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>.

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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

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`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 — *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 quemicals 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 quemicals, gender, 4 measured outcomes and Id.

Usage

```
data(expose_data)
```

Format

An object of class 'data frame'.

Examples

```
data(expose_data)
head(expose_data)
```

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 quemicals, gender, 4 measured outcomes and Id.

Usage

```
data(gen)
```

Format

An object of class `'data frame'`.

Examples

```
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

```
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

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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

```
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

```
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

```
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.

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simu *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 quemicals, gender, 4 measured outcomes and Id.

Usage

```
data(simu)
```

Format

An object of class `'data frame'`.

Examples

```
data(simu)
head(simu)
```

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