Package 'rexposome'

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Title Exposome exploration and outcome data analysis

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Description Package that allows to explore the exposome and to perform association analyses between exposures and health outcomes.

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Contents

`classification` *Method to get the classification of the samples from an ExposomeClust.*

Description

Method to get the classification of the samples from an ExposomeClust.

Usage

```
classification(object)
```

Arguments

`object`	An ExposomeClust to get the samples' classification.

Value

A labelled vector with the classification of each exposure.

See Also

clustering as a constructor for ExposomeClust, plotClassification to plot the groups

Examples

```
data("eclust")
tt <- classification(expo_c)
table(tt)
```

`clustering` *Method to perform clustering on the samples of an ExposomeSet*

Description

This method allows to create an ExposomeClust object from an ExposomeSet object by clustering samples through the exposure levels. The method is flexible to accept any clustering method (`method`) that allows to obtain a classification (`cmethod`) of the samples. The function assigned to argument `method` must have an argument called `data`, waiting for the matrix of exposures (samples as rows, exposures as columns). If the result object of the `method` has no accessor `$classification`, then a `cmethod` is required and will be applied on the result of `method` to obtain a labelled vector with the samples' classification.

Usage

```
clustering(object, method, cmethod, ..., warnings = TRUE)
```

Arguments

`object`	`ExposomeSet` containing the exposures used for the clustering process
`method`	Function applied to the exposures of `object`. This function must has an argument named as `data` that will receive the matrix of exposures.
`cmethod`	(optional) Function to obtain the classification from the object generated with `method`.
`...`	Passed to content of `method`.
`warnings`	(default `TRUE`) If set to `FALSE` warnings will not be displayed.

Value

`ExposomeClust` with the original exposures and the classification of each exposure.

Note

The function assigned to `cmethod` will be directy applied to the result of the `method` as: `cmethod(model)`; being `model` the result of `method`.

See Also

classification to see how to obtain the classification of the samples from an ExposomeClust, plotClassification to plot the groups

Examples

```
data("exposome")

# EXAMPLE 1: Clustering with mclust
library(mclust)
c <- clustering(expo[12:32, ], method = Mclust, G = 2)
table(classification(c))  # This works since the result of Mclust has an accessor
                   # $classification

# EXAMPLE 2: Cluseting with flexmix
library(flexmix)
# First we carete a function to apply flexmix to the ExposomeSet
flexmix_clust <- function(data, ...) {
  data <- as.matrix(data)
  flexmix(formula = data~1, ...)
}

# Then if we apply the method to the ExposomeSet it will crash:
# c <- clustering(expo[12:32, ], method = flexmix_clust, k = 2, model = FLXMCmvnorm())
# Because the method does not know how to obtain the classification for the result
# since flexmix has not an accessor called $classiciation

# We create a function to get the classification
flexmix_clas <- function(model, ...) {
  return(clusters(model))
}
```

```
# We put it to the ExposomeClust
c <- clustering(expo[12:32, ], method = flexmix_clust, cmethod = flexmix_clas,
    k = 2, model = FLXMCmvnorm())
classification(c) # This works because the ExposomeClust has a way to get
                  # the classification
```

`correlation` *Creation of an ExposomeCorr from an ExposomeSet.*

Description

Method to calculate the correlation between the exposures of an ExposomeSet. The correlation method takes into account the nature of each pair of exposures: continuous vs. continuous uses cor function from R base, categorical vs. categorical uses cramerV function from lsr R package and categorical vs. continuous exposures correlation is calculated as the square root of the adjusted r-square obtained from fitting a lineal model with the categorical exposures as dependent variable and the continuous exposure as independent variable. The function creates and returns an ExposomeCorr object.

Usage

```
correlation(object, ..., warnings = TRUE)
```

Arguments

`object`	`ExposomeSet` which exposures will be used to calculate their correlation
`...`	Other arguments passed to cor, cramersV or to lm.
`warnings`	(default `TRUE`) If set to `FALSE` warnings will not be displayed.

Value

`ExposomeCorr` with the correlation between the selected exposures and their description

See Also

plotCorrelation to plot the correlations of an ExposomeCorr, clustering to see how the exposures can cluster samples, pca to compute PCA on exposures

Examples

```
data("exposome")
expo.c <- correlation(expo)
expo.c
expo.c.table <- extract(expo.c)
```

`expo` `ExposomeSet` *for testing purpouses*

Description

`ExposomeSet` with full set of 104 exposures, 1200 simulated samples and 4 phenotypes (asthma status, BMI measure, sex, and age).

Usage

```
data("exposome")
```

Format

An object of class `ExposomeSet` of dimension 104 x 1200 x 4.

Value

An `ExposomeSet` object.

Examples

```
data("exposome")
dim(expo)
exposureNames(expo)
familyNames(expo)
sampleNames(expo)
phenotypeNames(expo)
```

`expos` *Returns the exposures matrix of an ExposomeSet.*

Description

Given an ExposomeSet it returns the inner matrix of exposures, having the exposures as columns and the samples as rows.

Usage

```
expos(object)
```

Arguments

`object`	An ExposomeSet.

Value

A matrix of exposures

Examples

```
data("exposome")
expos(expo)[1:3, 1:3]
```

`ExposomeClust` *Class ExposomeClust*

Description

Class `ExposomeClust` obtained from clustering on an ExposomeSet object, represents the groups of samples created applying a clustering method on the `ExposomeSet`' exposures.

Usage

```
## S4 method for signature 'ExposomeClust,ANY'
plot(x, y, ...)

## S4 method for signature 'ExposomeClust'
classification(object)

## S4 method for signature 'ExposomeClust'
plotClassification(object, type = "heatmap", ...)

## S4 method for signature 'ExposomeClust'
sampleNames(object)
```

Arguments

`x`	Object of class `ExposomeClust`
`y`	NOT USED
`...`	Argument given to `heatmap.2`
`object`	An object of class ExposomeClust
`type`	(default `"heatmap"`) Type of plot.

Value

An object of class `ExposomeClust`

Methods (by generic)

- `plot(x = ExposomeClust, y = ANY)`: Wrapper for `plotClassification` method.
- `classification(ExposomeClust)`: Return classe asigned to each sample
- `plotClassification(ExposomeClust)`: Draws a heatmap for the samples' classification.
- `sampleNames(ExposomeClust)`: Method to obtain samples' names

Slots

`model` Result obtained on applying `method` on the exposures.

`method` Function used to perform the clustering of the exposures.

`call` Call used to create this object.

`samples` Name of the exposures after the clustering process.

See Also

`clustering` to apply a clustering on an `ExposomeSet` and create an `ExposomeClust`.

`ExposomeCorr` *Class ExposomeCorr*

Description

Class `ExposomeCorr` contains a matrix of correlations between continuos exposures calculated using cor. It also contains the description of each exposures (`fData` of the original ExposomeSet) in order to maintain a coherence with the original source. It extends eSet-class.

Usage

```
## S4 method for signature 'ExposomeCorr,ANY'
plot(x, y, ...)

## S4 method for signature 'ExposomeCorr'
dim(x)

## S4 method for signature 'ExposomeCorr'
extract(object, sort, ...)

## S4 method for signature 'ExposomeCorr'
plotCorrelation(object, type = c("circos", "matrix"), ...)
```

Arguments

`x`	Object of class ExposomeCorr
`y`	NOT USED
`...`	Arguments passed to `corrplot` when `type="matrix"`.
`object`	An `ExposomeCorr` object.
`sort`	NOT USED
`type`	To choose between `"circos"` and `"matrix"`.

Value

An object of class `ExposomeCorr`

Methods (by generic)

- `plot(x = ExposomeCorr, y = ANY)`: Wrapper for `plotClassification` method.
- `dim(ExposomeCorr)`: Return the dimension of the internat matrix of correlation.
- `extract(ExposomeCorr)`: Return the raw correlation matrix
- `plotCorrelation(ExposomeCorr)`: Draws both a matrix of circos plot of correlations

Slots

`assayData` Contains the correlation matrix (see eSet, AssayData).

