Package ‘RCTrep’

March 29, 2023

Type Package

Title Validation of Estimates of Treatment Effects in Observational Data

Version 1.0.0

Author Lingjie Shen [aut, cre, cph],
    Gijs Geleijnse [aut],
    Maurits Kaptein [aut]

Maintainer Lingjie Shen <602249910@qq.com>

Description Validates estimates of (conditional) average treatment effects obtained using observational data by a) making it easy to obtain and visualize estimates derived using a large variety of methods (G-computation, inverse propensity score weighting, etc.), and b) ensuring that estimates are easily compared to a gold standard (i.e., estimates derived from randomized controlled trials). 'RCTrep' offers a generic protocol for treatment effect validation based on four simple steps, namely, set-selection, estimation, diagnosis, and validation. 'RCTrep' provides a simple dashboard to review the obtained results. The validation approach is introduced by Shen, L., Geleijnse, G. and Kaptein, M. (2023) <doi:10.21203/rs.3.rs-2559287/v1>.

License MIT + file LICENSE

URL https://github.com/duolajiang/RCTrep

Encoding UTF-8

LazyData true

Imports mvtnorm, MASS, MatchIt, ggplot2, ggrepubr, PSweight, numDeriv,
    R6, dplyr, geex, optmatch, BART, fastDummies, tidyr, copula,
    shiny, shinydashboard, glue, stats, utils, caret

Suggests rmarkdown, knitr, testthat (>= 3.0.0)

Config/testthat/edition 3

RoxygenNote 7.1.2

VignetteBuilder knitr

Depends R (>= 2.10), base

NeedsCompilation no

Repository CRAN

Date/Publication 2023-03-29 08:10:02 UTC
Visualizing validation results according to four steps, namely, set-selection, estimation, diagnosis, and validation

call_dashboard(source.obj = NULL, target.obj = NULL, source.obj.rep = NULL)

Arguments

source.obj an instantiated object of class TEstimator. The estimates of conditional average treatment effects are compared to those from target.obj.

target.obj an instantiated object of class TEstimator. The estimates of conditional average treatment effects are regarded as unbiased of truth.

source.obj.rep an instantiated object of class SEstimator. The estimates of conditional average treatment effects are compared to those from target.obj.

Value

an interactive interface visualizing results of four steps
Examples

```r
source.data <- RCTrep::source.data[sample(dim(RCTrep::source.data)[1],500),]
target.data <- RCTrep::target.data[sample(dim(RCTrep::target.data)[1],500),]

vars_name <- list(confounders_treatment_name = c("x1","x2","x3","x4","x5","x6"),
                  treatment_name = c('z'),
                  outcome_name = c('y'))

confounders_sampling_name <- c("x2","x6")

source.obj <- TEstimator_wrapper(
  Estimator = "G_computation",
  data = source.data,
  vars_name = vars_name,
  outcome_method = "glm",
  outcome_form = y ~ x1 + x2 + x3 + z + z:x1 + z:x2 + z:x3 + z:x6,
  name = "RWD",
  data.public = FALSE)

target.obj <- TEstimator_wrapper(
  Estimator = "Crude",
  data = target.data,
  vars_name = vars_name,
  name = "RCT",
  data.public = FALSE,
  isTrial = TRUE)

strata <- c("x1","x4")
source.rep.obj <- SEstimator_wrapper(Estimator = "Exact",
                                     target.obj = target.obj,
                                     source.obj = source.obj,
                                     confounders_sampling_name = confounders_sampling_name)

source.rep.obj$EstimateRep(stratification = strata, stratification_joint = TRUE)

call_dashboard(source.obj = source.obj,
               target.obj = target.obj,
               source.obj.rep = source.obj.rep)
```

Description

Generating RCT data or observational data for the examples used in the package
Usage

DGM(
  trial,
  n,
  var_name,
  p_success,
  tau,
  y0,
  log.ps = NULL,
  binary = FALSE,
  noise = 1,
  ...
)

Arguments

  trial  Logical indicating whether the treatment is randomly assigned in the generated data. If TRUE, RCT data is generated. Otherwise, observational data is generated.
  n      A numeric value indicating the number of observations in the generated data
  var_name  A character vector indicating the names of variables
  p_success  the success probability of binary variables
  tau  a character indicating the generation of the true treatment effect of each individual
  y0  a character indicating the generation of the potential outcome under control
  log.ps  a numeric value indicating the logit of propensity score
  binary  logical indicating whether the outcome is binary or continuous variable
  noise  a numeric value indicating the standard error of noise term of continuous outcome
  ...  an optional argument indicating pairwise correlations between variables

