generics

Suggests MASS, knitr, rmarkdown, broom, ebal

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Encoding UTF-8

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att	<i>Estimating the ATT from an hbal object</i>
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Description

att estimates the average treatment effect on the treated (ATT) from an hbal object returned by hbal.

Usage

att(hbalobject, method="lm_robust", dr=TRUE, displayAll=FALSE, ...)

Arguments

- hbalobject an object of class hbal as returned by hbal.
- method estimation method for the ATT. Default is the Lin (2016) estimator.
- dr doubly robust, whether an outcome model is included in estimating the ATT.
- displayAll only displays treatment effect by default.
- ... arguments passed to lm_lin or lm_robust

Details

This is a wrapper for lm_robust and lm_lin from the [estimatr](#) package.

Value

A matrix of estimates with their robust standard errors

Author(s)

Yiqing Xu, Eddie Yang

Examples

```
#EXAMPLE 1
set.seed(1984)
N <- 500
X1 <- rnorm(N)
X2 <- rbinom(N,size=1,prob=.5)
X <- cbind(X1, X2)
treat <- rbinom(N, 1, prob=0.5) # Treatment indicator
y <- 0.5 * treat + X[,1] + X[,2] + rnorm(N) # Outcome
dat <- data.frame(treat=treat, X, Y=y)
out <- hbal(Treat = 'treat', X = c('X1', 'X2'), Y = 'Y', data=dat)
sout <- summary(att(out))
```

contenderJudges

Data from Black and Owens (2016)

Description

Data on the contender judges from Black and Owens (2016): Courting the president: how circuit court judges alter their behavior for promotion to the Supreme Court. This dataset includes 10,171 period-judge observations for a total of 68 judges. The treatment variable of interest is `treatFinal0`, which indicates whether there was a vacancy in the Supreme Court. The outcome of interest is ideological alignment of judges' votes with the sitting President (`presIdeoVote`). The remaining variables are characteristics of the judges and courts, to be used as controls.

Format

A data frame with 10171 rows and 10 columns.

presIdeoVote ideological alignment of judges' votes with the sitting President (outcome)

treatFinal0 treatment indicator for vacancy period

judgeJCS judge's Judicial Common Space (JCS) score

presDist Ideological distribution of the sitting President

panelDistJCS ideological composition of the panel with whom the judge sat

circmed median JCS score of the circuit judges

setmed JCS score of the median justice on the Supreme Court

coarevtc indicator for whether the case decision was reversed by the circuit court

casepub indicator for the publication status of the court's opinion

judge name of the judge

References

- Black, R. C., and Owens, R. J. (2016). Courting the president: how circuit court judges alter their behavior for promotion to the Supreme Court. *American Journal of Political Science*, 60(1), 30-43.

Description

hbal performs hierarchically regularized entropy balancing such that the covariate distributions of the control group match those of the treatment group. hbal automatically expands the covariate space to include higher order terms and uses cross-validation to select variable penalties for the balancing conditions.

hbal performs hierarchically regularized entropy balancing such that the covariate distributions of the control group match those of the treatment group. hbal automatically expands the covariate space to include higher order terms and uses cross-validation to select variable penalties for the balancing conditions.

Usage

```
hbal(data, Treat, X, Y = NULL, w = NULL,
      X.expand = NULL, X.keep = NULL, expand.degree = 1,
      coefs = NULL, max.iterations = 200, cv = NULL, folds = 4,
      ds = FALSE, group.exact = NULL, group.alpha = NULL,
      term.alpha = NULL, constraint.tolerance = 1e-3, print.level = 0,
      grouping = NULL, group.labs = NULL, linear.exact = TRUE, shuffle.treat = TRUE,
      exclude = NULL, force = FALSE, seed = 94035)
```

Arguments

data	a dataframe that contains the treatment, outcome, and covariates.
Treat	a character string of the treatment variable.
X	a character vector of covariate names to balance on.
Y	a character string of the outcome variable.
w	a character string of the weighting variable for base weights
X.expand	a character vector of covariate names for serial expansion.
X.keep	a character vector of covariate names to keep regardless of whether they are selected in double selection.
expand.degree	degree of series expansion. 1 means no expansion. Default is 1.
coefs	initial coefficients for the reweighting algorithm (lambdas).
max.iterations	maximum number of iterations. Default is 200.
cv	whether to use cross validation. Default is TRUE.
folds	number of folds for cross validation. Only used when cv is TRUE.
ds	whether to perform double selection prior to balancing. Default is FALSE.
group.exact	binary indicator of whether each covariate group should be exact balanced.
group.alpha	penalty for each covariate group

<code>term.alpha</code>	named vector of ridge penalties, only takes 0 or 1.
<code>constraint.tolerance</code>	tolerance level for overall imbalance. Default is 1e-3.
<code>print.level</code>	details of printed output.
<code>grouping</code>	different groupings of the covariates. Must be specified if <code>expand</code> is FALSE.
<code>group.labs</code>	labels for user-supplied groups
<code>linear.exact</code>	seek exact balance on the level terms
<code>shuffle.treat</code>	whether to use cross-validation on the treated units. Default is TRUE.
<code>exclude</code>	list of covariate name pairs or triplets to be excluded.
<code>force</code>	binary indicator of whether to expand covariates when there are too many
<code>seed</code>	random seed to be set. Set random seed when <code>cv=TRUE</code> for reproducibility.