`featureData` Contains the description of the exposures including the family where they belong (see eSet, AnnotatedDataFrame).

See Also

`pca` to study the behavioud between samples and exposures in an `ExposomeSet`

`ExposomePCA` *Class ExposomePCA*

Description

Class `ExposomePCA` contains a matrix of exposures used to compute the PCA, also a table of phenotypes and a set congtaing the multiple results of computing the PCA.

Usage

```
## S4 method for signature 'ExposomePCA,ANY'
plot(x, y, ...)

## S4 method for signature 'ExposomePCA'
exposureNames(object)

## S4 method for signature 'ExposomePCA'
extract(object, table = "exposures", ...)

## S4 method for signature 'ExposomePCA'
ndim(object)

## S4 method for signature 'ExposomePCA'
phenotypeNames(object)

## S4 method for signature 'ExposomePCA'
plot3PCA(
  object,
  cmpX,
  cmpY,
  cmpZ,
  phenotype,
  main,
  angle = 35,
  pch = 16,
  legend = TRUE,
  plines = TRUE
)

## S4 method for signature 'ExposomePCA'
plotEXP(object, exposure)
```

```
## S4 method for signature 'ExposomePCA'
plotPCA(
  object,
  set,
  cmpX = 1,
  cmpY = 2,
  show.exposures = FALSE,
  show.samples = FALSE,
  phenotype
)

## S4 method for signature 'ExposomePCA'
plotPHE(object, phenotype, exp2fac = 5)
```

Arguments

`x`	Object of class `ExposomePCA`
`y`	NOT USED
`...`	NOT USED
`object`	An `ExposomePCA` object
`table`	Can takes values `"exposures"` or `"individuals"`.
`cmpX`	PC to place in X-axis
`cmpY`	PC to place in Y-axis
`cmpZ`	PC to place in Z-axis
`phenotype`	(when `set="samples"`) A phenotype can be selected so the samples are coloured by its value.
`main`	Title
`angle`	Point of view
`pch`	Size of the dots
`legend`	Boolean to show or hide the legend
`plines`	Boolean to show of hide the dotted lines that helps to place the dots in the X/Y axes
`exposure`	Vector of exposures to be shown in the plot
`set`	Can take values `"exposures"`, `"samples"` or `"all"`
`show.exposures`	When set to `TRUE`, labels for exposures are shown
`show.samples`	When set to `TRUE`, labels for samples are shown
`exp2fac`	Number of different values to considere an exposures continuous

Value

An object of class `ExposomePCA`

Methods (by generic)

- `plot(x = ExposomePCA, y = ANY)`: Wrapper for `plotPCA` method.
- `exposureNames(ExposomePCA)`: Getter to obtain the exposures's names.
- `extract(ExposomePCA)`: Method to extract the raw results of the PCA.
- `ndim(ExposomePCA)`: Number of principal components in an ExposomePCA.
- `phenotypeNames(ExposomePCA)`: Getter to obtain the phenotype's names.
- `plot3PCA(ExposomePCA)`: Methdo to draw a 3D plot for PCA
- `plotEXP(ExposomePCA)`: Plot correlation between exposures and PCA
- `plotPCA(ExposomePCA)`: Methdo to draw a 2D plot for PCA
- `plotPHE(ExposomePCA)`: Plot association score between phentoypes and PCA

Slots

`pca` list containing all elements of the PCA

`phenoData` Contains the phenotypes or variables experimenter-supplied (see eSet, AnnotatedDataFrame).

`featureData` Contains the description of the exposures including the family where they belong (see eSet, AnnotatedDataFrame).

See Also

`correlation` to study the correlation between exposures in a `ExposomeSet`

`ExposomeSet` *Class ExposomeSet*

Description

Class `ExposomeSet` contains the exposure levels, the exposure's description and the samples phenotype. It is the starting object for `rexposome` package and extends eSet.

Usage

```
## S4 method for signature 'ExposomeSet,ANY'
plot(x, y, ...)

## S4 method for signature 'ExposomeSet'
clustering(object, method, cmethod, ..., warnings = TRUE)

## S4 method for signature 'ExposomeSet'
correlation(object, ..., warnings = TRUE)

## S4 method for signature 'ExposomeSet'
dim(x)

## S4 method for signature 'ExposomeSet'
expos(object)

## S4 method for signature 'ExposomeSet'
```

```
exposureNames(object)

## S4 method for signature 'ExposomeSet'
exwas(
  object,
  formula,
  filter,
  family,
  ...,
  baselevels,
  tef = TRUE,
  verbose = FALSE,
  warnings = TRUE,
  robust = FALSE
)

## S4 method for signature 'ExposomeSet'
familyNames(object, by.exposure = FALSE)

## S4 method for signature 'ExposomeSet'
highAndLow(
  object,
  ngroups = 3,
  intervals = c("standard", "extreme"),
  select,
  drop = FALSE,
  warnings = TRUE
)

## S4 method for signature 'ExposomeSet'
ilod(
  object,
  seed = 1234,
  lod.col = "LOD",
  pNA = 0.2,
  tLog = FALSE,
  method = "QRILC",
  warnings = TRUE,
  ...
)

## S4 method for signature 'ExposomeSet'
imputation(object, select, ..., messages = FALSE)

## S4 method for signature 'ExposomeSet'
invExWAS(object, formula, filter, tef = TRUE, verbose = FALSE, warnings = TRUE)

## S4 method for signature 'ExposomeSet'
mexwas(object, phenotype, family, warnings = TRUE)

## S4 method for signature 'ExposomeSet'
normalityTest(
```

```
  object,
  exposure,
  th = 0.05,
  min.val = 5,
  na.rm = TRUE,
  warnings = TRUE
)

## S4 method for signature 'ExposomeSet'
pca(object, npc = 10, pca = FALSE, ...)

## S4 method for signature 'ExposomeSet'
phenotypeNames(object)

## S4 method for signature 'ExposomeSet'
plotFamily(x, family, group, group2, scatter = TRUE, na.omit = TRUE)

## S4 method for signature 'ExposomeSet'
plotHistogram(x, select, density = TRUE, show.trans = FALSE)

## S4 method for signature 'ExposomeSet'
plotLOD(object, lod.col = "LOD", x.max = 100, sort = TRUE)

## S4 method for signature 'ExposomeSet'
plotMissings(
  object,
  set = c("exposures", "phenotypes"),
  x.max = 100,
  sort = TRUE
)

## S4 method for signature 'ExposomeSet'
standardize(object, select, method = "normal", na.rm = TRUE, warnings = TRUE)

## S4 method for signature 'ExposomeSet'
Summary(x, set = c("exposures", "phenotypes"), select, ..., na.rm = FALSE)

## S4 method for signature 'ExposomeSet'
tableLOD(object, output = "n", lod.col = "LOD", sort = TRUE)

## S4 method for signature 'ExposomeSet'
tableMissings(
  object,
  set = c("exposures", "phenotypes"),
  output = "n",
  sort = TRUE
)

## S4 method for signature 'ExposomeSet'
trans(object, fun, select, by.exposure = FALSE, ...)
```