Value

a data frame; column names are variables names, z, y

Examples

n_rct <- 500; n_rwd <- 500
var_name <- c("x1","x2","x3","x4","x5","x6")
p_success_rct <- c(0.7,0.9,0.2,0.3,0.2,0.3)
p_success_rwd <- c(0.2,0.2,0.8,0.8,0.7,0.8)
tau <- "6*x2+x6+2"
y0 <- "x1"
log.ps <- "x1*x2+x3*x4+5*x5+x6"
rho1 <- c("x1","x2",0)
rho2 <- c("x2","x3",0)
Fusion

Validation of estimates of conditional average treatment effects in objects of class TEstimator and SEstimator.

Description

Validation of estimates of conditional average treatment effects in objects of class TEstimator and SEstimator.

Value

an R6 object

Methods

Public methods:
- Fusion$new()
- Fusion$plot()
- Fusion$print()
- Fusion$evaluate()
- Fusion$clone()

Method new():

Usage:
Fusion$new(..., stratification = NULL, stratification_joint = NULL)

Arguments:
... objects of class TEstimator and SEstimator.
stratification a character vector specifying variables. The variables are used to select subgroups individually or in combination depending on stratification_joint. Default value is NULL.
stratification_joint a logical indicating if subgroups are selected based on levels of individual variable in stratification or levels of combined variables in stratification. Default value is NULL.

Method plot():

```r
target.data <- RCTrep::DGM(trial=TRUE, n_rct, var_name,
                          p_success_rct, tau, y0, log.ps=0,
                          binary = FALSE, noise=1, rho1, rho2)
source.data <- RCTrep::DGM(trial=FALSE, n_rwd, var_name,
                          p_success_rwd, tau, y0, log.ps,
                          binary = FALSE, noise=1, rho1, rho2)
```
Usage:
Fusion$plot()

Method `print()`:
Usage:
Fusion$print()

Method `evaluate()`:
Usage:
Fusion$evaluate()

Method `clone()`: The objects of this class are cloneable with this method.
Usage:
Fusion$clone(deep = FALSE)

Arguments:
deep Whether to make a deep clone.

Examples

```r
source.data <- RCTrep::source.data[sample(dim(RCTrep::source.data)[1],500),]
target.data <- RCTrep::target.data[sample(dim(RCTrep::target.data)[1],500),]

vars_name <- list(confounders_treatment_name = c("x1","x2","x3","x4","x5","x6"),
  treatment_name = c("z"),
  outcome_name = c("y")
)
confounders_sampling_name <- c("x2","x6")

source.obj <- TEstimator_wrapper(
  Estimator = "G_computation",
  data = source.data,
  vars_name = vars_name,
  outcome_method = "glm",
  outcome_form = y ~ x1 + x2 + x3 + z + z:x1 + z:x2 + z:x3 + z:x6,
  name = "RWD",
  data.public = FALSE
)

target.obj <- TEstimator_wrapper(
  Estimator = "Crude",
  data = target.data,
  vars_name = vars_name,
  name = "RCT",
  data.public = FALSE,
  isTrial = TRUE
)

strata <- c("x1","x4")
source.rep.obj <- SEstimator_wrapper(Estimator = "Exact",

```
GenerateSyntheticData

Generating the synthetic RCT data given marginal distribution of each covariate

Usage

GenerateSyntheticData(margin_dis, N, margin, var_name, pw.cor = 0)

Arguments

margin_dis  a character indicating the distribution of each variable, allowable options are "bernoulli_categorical" and "bernoulli". If some variables have two categories and some have more than two categories, "bernoulli_categorical" should be specified; if all variables have two categories, "bernoulli" should be specified

N  a numeric value specifying the sample size for the simulated data

margin  a list containing the marginal distribution of variables; if margin_dis="bernoulli_categorical", then margin should be list(x1=c("x1",nlevels(x1),level1, level2,...,leveln, plelevel1, plelevel2,...,plelevel3), x2=c("x2",...)); if margin_dis="bernoulli", margin=list(p(x1=1),p(x2=1),...,p(xn=1))

var_name  a vector indicating the name of variables, the order of variables should be aligned with margin

pw.cor  a vector specifying the pairwise correlations of the variables, default is 0; when margin_dis="bernoulli", then pw.cor must be specified.

