Package ‘expose’

May 16, 2019

Type Package
Title Multiple Effect Estimation of Chemicals in Environmental Epidemiology
Version 0.0.3
Description Estimate individual and average joint effects of chemical mixtures, dose-response relationships, and potential interactions in environmental epidemiology. The visualization of interactions and the plotting of all the objects. For more information please, check next work: Youssef Oulhote, Marie-Abele Bind, Brent Coull, Chirag Patel, Philippe Grandjean (2017) <https://www.biorxiv.org/content/early/2017/06/30/147413.article-info>.
License MIT + file LICENSE
Encoding UTF-8
LazyData true
Imports RColorBrewer, ggplot2, repmis, SuperLearner, gam, splines, foreach, glmnet, Matrix, nnet, polspline, e1071, xgboost, Rcpp, stats
RoxygenNote 6.1.1
Suggests knitr, rmarkdown
VignetteBuilder knitr
NeedsCompilation no
Author Ibon Tamayo [aut, cre]
Maintainer Ibon Tamayo <itamuria@gmail.com>
Repository CRAN
Date/Publication 2019-05-16 11:50:07 UTC

R topics documented:

dose_resp .................................................. 2
dose_respe_ind ........................................... 3
expose_data .............................................. 3
gen ....................................................... 4
**dose_resp**

Extract the information from the simulation data frame to analyse the dose response effects

**Description**

Extract the information from the simulation data frame to analyse the dose response effects

**Usage**

dose_resp(allsim, dataset, exposures, dr, ic_dis = "IC", st)

**Arguments**

- **allsim**: dataset with all simulations values
- **dataset**: dataset with all variables
- **exposures**: a vector with exposures
- **dr**: a vector with dose response values
- **ic_dis**: choose between ic (interval confidences) and dis (distribution)
- **st**: summary table from general function

**Value**

a data frame with dose response values

**Examples**

data(expose_data)
data(simu)
data(gen)
delta=c(1,0)
seku <- seq(0,1,0.05)
Exposures<- c('Var1','Var2','Var3','Var4','Var5')
summary_table_lines <- gen[2]
drr.grp <- dose_resp (allsim = simu[[1]], dataset = expose_data, st = summary_table_lines, dr = seku, exposures = Exposures)
**dose_resp_ind**

| dose_resp_ind | Extract the information from the simulation data frame to analyse the dose response effects |

**Description**

Extract the information from the simulation data frame to analyse the dose response effects.

**Usage**

dose_resp_ind(allsim, dataset, dr = seq(0, 1, 0.1))

**Arguments**

- **allsim**: dataset with all simulations values
- **dataset**: dataset with all variables
- **dr**: a vector with dose response values

**Value**

a data frame with dose response values

---

**expose_data**

Multiple quacicals and several epidemiological outcomes

**Description**

Data from a epidemiological study on multiple-pollutants Dataset with 300 records each one representing an individual and 11 variables: 5 quacicals, gender, 4 measured outcomes and Id.

**Usage**

data(expose_data)

**Format**

An object of class 'data frame'.

**Examples**

data(expose_data)
head(expose_data)
**general_function**

---

**gen**

*One of the intermediate data frame*

---

**Description**

Data from a epidemiological study on multiple-pollutants Dataset with 300 records each one representing an individual and 11 variables: 5 quenicals, gender, 4 measured outcomes and Id.

**Usage**

```r
data(gen)
```

**Format**

An object of class `'data.frame`.

**Examples**

```r
data(gen)
head(gen)
```

---

**general_function**

*General function create the basic structure for the analysis*

---

**Description**

General function create the basic structure for the analysis

**Usage**

```r
general_function(dataset, exposures, confounders, outcomes, delta, dr)
```

**Arguments**

- `dataset` dataset with all variables
- `exposures` a vector with exposures
- `confounders` a vector with confounders
- `outcomes` outcome’s name
- `delta` a vector with two values
- `dr` a vector with dose response values

**Details**

.
Value

a list with 2 objects. One is the dataframe with all the values and the other is a summary of the
groups and the corresponding rows in the first dataframe.

Examples

data(expose_data)
N <- dim(expose_data)[1]
Outcome = 'Y4'
seku <- seq(0,1,0.05)  #c(0,0.1,0.2,0.25,0.3,0.4,0.5,0.6,0.7,0.75,0.8,0.9,1)
our.num.sim <- 5
delta = c(1,0)
Exposures <- c('Var1','Var2','Var3','Var4','Var5')
Confounders <- c('sex')
Outcome <- c('Y4')
gen <- general_function (dataset = expose_data, exposures = Exposures,
                          confounders = Confounders, 
                          outcomes = Outcome[1], delta=delta, dr = seku)

ice Extract the information from the simulation data frame to analyse the
individual conditional expectation

Description

Extract the information from the simulation data frame to analyse the individual conditional expectation