Arguments

`x`	An `ExposomeSet` object.
`y`	NOT USED
`...`	Arguments to be passed to imputeFAMD
`object`	An `ExposomeSet` object.
`method`	Method to be used.
`cmethod`	Function implementing a systsme to retrieve classification from clustering output
`warnings`	If set to `TRUE` it prints the warning messsages.
`formula`	Formula, not including exposures, to be tested. No need to provide response (left term)
`filter`	Expression to be used to filter `ExposomeSet`
`family`	Family descriving the nature of the health outcome
`baselevels`	Labeled vector with the default base level for categorical exposures.
`tef`	If `TRUE` it computed the threshold for effective tests.
`verbose`	If set to `TRUE` is shows messages on progression.
`by.exposure`	If set to `TRUE` ir returns the family which each exposure belongs
`ngroups`	Number of intervals to be used
`intervals`	If `"standard"` all levels are kept, if `"extreme"` intermetiate levels are set to `NA`.
`select`	Vector selecting thee xposures to be used.
`drop`	If set to `TRUE` exposures are replaced
`seed`	Numeric seed
`lod.col`	Indicator of the column where the LOD is located
`pNA`	Maximum percentage allowed of values under LOD
`tLog`	If set to `TRUE` it transforms all the exposures to lod before the imputation.
`messages`	If set to `TRUE` messages from `mice`'s function will be displayed.
`phenotype`	Health outcome to be used as dependent variable.
`exposure`	Vecror of exposures to be used.
`th`	Threshold of P-Value used to considere normalit
`min.val`	Minimum number of observations to perform test
`na.rm`	If set to `TRUE` removes `NA` values
`npc`	Number of PC to be kept
`pca`	Perform PCA (only numerical variables) or FAMD (numerical and categorical)
`group`	Phenotype to group exposures
`group2`	Phenotype to group exposures
`scatter`	If set to true it shows the samples value in the plot
`na.omit`	If set to `TRUE`, `NA` values are discarded
`density`	If set to `TRUE` a desntiry plot is draw on the histogram
`show.trans`	If set to `TRUE`, three extra plots are drawn with usual transformations
`x.max`	Threshold for x axis (in %)
`sort`	If set to `TRUE`, results are ordered
`set`	Cantake values `"exposures"` or `"phentoypes"`.
`output`	Can take values `"n"` (count) ot `"p"` (percentage)
`fun`	Function to bt used in the transformation process

Value

An object of class `ExposomeSet`

Methods (by generic)

- `plot(x = ExposomeSet, y = ANY)`: Wrapper for `plotFamily` method.
- `clustering(ExposomeSet)`: Performs clustering on samples based on exposure levels.
- `correlation(ExposomeSet)`: Computes correlation on exposures.
- `dim(ExposomeSet)`: Returns the number of exsures, samples and phenotypes.
- `expos(ExposomeSet)`: Returns a `data.frame` with exposures.
- `exposureNames(ExposomeSet)`: Getter to obtain the exposures's names.
- `exwas(ExposomeSet)`: Performs an EXposome-Wide Association Study
- `familyNames(ExposomeSet)`: Getter to obtain the families's names of the family of each exposure.
- `highAndLow(ExposomeSet)`: Performs a discretization of continuous exposures.
- `ilod(ExposomeSet)`: Imputation of under-LOD values of exposures.
- `imputation(ExposomeSet)`: Imputation of missing values of exposures.
- `invExWAS(ExposomeSet)`: Performs an EXposome-Wide Association Study (modelling the exposures as response)
- `mexwas(ExposomeSet)`: Performs a Multiple-EXposure-Wide Association Study.
- `normalityTest(ExposomeSet)`: Test the normality of each exposure.
- `pca(ExposomeSet)`: Performs a PCA
- `phenotypeNames(ExposomeSet)`: Getter to obtain the phenotypes's names.
- `plotFamily(ExposomeSet)`: Draws a boxplot or accumulated-bar plot for each exposure in a given family.
- `plotHistogram(ExposomeSet)`: Draws an histogram of a given continuous exposure or a pie chart if a given categorycal exposure.
- `plotLOD(ExposomeSet)`: Draws a barchart with the amount of under-LOD values.
- `plotMissings(ExposomeSet)`: Draws a bar-plot with the amount of missing values.
- `standardize(ExposomeSet)`: Standardization of exposures.
- `Summary(ExposomeSet)`: Summary of both continuous and categorical exposures
- `tableLOD(ExposomeSet)`: Returns a vector with the number of under-LOD values per exposure.
- `tableMissings(ExposomeSet)`: Returns a vector with the number of missing values per exposure.
- `trans(ExposomeSet)`: Transformation of exposures.

Slots

`assayData` Contains the exposures matrix with column number equal to `nrow(phenoData)` (see eSet, AssayData).

`featureData` Contains the description of the exposures including the family where they belong (see eSet, AnnotatedDataFrame).

`phenoData` Contains the phenotypes or variables experimenter-supplied (see eSet, AnnotatedDataFrame).

See Also

`readExposome` to create an `ExposomeSet` from files, `loadExposome` to create an `ExposomeSet` from `data.frames`

`exposureNames` *Getter to obtain the exposures's names of an ExposomeSet or ExposomePCA*

Description

Getter to obtain the exposures's names of an ExposomeSet or ExposomePCA

Usage

```
exposureNames(object)
```

Arguments

`object`	ExposomeSet that will be queried for the exposures's names.

Value

The name of the exposures as a character vector.

Warning

exposureNames collides with featureNames of eSet. Although in `rexposome 1.0.0` both function can be used as synonyms, this usage is discouraged and it is not assured.

See Also

phenotypeNames to get the phenotypes, familyNames to get the families of exposures

Examples

```
data("exposome")
exposureNames(expo)
```

`expo_c` `ExposomeClust` *for testing purpouses*

Description

`ExposomeClust` created from an `ExposomeSet` with full set of 104 exposures, 1200 simulated samples and 4 phenotypes (asthma status, BMI measure, sex, and age). The clustering was done using `hclust` and `cutree` with `k = 3`.

Usage

```
data("eclust")
```

Format

An object of class `ExposomeClust` of dimension 99 x 1200 x 5.

Value

An `ExposomeSet` object.

Examples

```
data("eclust")
dim(expo_c)
table(classification(expo_c))
```

`extract` *Raw data from* `ExWAS`, `ExposomeClust` *and* `ExposomeCorr`.

Description

Returns internal table of results of objects of class `ExWAS`, `ExposomeClust` and `ExposomeCorr`.

Usage

```
extract(object, ...)
```

Arguments

`object`	Object of class `ExWAS`, `ExposomeClust` or `ExposomeCorr`
`...`	NO USED

Value

A `data.frame` containing the raw result from PsyGeNET or a `data.frame` with the result Jaccard Index for each disease.

`ExWAS` *Class ExWAS*

Description

Class `ExWAS` obtained from exwas method of an ExposomeSet object, contains the result of testing the association of exposures of an `ExposomeSet` to its phenotypes. "ExWAS" is the acronym of "Exposome-Wide Association Study". The function can be applied to one of to many phenotypes in the `ExposomeSet` object.

Usage

```
## S4 method for signature 'ExWAS,ANY'
plot(x, y, ...)

## S4 method for signature 'ExWAS'
extract(object, sort = TRUE, ...)

## S4 method for signature 'ExWAS'
get_robust_sd(object, sort = TRUE, ...)

## S4 method for signature 'ExWAS'
names(x)

## S4 method for signature 'ExWAS'
plotEffect(x, y, select, labels, xlab, ylab)

## S4 method for signature 'ExWAS'
plotExwas(
  object,
  ...,
  subtitles,
  color,
  exp.order,
  labels,
  show.effective = TRUE
)

## S4 method for signature 'ExWAS'
plotVolcano(x, p.value = -log10(0.001), labels, show.effect = FALSE)

## S4 method for signature 'ExWAS'
tef(object)
```

Arguments

`x`	An `ExWAS` object
`y`	An `ExWAS` object
`...`	NOT USED
`object`	An object of class `ExWAS`, `mExWAS` or `nlExWAS`.

`sort`	If `TRUE`, the results are ordered by pvalue.
`select`	(optional) Vector with the selected exposures
`labels`	(optional) Character vector with the labels for each exposure. It must be labeled vector.
`xlab`	(optional) Label for x-axis
`ylab`	(optional) Label for y-axis
`subtitles`	Character vector with the "subtitle" for each plot when given more than one `ExWAS`.
`color`	(optional) A vector of colors. The vector must have length equal to the number of families. The vector must be names with the name of the families.
`exp.order`	(optional) Order of the exposures.
`show.effective`	(default TRUE) draws a brown line on the threshold given by the effective number of tests.
`p.value`	(default `-log10(0.001)`) Is the threshold from where the exposures can be taken as significants.
`show.effect`	(default `false`) Apply `exp` to obtained beta.