Value

a data frame with columns names x1, x2,....
quasar.agg

*Aggregated data derived from paper of QUASAR trial*

**Description**

Aggregated data derived from paper of QUASAR trial

**Usage**

quasar.agg

**Format**

An object of class `list` of length 5.

---

quasar.obj

*An object of class TEstimator_Synthetic using quasar.synthetic*

**Description**

An object of class TEstimator_Synthetic using quasar.synthetic

**Usage**

quasar.obj

**Format**

An object of class Synthetic_TEstimator (inherits from TEstimator, R6) of length 14.

---

quasar.synthetic

*A synthetic QUASAR trial dataset, where outcome is a binary variable, treatment is a binary variable.*

**Description**

A synthetic QUASAR trial dataset, where outcome is a binary variable, treatment is a binary variable.

**Usage**

quasar.synthetic
Format

```r
## 'quasar.synthetic' A data frame with 5934 rows and 3 variables:
Stage2  binary variable, 1 indicating stage 2 and 0 indicating stage 3
male    binary variable, 1 indicating male and 0 indicating female
age     categorical variable, 1 indicating [23,50], 2 indicating [50,59], 3 indicating [60,69], 4 indicating [70,86]
```

Description

The function `RCTREP` is used to validate the estimates of treatment effects obtained from observational data by comparing to estimates from a target randomized control trial. The function currently implements the following types of estimators of treatment effects: G_computation, inverse propensity score weighting (IPW), and augmented propensity score weighting. The function implements the following three types of weighting estimators to compare the resulting estimates of treatment effects from RWD to the target RCT: exact matching weights, inverse selection probability weighting, and sub-classification. Since we regard the sample in the RCT as the target population, weights for each individual in observational data is $p/(1 - p)$ so that the weighted population of observational data is representative to the target population.