Details

In the simplest set-up, user can just pass in {Treatment, X, Y}. The default settings will serially expand X to include higher order terms, hierarchically residualize these terms, perform double selection to only keep the relevant variables and use cross-validation to select penalties for different groupings of the covariates.

Value

An list object of class `hbal` with the following elements:

<code>coefs</code>	vector that contains coefficients from the reweighting algorithm.
<code>mat</code>	matrix of serially expanded covariates if <code>expand=TRUE</code> . Otherwise, the original covariate matrix is returned.
<code>penalty</code>	vector of ridge penalties used for each covariate
<code>weights</code>	vector that contains the control group weights assigned by <code>hbal</code> .
<code>W</code>	vector of treatment status
<code>Y</code>	vector of outcome

Author(s)

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References

Xu, Y., & Yang, E. (2022). Hierarchically Regularized Entropy Balancing. *Political Analysis*, 1-8. doi:10.1017/pan.2022.12

Examples

```
# Example 1
set.seed(1984)
N <- 500
X1 <- rnorm(N)
X2 <- rbinom(N,size=1,prob=.5)
X <- cbind(X1, X2)
treat <- rbinom(N, 1, prob=0.5) # Treatment indicator
y <- 0.5 * treat + X[,1] + X[,2] + rnorm(N) # Outcome
dat <- data.frame(treat=treat, X, Y=y)
out <- hbal(Treat = 'treat', X = c('X1', 'X2'), Y = 'Y', data=dat)
summary(hbal::att(out))

# Example 2
## Simulation from Kang and Shafer (2007).
library(MASS)
set.seed(1984)
n <- 500
X <- mvrnorm(n, mu = rep(0, 4), Sigma = diag(4))
prop <- 1 / (1 + exp(X[,1] - 0.5 * X[,2] + 0.25*X[,3] + 0.1 * X[,4]))
# Treatment indicator
treat <- rbinom(n, 1, prop)
# Outcome
y <- 210 + 27.4*X[,1] + 13.7*X[,2] + 13.7*X[,3] + 13.7*X[,4] + rnorm(n)
# Observed covariates
X.mis <- cbind(exp(X[,1]/2), X[,2]*(1+exp(X[,1]))^(-1)+10,
               (X[,1]*X[,3]/25+.6)^3, (X[,2]+X[,4]+20)^2)
dat <- data.frame(treat=treat, X.mis, Y=y)
out <- hbal(Treat = 'treat', X = c('X1', 'X2', 'X3', 'X4'), Y='Y', data=dat)
summary(att(out))
```

lalonge

Data from Hazlett (2020)

Description

Data on the treated units is from Dehejia and Wahba (1999), containing 185 individuals; data on the control units is from Panel Study of Income Dynamics (PSID-1), containing 2,490 individuals.

Format

A data frame with 2675 rows and 13 columns.

nsw treatment indicator of whether an individual participated in the National Supported Work (NSW) program

age

educ years of education

black demographic indicator variables for Black

hisp idemographic indicator variables for Hispanic
married demographic indicator variables for married
re74 real earnings in 1974
re75 real earnings in 1975
re78 real earnings in 1978, outcome
u74 unemployment indicator for 1974
u75 unemployment indicator for 1975
u78 unemployment indicator for 1978
nodegr indicator for no high school degree

References

- Dehejia, R. H., and Wahba, S. (1999). Causal effects in nonexperimental studies: Reevaluating the evaluation of training programs. *Journal of the American statistical Association*, 94(448), 1053-1062.
- Hazlett, C. (2020). KERNEL BALANCING. *Statistica Sinica*, 30(3), 1155-1189.

plot.hbal

Plotting Covariate Balance from an hbal Object

Description

This function plots the covariate difference between the control and treatment groups in standardized means before and after weighting.

Usage

```
## S3 method for class 'hbal'
plot(x, type = 'balance', log = TRUE, base_size = 10, ...)
```

Arguments

x	an object of class hbalobject as returned by hbal.
type	type of graph to plot.
log	log scale for the weight plot
base_size	base font size
...	Further arguments to be passed to plot.hbal().

Value

A matrix of ggplots of covariate balance by group

Author(s)

Yiqing Xu, Eddie Yang

`summary.hbal`*Summarizing from an hbal Object*

Description

This function prints a summary from an hbal Object.

Usage

```
## S3 method for class 'hbal'  
summary(object, print.level = 0, ...)
```

Arguments

<code>object</code>	an object of class <code>hbalobject</code> as returned by <code>hbal</code> .
<code>print.level</code>	level of details to be printed
<code>...</code>	Further arguments to be passed to <code>summary.hbal()</code> .

Value

a summary table

Author(s)

Yiqing Xu, Eddie Yang

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