Value

An object of class `ExWAS`

Methods (by generic)

- `plot(x = ExWAS, y = ANY)`: Wrapper for `plotExwas` method.
- `extract(ExWAS)`: Method to obtain the matrix of association scores
- `get_robust_sd(ExWAS)`: Method to obtain the matrix of association scores
- `names(ExWAS)`: Method to obtain the Threshold for effective tests (TEF)
- `plotEffect(ExWAS)`: Draws a plot with the confidence interval of each exposure. Alows to compare two ExWAS instances.
- `plotExwas(ExWAS)`: Method to plot a manhatan plot for association between exposures and phenitypes
- `plotVolcano(ExWAS)`: Method to plot a volcano plot for association between exposures and phenotypes
- `tef(ExWAS)`: Method to obtain the Threshold for effective tests (TEF)

Slots

`effective` Number containing the effective number of tests.

`formula` Tested formula.

`comparison` Result of performing the test to find association between levels of exposures and phenotype.

`description` Description of the exposures used in the ExWAS. (in description file).

See Also

`exwas` to perform an Exposome-Wide Association Study and to create an `ExWAS`, `mexwas` to perform a Multivariate Exposome-Wide Association Study and to create a `mExWAS`

`exwas` *Testing the association between an exposure and a phenotype of an ExposomeSet*

Description

The `exwas` method performs an "Exposome-Wide Association Study" (ExWAS) using the exposures in ExposomeSet and one of its phenotype.

Usage

```
exwas(
  object,
  formula,
  filter,
  family,
  ...,
  baselevels,
  tef = TRUE,
  verbose = FALSE,
  warnings = TRUE,
  robust = FALSE
)
```

Arguments

`object`	`ExposomeSet` that will be used for the ExWAS.
`formula`	`formula` indicating the test to be done. If any exposure is included it will be used as covariate. `exwas` metho will perform the test for each exposure.
`filter`	`expression` to be used to filter the individuals included into the test.
`family`	Family of the distribution followed by the health outcome to be tested (gaussian, bionomal, ... check glm).
`...`	NOT USED
`baselevels`	(optional) If set, must be a labeled vector with the default base level for categorical exposures.
`tef`	(default `TRUE`) If `TRUE` it computed the effective number of tests and the threhold for the effective number of tests. Usually it needs imputed data.
`verbose`	(default `FALSE`) If set o true messages along the tests are shown.
`warnings`	(default `TRUE`) If set to `FALSE` warnings will not be displayed.

Value

An codeExWAS object with the result of the association study

References

An Environment-Wide Association Study (ExWAS) on Type 2 Diabetes Mellitus. Chirag J. Patel, Jayanta Bhattacharya, Atul J. Butte. May 20, 2010 Plos One

Evaluating the effective numbers of independent tests and significant p-value thresholds in commercial genotyping arrays and public imputation reference datasets. Miao-Xin Li, Juilian M. Y. Yeung, Stacey S. Cherny and Pak C. Sham. May 2012 Hum Genet.

See Also

extract to obtain a table with the result of the ExWAS, plotExwas to plot the results of the ExWAS

Examples

```
data(exposome)
w1 <- exwas(expo[1:5, ], asthma~1, family = "binomial")
w2 <- exwas(expo[1:5, ], asthma~sex+age, family = "binomial")
w3 <- exwas(expo[1:5, ], asthma~age, family = "binomial", filter = sex=="boy")
```

`ex_imp` `imExposomeSet` *for testing purpouses*

Description

`imExposomeSet` created from the raw data included in the package. The creation process is ilustrated in the vignette.

Usage

```
data("ex_imp")
```

Format

An object of class `imExposomeSet` of dimension 47 x 109 x 10.

Value

An `imExposomeSet` object.

Examples

```
data("ex_imp")
ex_imp
```

`familyNames` *Getter to obtain the exposures's names of an ExposomeSet.*

Description

This method returns the name of the families in an ExposomeSet, but it can return a vector, labeled with the exposures in the ExposomeSet, containing the family belonging to each exposure.

Usage

```
familyNames(object, by.exposure = FALSE)
```

Arguments

`object`	`ExposomeSet` that will be queried for the exposures's family-names.
`by.exposure`	(default `FALSE`) If `TRUE` a vector labeled with each exposure name will be returned with the family of each exposures. If `FALSE` a vector with the (unique) name of the families of exposures will be returned.

Value

The families of the exposures into the ExposomeSet, or the family of each exposure into the ExposomeSet.

See Also

exposureNames to get the name of the exposures, phenotypeNames to get the phenotypes

Examples

```
data("exposome")
# Get families
familyNames(expo)
# Get the family of each exposure
familyNames(expo, by.exposure = TRUE)
```

`get_robust_sd` *Raw data from* `ExWAS`

Description

Returns internal table of robust SD of objects of class `ExWAS`

Usage

```
get_robust_sd(object, ...)
```

Arguments

`object`	Object of class `ExWAS`
`...`	NO USED

Value

A `data.frame` containing the raw result from robust SD

`highAndLow` *Function to convert continuous exposures to categorical exposures*

Description

This method allows to convert continuous exposures of an `ExposomeSet` to categorical exposures using the n-percentile groups, defined by `ngroups` argument. By default, all levels are kept but if `intervals` is set to `"extrem"`, the levels between the extrems (aka. lowes and highest) are discarted and their values set to `NA`.

Usage

```
highAndLow(
  object,
  ngroups = 3,
  intervals = "standard",
  select,
  drop = FALSE,
  warnings = TRUE
)
```

Arguments

`object`	An object of class `ExposomeSet`.
`ngroups`	(default `3`) Number of intervals to be created.
`intervals`	(default `"standard"`) If set to `"sctandard"` all levels are set. If set to `"extreme"` obly lowes and highest levels are kept (others are set to `NA`).
`select`	(optional) Subset of exposures where the discretization is applied. If missing, all exposures are used.
`drop`	(default `FALSE`) If set to `FALSE` original exposures are kept and discretized exposures are add to `ExposomeSet`. If set to `TRUE`, original exposures are replaced by categorical exposures.
`warnings`	(defaulr `TRUE`) If set to `FALSE` warnings are not shown.

Value

A new `ExposomeSet` with categorical exposures.

See Also

`trans` to transform exposures, `standardize` to standardize exposures.

Examples

```
# No drop
data("exposome")
exp.hl <- highAndLow(expo, intervals = "standard", select = "ldde_lip")
dim(exp.hl)
# exposures   samples phenotyes
#       105      1200         4
dim(expo)
```

```
# exposures   samples phenotyes
#       104      1200         4
# exps.hl has 107 exposures: the original 104 plus the new
#         3 factored exposures

# Drop
exp.hl <- highAndLow(expo, intervals = "standard",
    select = "ldde_lip", drop = TRUE)
dim(exp.hl)
# exposures   samples phenotyes
#       104      1200         4
dim(expo)
# exposures   samples phenotyes
#       104      1200         4
```

`ilod` *Function to impute under-LOD values from an ExposomeSet*

Description

This function is a wrapper of the functions `impute.MinProb` from the package `imputeLCMD`.

Usage

```
ilod(
  object,
  seed = 1234,
  lod.col = "LOD",
  pNA = 0.2,
  tLog = FALSE,
  method = "QRILC",
  warnings = TRUE,
  ...
)
```

Arguments

`object`	`ExposomeSet` which exposures will be imputed.
`seed`	(default `1234`) Seed to make the imputation reproducible.
`lod.col`	(default `"LOD"`) Name of the column in `fData` with the threshold of the LOD.
`pNA`	(default `0.2`) Maximum percentage allowed of values under LOD
`tLog`	(default `FALSE`) If set to `TRUE` it transforms all the exposures to lod before the imputation.
`method`	(default `"QRILC"`) Method to be used to impute the under-LOD values. Two allowed: QRILC method (value `"QRILC"`) and stochastic minimal value approach (value `"MinProb"`).
`warnings`	(default `TRUE`) If set to `FALSE` warnings will not be displayed.
`...`	Arguments passed to `impute.QRILC` or impute.MinProb from `imputeLCMD`.

Value

A new `ExposomeSet` with the imputed exposures.