Usage

```r
RCTREP(
    TEstimator = "G_computation",
    SEstimator = "Exact",
    source.data = source.data,
    target.data = target.data,
    source.name = "RWD",
    target.name = "RCT",
    vars_name,
    confounders_sampling_name,
    outcome_method = "glm",
    treatment_method = "glm",
    weighting_method = "glm",
    outcome_formula = NULL,
    treatment_formula = NULL,
    selection_formula = NULL,
    stratification = NULL,
    stratification_joint = FALSE,
    strata_cut_source = NULL,
    strata_cut_target = NULL,
    two_models = FALSE,
)```

data.public = TRUE,
...

Arguments

TEstimater A character specifying an estimator for conditional average treatment effects. The allowed estimators for TEstimator are: "G_computation", "IPW", and "DR". The corresponding object will be created by the wrapper function TEstimator_wrapper(). The default is "G_computation", which, along with outcome_method="glm" models the potential outcomes.

SEstimater A character specifying an estimator for weight. The allowed estimators are: "Exact", "Subclass", "ISW". The default is "Exact", which, implements the exact matching on variables in confounders_sampling_name to balance the population covariates between source.data and target.data.

source.data A data frame containing variables named in vars_name and possible other variables. source.obj is instantiated using source.data.

target.data A data frame containing variables named in vars_name and possible other variables. target.obj is instantiated using target.data.

source.name A character indicating the name of source.obj.

target.name A character indicating the name of target.obj.

vars_name A list containing four vectors confounders_treatment_name, treatment_name, and outcome_name. confounders_treatment_name is a character vector containing the adjustment variables, which, along with TEstimator and the corresponding outcome_method or treatment_method to correct for confounding; outcome_name is a character vector of length one containing the variable name of outcome; treatment_name is a character vector of length one containing the variable name of treatment.

confounders_sampling_name a character vector specifying variable names. The weights are estimated based on the variables.

outcome_method, treatment_method, weighting_method A character specifying model for outcome, treatment, and weight to use. Possible values are found using names(getModelInfo()). See http://topepo.github.io/caret/train-models-by-tag.html.

outcome_formula, treatment_formula, selection_formula An optional object of class formula describing the outcome model specification, treatment model specification, and selection model specification.

stratification An optional character vector containing variables to select subgroups. source.obj will compute both weighted and unweighted average treatment effects of the subgroups, target.obj will calculate the average treatment effects of the subgroups.

stratification_joint An optional logical indicating if the subgroups are selected based on levels of combined variables in stratification or levels of individual variable in stratification.
strata_cut_source
An optional list containing lists. Each component is a list with tag named by a variable in source.data to discretize, containing break which is a vector specifying the interval of range of the variable to divide, label which is a character vector specifying how to code value in the variable according to which interval they fall. The leftmost interval corresponds to level one, the next leftmost to level two and so on. This parameter is useful in the case we concern the integrated treatment effect conditioning on variables with multiple levels (for instance, continuous variable or ordinal variable with multiple levels). Note that we first model based on these continuous variables, then we discretize these variables according to strata_cut. The variables in data of TEstimator object are discretized, and the weight is calculated based on the discretized variables.

strata_cut_target
An optional list containing lists. Each component is a list with tag named by a variable in target.data to discretize.

two_models
An optional logical indicating whether potential outcomes should be modeled separately when TEstimator="DR". Default is FALSE.

data.public
An optional logical indicating whether the data in the output objects are public. Default is TRUE.

... An optional argument passed to fit() of each estimator object for model training and tuning. See https://topepo.github.io/caret/model-training-and-tuning.html for details.

Details
An R6 object is constructed by a wrapper function TEstimator_wrapper and SEstimator_wrapper with user's input of data and estimators for treatment effect and weight. TEstimator_wrapper() returns initialized objects source.obj and target.obj. SEstimator_wrapper() weights the estimates of source.obj via the class method RCTrep(). The weights are computed using data in the source object source.obj, target object target.obj, and estimator of weights SEstimator.

Value
A list of length three with three R6 class objects, source.obj, target.obj and source.rep.obj

Examples
```
output <- RCTREP(TEstimator = "G_computation", SEstimator = "Exact",
                 outcome_method = "BART",
                 source.data = RCTrep::source.data[sample(dim(RCTrep::source.data)[1],500),],
                 target.data = RCTrep::target.data[sample(dim(RCTrep::target.data)[1],500),],
                 vars_name = list(confounders_treatment_name =
                                  c("x1","x2","x3","x4","x5","x6"),
                                  treatment_name = c("z"),
                                  outcome_name = c("y")),
                 confounders_sampling_name = c("x2","x6"),
                 stratification = c("x1","x3","x4","x5"),
                 stratification_joint = TRUE)
```
SEstimator_wrapper

Estimating the weighted conditional average treatment effects in source.obj based on input objects source.obj and target.obj of class TEstimator.

Description

Estimating the weighted conditional average treatment effects in source.obj based on input objects source.obj and target.obj of class TEstimator.

Usage

SEstimator_wrapper(
  Estimator,
  target.obj,
  source.obj,
  confounders_sampling_name,
  method = "glm",
  sampling_formula = NULL,
  ...
)

Arguments

Estimator a character specifying an estimator for weight. The allowed estimators are "Exact", "ISW", and "Subclass".

target.obj, source.obj an instantiated object of class TEstimator.

confounders_sampling_name a character vector specifying the names of variables in data of source.obj and target.obj. Weights are estimated based on the variables.

method an optional character specifying a model for estimating sampling probability when Estimator='ISW' or Estimator='Subclass'.

sampling_formula an object of class formula specifying a model specification for sampling probability. Default value is NULL.

... an optional argument specifying training and tuning for a model of sampling probability. See https://topepo.github.io/caret/model-training-and-tuning.html for details.

Value

An object of class SEstimator
Examples

```r
source.data <- RCTrep::source.data[sample(dim(RCTrep::source.data)[1],500),]
target.data <- RCTrep::target.data[sample(dim(RCTrep::target.data)[1],500),]

vars_name <- list(confounders_treatment_name = c("x1","x2","x3","x4","x5","x6"),
                  treatment_name = c('z'),
                  outcome_name = c('y'))

target.obj <- TEstimator_wrapper(
  Estimator = "Crude",
  data = target.data,
  vars_name = vars_name,
  name = "RCT",
  data.public = FALSE,
  isTrial = TRUE)

source.obj <- TEstimator_wrapper(
  Estimator = "G_computation",
  data = source.data,
  vars_name = vars_name,
  outcome_method = "glm",
  outcome_form=y ~ x1 + x2 + x3 + z + z:x1 + z:x2 + z:x3+ z:x6,
  name = "RWD",
  data.public = TRUE)

source.rep.obj <- SEstimator_wrapper(Estimator="Exact",
  target.obj=target.obj,
  source.obj=source.obj,
  confounders_sampling_name=c("x2","x6"))