Usage

ice(allsim, dataset, dr = seq(0, 1, 0.1), squem, remove_extrem = FALSE)

Arguments

  allsim  dataset with all simulations values
  dataset  dataset with all variables
  dr  a vector with dose response values
  squem  squeme of the values of the prediction values
  remove_extrem  boolean parameter to remove the extrem values

Value

a data frame with interactions
Examples

```r
data(expose_data)
data(simu)
data(gen)
delta=c(1,0)
seku <- seq(0,1,0.05)
Exposures<- c('Var1','Var2','Var3','Var4','Var5')
summary_table_lines <- gen[[2]]
ice_res <- ice(allsim = simu[[1]], dataset = expose_data, dr = seku,
squem = summary_table_lines, remove_extrem = FALSE)
```

interact Extract the information from the simulation data frame to analyse the interaction effects

Description

Extract the information from the simulation data frame to analyse the interaction effects

Usage

```r
interact(allsim, dataset, exposures, confounders, squem)
```

Arguments

- **allsim**: dataset with all simulations values
- **dataset**: dataset with all variables
- **exposures**: a vector with exposures
- **confounders**: a vector with confounders
- **squem**: squeme of the values of the prediction values

Value

data frame with interaction values

Examples

```r
data(expose_data)
data(simu)
data(gen)
delta=c(1,0)
seku <- seq(0,1,0.05)
Exposures<- c('Var1','Var2','Var3','Var4','Var5')
summary_table_lines <- gen[[2]]
it <- interact (allsim = simu[[1]], dataset = expose_data, exposures = Exposures,
confounders = c('sex'), squem = summary_table_lines)
```
naive_ace

Extract the information from the simulation data frame to analyse the naive causal effects

Description

Extract the information from the simulation data frame to analyse the naive causal effects

Usage

naive_ace(allsim, dataset, exposures, delta = c(0, 1), ic_dis = "IC", st)

Arguments

allsim dataset with all simulations values
dataset dataset with all variables
exposures a vector with exposures
delta a vector with two values
ic_dis choose between ic (interval confidences) and dis (distribution)
st summary table from general function

Value

a data frame with naive ace and confident intervals

Examples

data(expose_data)
data(simu)
data(gen)
delta=c(1,0)
Exposures<- c('Var1','Var2','Var3','Var4','Var5')
summary_table_lines <- gen[[2]]
ace.df.g <- naive_ace (allsim = simu[[1]], dataset = expose_data,
ic_dis = 'IC', st = summary_table_lines,
exposures = Exposures, delta = delta)
naive_ace_ind

Extract the information from the simulation data frame to analyse the interaction effects

Description

Extract the information from the simulation data frame to analyse the interaction effects

Usage

naive_ace_ind(allsim, dataset, ic_dis = "IC")

Arguments

allsim dataset with all simulations values
dataset dataset with all variables
ic_dis choose between ic (interval confidences) and dis (distribution)

Value

a data frame with naive ace and confident intervals

run_simulations

This function run all the simulations based on the structure of the basic data frame.

Description

This function run all the simulations based on the structure of the basic data frame.

Usage

run_simulations(dataset, exposures, confounders, libraries, outcomes,
num.sim = 50, delta = c(0, 1), dr, newdata, show_times = FALSE,
show_num_sim = TRUE, save_time = FALSE, verbose = FALSE,
family = "gaussian", method = "method.NNLS")

Arguments

dataset dataset with all variables
exposures a vector with exposures
confounders a vector with confounders
libraries a vector of libraries to use
outcomes outcome’s name
num_sim  number of simulations
delta    a vector with two values
dr       a vector with dose response values
newdata  the dataframe with new values
show_times boolean parameter to see the time
show_num_sim boolean parameter to see the iteration of simulations
save_time boolean parameter to save the time in the result list
verbose  boolean parameter to see the verbose of superlearner
family   a character parameter to describe the family of the model
method   a character parameter to choose the method in the superlearner

details

libraries could be SL if we don't select nothing or 'SL.glm', 'SL.glm.interaction', 'SL.glmnet', 'SL.gam', 'SL.xgboost', 'SL.polymars', 'SL.randomForest'

value

a list with 4 objects: a data frame with all simulations, risk and coefficients of the crossvalidation and the time of the proces.

Description

Data from a epidemiological study on multiple-pollutants Dataset with 300 records each one representing an individual and 11 variables: 5 chemicals, gender, 4 measured outcomes and Id.

Usage

data(simu)

Format

An object of class 'data frame'.

Examples

data(simu)
head(simu)
Index

• Topic **datasets**
  - expose_data, 3
  - gen, 4
  - simu, 9

  - dose Resp, 2
  - dose Resp Ind, 3

  - expose_data, 3

  - gen, 4
  - general function, 4

  - ice, 5
  - interact, 6

  - naive ace, 7
  - naive ace Ind, 8

  - run simulations, 8

  - simu, 9