See Also

plotMissings to plot the missing data of an ExposomeSet, tableMissings to get a table with the missing data of an ExposomeSet

Examples

```
## Not run:
#Being x an ExposomeSet
x <- ilod(x)

## End(Not run)
```

`imExposomeSet` *Class imExposomeSet*

Description

Class `imExposomeSet` was designed to store the exposures obtained after a multiple imputation process done using `mice`. The `data.frame` obtained from `mice` has the particulatiry to contain the columns `.imp` and `.id` joint to phenotypes and exposures. The slots `assayData`, `featureData`, and `phenoData` are coordinated.

Usage

```
## S4 method for signature 'imExposomeSet,ANY'
plot(x, y, ...)

## S4 method for signature 'imExposomeSet'
dim(x)

## S4 method for signature 'imExposomeSet'
expos(object)

## S4 method for signature 'imExposomeSet'
exposureNames(object)

## S4 method for signature 'imExposomeSet'
extract(object, rid = -1, ...)

## S4 method for signature 'imExposomeSet'
exwas(
  object,
  formula,
  filter,
  family,
  ...,
  baselevels,
```

```
  tef = TRUE,
  verbose = FALSE,
  warnings = TRUE,
  robust = FALSE
)

## S4 method for signature 'imExposomeSet'
familyNames(object, by.exposure = FALSE)

## S4 method for signature 'imExposomeSet'
phenotypeNames(object)

## S4 method for signature 'imExposomeSet'
plotFamily(x, family, group, group2, scatter = FALSE, na.omit = TRUE)

## S4 method for signature 'imExposomeSet'
sampleNames(object)

## S4 method for signature 'imExposomeSet'
x[[i]]

## S4 method for signature 'imExposomeSet,ANY,ANY,ANY'
x[i, j, k, ..., drop = FALSE]

## S4 method for signature 'imExposomeSet'
toES(object, rid = 1)
```

Arguments

`x`	An `imExposomeSet` object.
`y`	NOT USED
`...`	Other used arguments
`object`	An object of class `imExposomeSet`
`rid`	Number of the imputation to be extracted
`formula`	Formula, not including exposures, to be tested.
`filter`	Expression to be used to filter `ExposomeSet`
`family`	Family descriving the nature of the health outcome
`baselevels`	Labeled vector with the base-level of the categorical exposures
`tef`	If set to `TRUE` the threshold for effective test is computed.
`verbose`	If set to `TRUE` it shows messages on progression.
`warnings`	If set to `TRUE` it shows warnings on progession.
`by.exposure`	If set to `TRUE` ir returns the family which each exposure belongs
`group`	Phenotype to group exposures
`group2`	NOT USED
`scatter`	If set to true it shows the samples value in the plot
`na.omit`	NOT USED
`i`	Character coresponding to selected exposures.

`j`	Character corresponding to selected sample names.
`k`	Character corresponding to selected phenotypes.
`drop`	NOT USED

Value

An object of class `imExposomeSet`

Methods (by generic)

- `plot(x = imExposomeSet, y = ANY)`: Wrapper for `plotFamily` method.
- `dim(imExposomeSet)`: Returns the number of exsures, samples and phenotypes.
- `expos(imExposomeSet)`: Returns a `data.frame` with exposures.
- `exposureNames(imExposomeSet)`: Method to obtain samples' names
- `extract(imExposomeSet)`: Method to extract exposures for a single imputation
- `exwas(imExposomeSet)`: Performs an EXposome-Wide Association Study
- `familyNames(imExposomeSet)`: Getter to obtain the families's names of the family of each exposure.
- `phenotypeNames(imExposomeSet)`: Getter to obtain the families's names of the family of each exposure.
- `plotFamily(imExposomeSet)`: Draws a boxplot or accumulated-bar plot for each exposure in the all imputed sets.
- `sampleNames(imExposomeSet)`: Method to obtain samples' names
- `[[`: Get an `ExposomeSet` with the selected imputation
- `x[i`: Subset an `imExposomeSet`
- `toES(imExposomeSet)`: Returns an `ExposomeSet` with ethe given imputation.

Slots

`nimputation` Number of imputations done with `mice`.

`assayData` `data.frame` containing `.imp`, `.id` and the exposures.

`featureData` `data.frame` containing the description of the exposures.

`phenoData` `data.frame` containing `.imp`, `.id` and the phenotypes.

Note

Sample order is not guarantee

See Also

`loadImputed` to create an `imExposomeSet` from `data.frames`

`imputation` *Function to impute missing values from an ExposomeSet*

Description

This function is a wrapper of the functions `mice` and `complete` from the package `mice`. Also to the `impute` from the package `Hmisc`. The function is designed to use those functions to impute missing values on exposures (not in phenotypes).

Usage

```
imputation(object, select, ..., messages = FALSE)
```

Arguments

`object`	`ExposomeSet` which exposures will be imputed.
`select`	Exposures to be imputed. If missing, all exposes will be imputed.
`...`	Argument given to function `mice` of pakcage `mice` (`printFlag` is set from `messages`).
`messages`	(default `FALSE`) If set to `TRUE` messages from `mice`'s function will be displayed.

Value

A new `ExposomeSet` with the imputed exposures.

See Also

plotMissings to plot the missing data of an ExposomeSet, tableMissings to get a table with the missing data of an ExposomeSet

Examples

```
## Not run:
#Being x an ExposomeSet
x <- imputation(x)

## End(Not run)
```

`imputeLOD` *Function to impute values under limit of detection*

Description

Homologous function to the ilod method of ExposomeSet for a given `data.frame` of exposures and a `vector` of threshold. The use of this function is related to HELIX Project.

Usage

```
imputeLOD(
  x,
  lod,
  description = NULL,
  pNA = 0.2,
  pLOD = 0,
  log = TRUE,
  seed = NULL
)
```

Arguments

`x`	`data.frame` containing the exposures as columns and the samples as rows.
`lod`	`vectro` containing the
`description`	`1` means values under LOD while `2` means quantifiable value, `3`
`pNA`	(default: `0.2`) maximum percentage of allowed missing data
`pLOD`	(default: `0`) minimum percentave of values under LOD
`log`	(default: `NA`) log transformation to normalize data
`seed`	(default: `NULL`)

Value

A new `data.frame` with the imputed exposures.

Examples

```
## Not run:
inma.imp <- imputeLOD(x = raw, lod = lod, description = desc,
     pNA = pNA, pLOD = pLOD, log = log, seed = seed)

## End(Not run)
```

`invExWAS` *Testing the association between an exposure and a phenotype of an ExposomeSet (modelling the exposures as response)*

Description

The `invExWAS` method performs an "Exposome-Wide Association Study" (ExWAS) using the exposures in ExposomeSet and one of its phenotype. (modelling the exposures as response)

Usage

```
invExWAS(object, formula, filter, tef = TRUE, verbose = FALSE, warnings = TRUE)
```

Arguments

`object`	`ExposomeSet` that will be used for the ExWAS.
`formula`	`formula` indicating the test to be done. If any exposure is included it will be used as covariate. `exwas` metho will perform the test for each exposure.
`filter`	`expression` to be used to filter the individuals included into the test.
`tef`	(default `TRUE`) If `TRUE` it computed the effective number of tests and the threhold for the effective number of tests. Usually it needs imputed data.
`verbose`	(default `FALSE`) If set o true messages along the tests are shown.
`warnings`	(default `TRUE`) If set to `FALSE` warnings will not be displayed.

Value

An codeExWAS object with the result of the association study

See Also

extract to obtain a table with the result of the ExWAS, plotExwas to plot the results of the association

Examples

```
data(exposome)
w1 <- invExWAS(expo, ~BMI)
w2 <- invExWAS(expo, ~BMI + sex)
plotExwas(w1, w2)
```

`loadExposome` *Creation of an ExposomeSet from* `data.frames`

Description

Given three `data.frames` that defines the exposome (measures of exposome, exposome description and individuals phentype) it loads them and creates an object of type ExposomeSet.