source.rep.obj$EstimateRep(stratification = c("x1","x3","x4","x5"),
                           stratification_joint = TRUE)
```

source.binary.data  A dataset of simulated observational data, where outcome is binary variable. The data is filtered after compared to target.binary.data

Description

A dataset of simulated observational data, where outcome is binary variable. The data is filtered after compared to target.binary.data

Usage

source.binary.data
Format

A data frame with 2624 rows and 9 variables.

- **x1** binary variable, x1 ~ rbinom(5000,1,0.2)
- **x2** binary variable, x2 ~ rbinom(5000,1,0.2)
- **x3** binary variable, x3 ~ rbinom(5000,1,0.8)
- **x4** binary variable, x4 ~ rbinom(5000,1,0.8)
- **x5** binary variable, x5 ~ rbinom(5000,1,0.7)
- **x6** binary variable, x6 ~ rbinom(5000,1,0.8)
- **z** binary variable. pp = x1*x2+x3*x4+5*x5+x6, p(z=1) = p = 1/1+e^-(pp-mean(pp))/sd(pp)*sqrt(3)/pi, z ~ rbinom(5000,1,p)
- **y** binary variable. pp = x1 + (6*x2+x6+2)*z, p(y=1) = p = 1/1+e^-(pp-mean(pp))/sd(pp)*sqrt(3)/pi, y ~ rbinom(5000,1,p)
- **pt** a continuous variable within 0 and 1, specifying the probability of p(z=1) given x1,x2,x3,x4,x5,x6

source.data

A data set of simulated observational data, where outcome is continuous variable, treatment is a binary variable.

Description

A data set of simulated observational data, where outcome is continuous variable, treatment is a binary variable.

Usage

source.data

Format

```r
# 'source.data' A data frame with 5000 rows and 8 variables:

- **x1** binary variable, x1 ~ rbinom(5000,1,0.2)
- **x2** binary variable, x2 ~ rbinom(5000,1,0.2)
- **x3** binary variable, x3 ~ rbinom(5000,1,0.8)
- **x4** binary variable, x4 ~ rbinom(5000,1,0.8)
- **x5** binary variable, x5 ~ rbinom(5000,1,0.7)
- **x6** binary variable, x6 ~ rbinom(5000,1,0.8)
- **z** binary variable indicating treatment and control. pp = x1*x2+x3*x4+5*x5+x6, p(z=1) = p = 1/1+e^-(pp-mean(pp))/sd(pp)*sqrt(3)/pi, z ~ rbinom(5000,1,p)
- **y** continuous variable indicating outcome, y ~ x1 + 6*x2+x6+2*z + rnorm(5000,0,1)
```
**target.binary.data**

A dataset of simulated RCT data, where outcome is binary variable. The data is filtered after compared to source.binary.data

**Description**

A dataset of simulated RCT data, where outcome is binary variable. The data is filtered after compared to source.binary.data

**Usage**

target.binary.data

**Format**

A data frame with 3194 rows and 9 variables.

- **x1** binary variable, \( x_1 \sim \text{rbinom}(5000,1,0.7) \)
- **x2** binary variable, \( x_2 \sim \text{rbinom}(5000,1,0.9) \)
- **x3** binary variable, \( x_3 \sim \text{rbinom}(5000,1,0.2) \)
- **x4** binary variable, \( x_4 \sim \text{rbinom}(5000,1,0.3) \)
- **x5** binary variable, \( x_5 \sim \text{rbinom}(5000,1,0.2) \)
- **x6** binary variable, \( x_6 \sim \text{rbinom}(5000,1,0.3) \)
- **z** binary variable. \( pp = x_1*x_2+x_3*x_4+5*x_5+x_6, \ p(z=1) = p = 1/1+\exp^{-(pp-mean(pp))/sd(pp)*sqrt(3)/pi}, \ z \sim \text{rbinom}(5000,1,p) \)
- **y** binary variable. \( pp = x_1 + (6*x_2+x_6+2)*z, \ p(y=1) = p = 1/1+\exp^{-(pp-mean(pp))/sd(pp)*sqrt(3)/pi}, \ y \sim \text{rbinom}(5000,1,p) \)
- **pt** a continuous variable within 0 and 1, specifying the probability of \( p(z=1) \) given \( x_1,x_2,x_3,x_4,x_5,x_6 \)

---

**target.data**

A dataset of simulated RCT data, where outcome is continuous variable, treatment is a binary variable.

**Description**

A data set of simulated RCT data, where outcome is continuous variable, treatment is a binary variable.

**Usage**

target.data
`TEstimator_wrapper` Estimating conditional average treatment effects

Description

Estimating conditional average treatment effects

Usage

```r
TEstimator_wrapper(
  Estimator,
  data,
  vars_name,
  name = "",
  outcome_method = "glm",
  treatment_method = "glm",
  two_models = FALSE,
  outcome_formula = NULL,
  treatment_formula = NULL,
  data.public = TRUE,
  isTrial = FALSE,
  strata_cut = NULL,
  ...
)
```

Arguments

- `Estimator` A character specifying an estimator for conditional average treatment effects. The allowed estimators are: "G_computation", "IPW", and "DR". The corresponding object will be created by the function `TEstimator_wrapper()`. The default is "G_computation", which, along with `outcome_method="glm"` models the potential outcomes.

Format

```r
## 'target.data' A data frame with 5000 rows and 8 variables:

x1 binary variable, x1 ~ rbinom(5000,1,0.7)
x2 binary variable, x2 ~ rbinom(5000,1,0.9)
x3 binary variable, x3 ~ rbinom(5000,1,0.2)
x4 binary variable, x4 ~ rbinom(5000,1,0.3)
x5 binary variable, x5 ~ rbinom(5000,1,0.2)
x6 binary variable, x6 ~ rbinom(5000,1,0.3)
z binary variable indicating treatment and control, z ~ rbinom(5000,1,0.5)
y continuous variable indicating outcome, y ~ x1 + 6*x2+x6+2*z + rnorm(5000,0,1)
```
data  A data frame containing variables named in vars_name and possible other variables.

vars_name  A list containing four character vectors confounders_treatment_name, treatment_name, and outcome_name. confounders_treatment_name is a character vector containing the adjustment variables, which, along with TEstimator and the corresponding outcome_method or treatment_method to correct for confounding; outcome_name is a character vector of length one containing the name of outcome; treatment_name is a character vector of length one containing the name of treatment.

name  A character indicating the name of the output object

outcome_method  A character specifying a model for outcome. Possible values are found using names(getModelInfo()). See http://topepo.github.io/caret/train-models-by-tag.html. Default is "glm".

treatment_method  A character specifying a model for treatment. Possible values are found using names(getModelInfo()). See http://topepo.github.io/caret/train-models-by-tag.html. Default is "glm".

two_models  An optional logical indicating whether potential outcomes should be modeled separately when TEstimator="DR". Default is FALSE.

outcome_formula  An optional object of class formula describing the outcome model specification when Estimator="G_computation" or Estimator="DR".

treatment_formula  An optional object of class formula describing the treatment model specification when Estimator="IPW" or Estimator="DR".

data.public  An optional logical indicating whether individual-level data is public in the output object. Default is TRUE.

isTrial  An optional logical indicating whether the treatment assignment of data is random or unknown.

strata_cut  An optional list containing lists. Each component is a list with tag named by a variable in data to discretize, containing break which is a vector specifying the interval of range of the variable to divide, lable which is a character vector specifying how to code value in the variable according to which interval they fall. The leftmost interval corresponds to level one, the next leftmost to level two and so on. This parameter is useful in the case we concern the integrated treatment effect conditioning on variables with multiple levels (for instance, continuous variable or ordinal variable with multiple levels). Note that we first model based on these continuous variables, then we discretize these variables according to strata_cut. The variables in data of the output object are discretized.

...  An optional argument passed to the private function fit() of each class for model training and tuning. See https://topepo.github.io/caret/model-training-and-tuning.html for details.

Value

An object of class TEstimator.
Examples

data <- RCTrep::source.data[sample(dim(RCTrep::source.data)[1], 500),]
vars_name <- list(confounders_treatment_name = c("x1", "x2", "x3", "x4", "x5", "x6"),
                 treatment_name = c('z'),
                 outcome_name = c('y'))

obj <- TEstimator_wrapper(
    Estimator = "G_computation",
    data = data,
    vars_name = vars_name,
    name = "RCT",
    data.public = TRUE,
    isTrial = FALSE)
Index

* **datasets**

  quasar.agg, 8
  quasar.obj, 8
  quasar.synthetic, 8
  source.binary.data, 13
  source.data, 14
  target.binary.data, 15
  target.data, 15

  call_dashboard, 2

  DGM, 3

  Fusion, 5

  GenerateSyntheticData, 7

  quasar.agg, 8
  quasar.obj, 8
  quasar.synthetic, 8

  RCTREP, 9

  SEstimator_wrapper, 11, 12
  source.binary.data, 13
  source.data, 14

  target.binary.data, 15
  target.data, 15

  TEstimator_wrapper, 11, 16