Usage

```
loadExposome(
  exposures,
  description,
  phenotype,
  description.famCol = "family",
  exposures.asFactor = 5,
  warnings = TRUE
)
```

Arguments

`exposures`	`data.frame` of exposures.
`description`	`data.frame` with the description of the exposures (relation between exposures and exposure-family).
`phenotype`	`data.frame` with the phenotypes of interest.
`description.famCol`	(default `"family"`) Index where the family's name (per exposures) if found in file "description". It can be both numeric or character.
`exposures.asFactor`	(default `5`) The exposures with more than this number of unique items will be considered as "continuous" while the exposures with less or equal number of items will be considered as "factor".
`warnings`	(default `TRUE`) If `TRUE` shows useful information/warnings from the process of loading the exposome.

Details

The rows of the exposure's `data.frames`, that corresponds to samples' names, must be the same than the phenotype's `data.frames`. In the same way, the columns in exposure's `data.frames` must be the same in description `data.frame`.

Value

An object of class ExposomeSet.

Note

ExposomeSet's `fData` will contain some inner columns called `.std`, `.trn`, `.fct` and `.type` in order to trace the transformations an exposure suffers and to know, at eny moment, if an exposure is categorical or continuous. The "description" file can contains a column called `type` with values `"factor"` and `"numeric"` to speficy how an exposure needs to be understood. If given, this column will be renamed to `.type`. If not given, it will be created using `exposures.asFactor` value.

See Also

ExposomeSet for class description, readExposome for constructor from txt/csv files.

Examples

```
path <- file.path(path.package("rexposome"), "extdata")
description <- file.path(path, "description.csv")
phenotype <- file.path(path, "phenotypes.csv")
exposures <- file.path(path, "exposures.csv")
dd <- read.csv(description, header=TRUE)
ee <- read.csv(exposures, header=TRUE)
pp <- read.csv(phenotype, header=TRUE)
rownames(dd) <- dd[, 2]
dd <- dd[ , -2]
rownames(ee) <- ee[ , 1]
ee <- ee[ , -1]
rownames(pp) <- pp[ , 1]
pp <- pp[ , -1]
exp <- loadExposome(
```

```
exposures = ee,
description = dd,
phenotype = pp,
description.famCol = "Family"
)
```

`loadExposome_plain` *Creation of an ExposomeSet from single* `data.frame`

Description

Creation of an ExposomeSet from single `data.frame`

Usage

```
loadExposome_plain(
  data,
  data_id,
  sep = ",",
  pheno_cols,
  na.strings = c("NA", "-", "?", " ", ""),
  families = NULL,
  exposures.asFactor = 5,
  warnings = TRUE
)
```

Arguments

`data`	`data.frame` With the exposures and phenotypes (in no particular order!) or `string` with the path to a file (.csv, .tsv, .txt) with the table of exposures and phenotypes
`data_id`	`character` Name of the column on the selected table that contains the ID
`sep`	`character` (default `","`) Separator used by `read.table` to load the files "exposures", "description" and "phenotype". Only applies when providing a path on the data argument
`pheno_cols`	`character` Character vector of the phenotype columns (all the other columns are considered exposures)
`na.strings`	`character` (default `c("NA", "-", "?", " ", "")`) Character defining the `NA` values in expsome's files.
`families`	`list` (default `NULL`) List to specify the families of the exposures, construct it as: `list(Family1 = c("exposure_1_1", "exposure_1_2", "exposure_1_n"), Family2 = c("exposure_2_1", "exposure_2_2", "exposure_2_n"), FamilyM = c("exposure_M_1", "exposure_M_2", "exposure_M_n"))`. All the exposures on the data table have to be on this provided list with their respective families. The family classification is optional, input `NULL` to bypass the family classifier
`exposures.asFactor`	`numeric` (default 5) The exposures with more than this number of unique items will be considered as "continuous" while the exposures with less or equal number of items will be considered as "factor".
`warnings`	(default `TRUE`) If `TRUE` shows useful information/warnings from the process of loading the exposome.

Value

An object of class ExposomeSet.

Examples

```
path <- file.path(path.package("rexposome"), "extdata")
phenotype <- file.path(path, "phenotypes.csv")
exposures <- file.path(path, "exposures.csv")
ee <- read.csv(exposures, header=TRUE)
pp <- read.csv(phenotype, header=TRUE)
# Create fake dataset with exposures and phenotypes combined
data <- cbind(ee, pp)

loadExposome_plain <- function(data, data_id = "idnum",
pheno_cols = c("rhinitis", "wheezing", "sex", "age", "cbmi", "blood_pre", "whistling_chest","flu"))
```

`loadImputed` *Creation of an imExposomeSet from* `data.frames`

Description

Given a `data.frame` from code with the multiple imputations of both exposures and phenotypes, join with a `data.frame` with exposures' description, and object of class `imExposomeSet` is created.

Usage

```
loadImputed(
  data,
  description,
  description.famCol = "family",
  description.expCol = "exposure",
  exposures.asFactor = 5,
  warnings = TRUE
)
```

Arguments

`data`	The `data.frame` of both exposures and phentoypes obtained from `mice`.
`description`	`data.frame` with the description of the exposures (relation between exposures and exposure-family).
`description.famCol`	(default `"family"`) Index where the family's name (per exposures) if found in file "description". It can be both numeric or character.
`description.expCol`	(default `"exposures"`) Index where the exposure's name if found in file "description". It can be both numeric or character.
`exposures.asFactor`	(default `5`) The exposures with more than this number of unique items will be considered as "continuous" while the exposures with less or equal number of items will be considered as "factor".
`warnings`	(default `TRUE`) If `TRUE` shows useful information/warnings from the process of loading the exposome.

Details

The coordination of the information is based in the columns `.imp` and `.id` from the `data.frame` obtained from `mice`. The division of exposures and phenotypes is based in description `data.frame`, that are the exposures. Hence, the elements in the main `data.frame` that are not in the description, are the phentoypes.

Value

An object of class imExposomeSet.

See Also

imExposomeSet for class description

Examples

```
data("me") # me is an imputed matrix of exposure and phenotyes
path <- file.path(path.package("rexposome"), "extdata")
description <- file.path(path, "description.csv")
dd <- read.csv(description, header=TRUE, stringsAsFactors=FALSE)
dd <- dd[dd$Exposure %in% colnames(me), ]
ex_imp <- loadImputed(data = me, description = dd,
description.famCol = "Family",
description.expCol = "Exposure")
```

`me` `data.frame` *for testing purpouses*

Description

`data.frame` created with `mice` used to test and ilustrate the creation of `imExposomeSet`.

Usage

```
data("me")
```

Format

An object of class `data.frame` with 654 rows and 57 columns.

Value

A `data.frame`.

Examples

```
data("me")
dim(me)
colnames(me)
```

`mExWAS` *Class mExWAS*

Description

Class `mExWAS` obtained from mexwas method of an ExposomeSet object, contains the result of testing the multiple models of exposures of an `ExposomeSet` to a set of given phenotypes. "mExWAS" is the #' acronym of "Multivariate Exposome-Wide Association Study".

Usage

```
## S4 method for signature 'mExWAS,ANY'
plot(x, y, ...)

## S4 method for signature 'mExWAS'
extract(object, type = "test", sort = TRUE)

## S4 method for signature 'mExWAS'
plotExwas(
  object,
  ...,
  subtitles,
  color,
  exp.order,
  labels,
  show.effective = TRUE
)
```

Arguments

`x`	Object of class `mExWAS`
`y`	NOT USED
`...`	Other used arguments.
`object`	object of class `mExWAS`.
`type`	(default `"test"`). Can take `"test"` or `"raw"` to obtain a `data.frame` of `glmnet` result.
`sort`	NOT USED
`subtitles`	NOT USED
`color`	NOT USED
`exp.order`	NOT USED
`labels`	NOT USED
`show.effective`	NOT USED

Value

An object of class `mExWAS`

Methods (by generic)

- `plot(x = mExWAS, y = ANY)`: Wrapper for `plotExwas` method.
- `extract(mExWAS)`: Method to obtain the generated model
- `plotExwas(mExWAS)`: Method to plot a heap-map with the coeficient of each exposure

Slots

`result` klist with the fitted model and result.

`phenotype` Name of the phenotype used in the analysys.

`description` feature data from original ExposomeSet.

See Also

`mexwas` to perform a Multivariate Exposome-Wide Association Study and to create a `mExWAS`, `exwas` to perform an Exposome-Wide Association Study and to create an `ExWAS`

`mexwas` *Testing the association between an exposure and a phenotype of an ExposomeSet using a multivariate aproach.*

Description

The `mexwas` method performs an "Multi Exposome-Wide Association Study" (m-ExWAS) using the exposures in ExposomeSet and one of its phenotype. It uses the packages `glmnet` and `partDSA`.

Usage

```
mexwas(object, phenotype, family, warnings = TRUE)
```

Arguments

`object`	`ExposomeSet` that will be used for the ExWAS.
`phenotype`	Target phenotype used for the study. If missing all the phenotypes in the ExposomeSet will be used.
`family`	It must decrive the nature of the outcome. Can take values `"gaussian"`, `"binomial"`, `"poisson"`, `"multinomial"`, `"cox"` or `"mgaussian"`.
`warnings`	(default `TRUE`) If set to `FALSE` warnings will not be displayed.

Value

Returns an object of class mExWAS

See Also

extract to obtain a table with the result of the ExWAS, plotExwas to plot the results of the ExWAS

Examples

```
data("exposome")
wt <- mexwas(expo[3:7, 1:100], phenotype = "asthma", family = "binomial")
```

`ndim` *Number of principal components in an ExposomePCA.*

Description

Number of principal components in an ExposomePCA.

Usage

```
ndim(object)
```

Arguments

`object`	`ExposomePCA` to obtain the number of components.

Value

The number of components in the `ExposomePCA`.

See Also

plotPCA to plot the PCA values of an ExposomePCA, clustering to see how the exposures can cluster samples, correlation to compute the correlation between exposures

Examples

```
data("exposome")
epca <- pca(expo[3:7, 1:100])
ndim(epca)
```

`normalityTest` *It creates a* `data.frame` *of boolean indicating if the exposures follows a normal distribution or not.*

Description

This functions uses `shapiro.test` to test the normality of the exposures and returns a `data.frame` with a boolean value and a p-value for each exposure.

Usage

```
normalityTest(
  object,
  exposure,
  th = 0.05,
  min.val = 5,
  na.rm = TRUE,
  warnings = TRUE
)
```

Arguments

`object`	ExposomeSet with the exposome to be tested.
`exposure`	Name of the exposure to be tested, if missing all the exposures will be tested.
`th`	(by default `0.05`) Threshold to considere an exposure to follow a normal distribution.
`min.val`	(by default `5`) Minimum number of values not missings to test the exposures.
`na.rm`	(by default `TRUE`) Removes the NA values to test the normality on the exposure.
`warnings`	(by default: `TRUE`) Show warnings if required.

Value

A `data.frame` with three columns: exposure, normality and p.value. "exposure" column contains the name of each exposure. "normalty" column contains a `logical` value indicating if the obtained p-value is under the given threshold. "p.value" column contains the obtained p-value from `shapiro.test`.

See Also

plotHistogram to draw the shape of an exposure, plotMissings to draw a plot with the missing data an ExposomeSet, imputation to impute missing data on the exposures of an ExposomeSet

Examples

```
data("exposome")
normalityTest(expo)
```

`pca` *Creation of an ExposomePCA from an ExposomeSet.*

Description

Method to calculate a PCA based on the exposures of an ExposomeSet. Only numerical-exposures (non categorical) will be computed. The function resurns an ExposomePCA object. This PCA is performed by using FactoMineR package.

Usage

```
pca(object, npc = 10, pca = FALSE, ...)
```

Arguments

`object`	`ExposomeSet` which exposures will be used for the PCA
`npc`	(by default 10) number of dimensions kept in the results
`pca`	(default `FALSE`) Set to `TRUE` to Perform PCA (only numerical variables) or `FALSE` to perform FAMD (numerical and categorical)
`...`	Arguments to be passed to imputeFAMD

Value

An `ExposomePCA` with the values of the PCA.

See Also

plotPCA to plot the PCA values of an ExposomePCA, clustering to see how the exposures can cluster samples, correlation to compute the correlation between exposures

Examples

```
data("exposome")
epca <- pca(expo[12:20, ])
```

`phenotypeNames` *Getter to obtain the phenotype's names of an ExposomeSet or ExposomePCA.*

Description

Getter to obtain the phenotype's names of an ExposomeSet or ExposomePCA.

Usage

```
phenotypeNames(object)
```

Arguments

`object`	`ExposomeSet` that will be queried for the phenotype's names.

Value

The name of the phenotypes as a a character vector.

See Also

exposureNames to get the name of the exposures, familyNames to get the families of exposures

Examples

```
data("exposome")
phenotypeNames(expo)
```

`plot3PCA` *Ploting PCA in a 3D space*

Description

Methdo to draw a plot for samples using three PC contained in an ExposomePCA

Usage

```
plot3PCA(
  object,
  cmpX,
  cmpY,
  cmpZ,
  phenotype,
  main,
  angle = 35,
  pch = 16,
  legend = TRUE,
  plines = TRUE
)
```

Arguments

`object`	An onbject of class ExposomePCA
`cmpX`	Component to be placed at X axis
`cmpY`	Component to be placed at Y axis
`cmpZ`	Component to be placed at Z axis
`phenotype`	Used to color samples by phentoype
`main`	Title for the plot
`angle`	(default `35`) angle between x and y axis.
`pch`	(default `16`) plotting "character", i.e. symbol to use.
`legend`	(default `TRUE`) If `TRUE` shows the legend.
`plines`	(default `TRUE`) If `TRUE` it draws the lines from each dot to the base plane.

Value

A `list` with different graphics option from `scatterplot3d`.

See Also

pca to compite PCA on an ExposomeSet, plotPCA to plot the PCA, ExposomePCA as main class data("exposome") epca <- pca(expo[3:7, 1:100]) plot3PCA(epca, cmpX = 1, cmpY = 2, cmpZ = 3, phenotype = "sex")

`plotClassification` *Draw the profile of the levels exposures after a classification with a clustering method*

Description

Draw the profile of the levels exposures after a classification with a clustering method

Usage

```
plotClassification(object, type = "heatmap", ...)
```

Arguments

`object`	Object of class `Exposomeclust`
`type`	Two types are available: `"heatmap"` or `"valuemap"`.
`...`	NOT USED

Value

A `list` with different graphics parameters.

See Also

clustering as a constructor for ExposomeClust, classification to see how to obtain the classification of the samples from an ExposomeClust

Examples

```
## Not run:
data("eclust")
plotClassification(expo_c)

## End(Not run)
```

`plotCorrelation` *It draws both circos or matrix plot for the correlation in ExposomeCorr*

Description

While the circos plot can be used to see the general behaviours intra and extra families of exposures, the matrix plot allows for a detailed view of the correlations within an `ExposomeCorr` object.

Usage

```
plotCorrelation(object, type = "circos", ...)
```

Arguments

`object`	`ExposomeCorr` which correlations will be plotted.
`type`	(default `"circos"`) Can take both `"circos"` or `"matrix"`.
`...`	Arguments given to `corrplot` of package corrplot if a matrix is draw. Moreover extra arguments are can be passed to inner functions to draw both the matrix and the circos of correlations.

Value

A `list` with different graphics parameters.

See Also

correlation as a constructor for ExposomeCorr objects, pca to compute PCA on exposures

Examples

```
data("exposome")
expo.c <- correlation(expo)
plotCorrelation(expo.c, type="circos")
plotCorrelation(expo.c, type="matrix")
```

`plotEffect` *Function to draw a plot of the pvalues stored in an* `ExWAS` *object*

Description

This function draws a sort of manhattan plots using the p-value of the association of the exposures with phenotypes of an `ExWAS` object.

Usage

```
plotEffect(x, y, select, labels, xlab, ylab)
```

Arguments

`x`	An `ExWAS` object which effect will be ploted.
`y`	(optional) Another `ExWAS` object. If provded its effects will be ploted in Y-axis.
`select`	(optional) Character with exposures to be shown.
`labels`	(optional) Character vector with the labels for each exposure. It must be labeled vector.
`xlab`	(optional) Label for X-axis.
`ylab`	(optional) Label for Y-axis.

Value

An object of class `ggplot`.

See Also

exwas as a constructor for ExWAS objects, extract to obtain a table with the result of the ExWAS

Examples

```
data(exposome)
w1 <- exwas(expo[1:5, ], asthma~1, family = "binomial")
w2 <- exwas(expo[1:5, ], asthma~sex+age, family = "binomial")
plotEffect(w1, w2)
```

`plotEXP` *Plot correlation between exposures and PCA*

Description

Function used to plot the correlation between the exposures in an ExposomePCA and the values for each component of the PCA in the same ExposomePCA

Usage

```
plotEXP(object, exposure)
```

Arguments

`object`	An object of class ExposomePCA
`exposure`	(optional) to select a set of exposures to be ploted. If not given all are used.

Value

An object of class `ggplot`.

See Also

pca to compute PCA on an ExposomeSet, plotPHE to plot the P-Value of association between phenotypes ans PCA, ExposomePCA as main class

Examples

```
data("exposome")
epca <- pca(expo[3:7, 1:100])
plotEXP(epca)
```

`plotExwas` *Function to draw a plot of the pvalues stored in an* `ExWAS` *object*

Description

This function draws a sort of manhattan plots using the p-value of the association of the exposures with phenotypes of an `ExWAS` object.

Usage

```
plotExwas(
  object,
  ...,
  subtitles,
  color,
  exp.order,
  labels,
  show.effective = TRUE
)
```

Arguments

`object`	An `ExWAS` object which p-values will be plotted.
`...`	Other objects of class `ExWAS`.
`subtitles`	(optional) Characters used as "substitle" when more than one `ExWAS` is given.
`color`	(optional) Character vector of HTML colors, labeled with family's names. Used to colore the exposures.
`exp.order`	(optional) Character vector of exposures used to order and subset the plot.
`labels`	(optional) Character vector with the labels for each exposure. It must be labeled vector.
`show.effective`	(default `TRUE`) If set to `FALSE`, line showing effective test threshold is not shown.

Value

An object of class `ggplot`.

See Also

exwas as a constructor for ExWAS objects, extract to obtain a table with the result of the ExWAS

Examples

```
data(exposome)
w1 <- exwas(expo[1:5, ], asthma~1, family = "binomial")
plotExwas(w1)
```

`plotFamily` *It draws the profile of the exposome in an ExposomeSet*

Description

This function draw a profile of the full exposome into an ExposomeSet or the profile of the exposures in a specific family. For continuous families, box-plots are drawn; while for categorical families accumulative bar-charts.

Usage

```
plotFamily(x, family, group, group2, scatter = TRUE, na.omit = TRUE)
```

Arguments

`x`	ExposomeSet which exposome will be plotted.
`family`	Name of the familty that will be drawn. `'all'` is allowed to draw a grid with all the families.
`group`	If set it displays the family grouped by the given phenotype.
`group2`	If set it displays the family grouped by the given phenotype.
`scatter`	(default `TRUE`) If the family to be plotted is continuous, the samples will be shown.
`na.omit`	(default `TRUE`) Do not show `NA` values.

Value

A `ggplot` object if a family was selected. `invisible()` if argument `family` was set to `"all"`.

See Also

plotHistogram to draw the shape of an exposure, plotMissings to plot the missing data from an ExposomeSet

Examples

```
data("exposome")
plt <- plotFamily(expo, family = "Metals")
plt <- plt + ggplot2::ggtitle("Metals")
plt
plt <- plotFamily(expo, family = "Indoor air")
plt <- plt + ggplot2::ggtitle("Indoor air")
plt
```

`plotHistogram` *It draws a histogram for each exposure in an ExposomeSet*

Description

It draws a grid with an histogram per exposure in an ExposomeSet.

Usage

```
plotHistogram(x, select, density = TRUE, show.trans = FALSE)
```

Arguments

`x`	ExposomeSet which exposome will be plotted.
`select`	Name fo the exposure to be plotted. If missing, all exposures will be used.
`density`	(default `TRUE`) If `TRUE` a density plot is drawn overlapping the histogram.
`show.trans`	(default `FALSE`) If set to `TRUE` it will draw a panel of auxiliar plots with the continuous exposure transformed with `log` and `sqrt`.

Value

A `ggplot` object.

See Also

plotFamily to draw the profile of a family of exposures, plotMissings to plot the missing data from an ExposomeSet

Examples

```
data("exposome")
plotHistogram(expo[1:3, ], select = "ldde_lip")
```

`plotLOD` *It draws a chart with the percentage of under-LOD values in an ExposomeSet*

Description

This function can be used to draw the amount of under-LOD values in the exposures of an ExposomeSet.

Usage

```
plotLOD(object, lod.col = "LOD", x.max = 100, sort = TRUE)
```

Arguments

`object`	ExposomeSet which exposome will be plotted.
`lod.col`	(default `"LOD"`) Name of the column in `fData` containing the LOD thresholds.
`x.max`	(default `100`) Fix the maxium value of the X-axis.
`sort`	(default `TRUE`) If `TRUE` the chart will be ordered from the features with less missing data to the ones with more under-LOD values.

Value

A `ggplot` object.

See Also

plotFamily to draw the profile of a family of exposures, plotHistogram to draw the shape of an exposure, tableMissings to get a table with the missing data of an ExposomeSet, imputation to impute missing data on the exposures of an ExposomeSet

Examples

```
data("exposome")
# The included has no missing data
plotLOD(expo)
```

`plotMissings` *It draws a chart with the percentage of missing in an ExposomeSet*

Description

This function can be used to draw the number of missing data in exposures and in phenotypes of an ExposomeSet.

Usage

```
plotMissings(object, set, x.max = 100, sort = TRUE)
```

Arguments

`object`	ExposomeSet which exposome will be plotted.
`set`	Can be set to `"exposures"` or to `"phenotypes"`.
`x.max`	(default `100`) Fix the maxium value of the X-axis.
`sort`	(default `TRUE`) If `TRUE` the chart will be ordered from the features with less missing data to the ones with more missing data.

Value

A `ggplot` object.

See Also

plotFamily to draw the profile of a family of exposures, plotHistogram to draw the shape of an exposure, tableMissings to get a table with the missing data of an ExposomeSet, imputation to impute missing data on the exposures of an ExposomeSet

Examples

```
data("exposome")
# The included has no missing data
plotMissings(expo, set = "exposures")
plotMissings(expo, set = "phenotypes")
```

`plotPCA` *Ploting PCA*

Description

Methdo to draw a plot for PCA contained in an ExposomePCA

Usage

```
plotPCA(
  object,
  set,
  cmpX = 1,
  cmpY = 2,
  show.exposures = FALSE,
  show.samples = FALSE,
  phenotype
)
```

Arguments

`object`	An onbject of class ExposomePCA
`set`	Group (`"all"`, `"samples"` or `"exposures"`) taht will be ploted.
`cmpX`	(default: `1`) component to be placed at X axis
`cmpY`	(default: `2`) component to be placed at Y axis
`show.exposures`	(default: `FALSE`) If set to true, labels indicating the exposures are shown.
`show.samples`	(default: `FALSE`) If set to true, labels indicating the samples are shown.
`phenotype`	If `set` is set to `"samples"` can be used to color samples by phenotype

Value

An object of class `ggplot` or an object of class `gtable` if argument `set` was set to `"all"`.

See Also

pca to compite PCA on an ExposomeSet, plotPCA to plot the PCA, ExposomePCA as main class

Examples

```
data("exposome")
epca <- pca(expo[3:7, 1:100])
# A grid with exposures space, samples space and explained variance
plotPCA(epca, set = "all")
# Only exposures space
plotPCA(epca, set = "exposures") + ggplot2::theme(legend.position = "bottom")
# Only samples space
plotPCA(epca, set = "samples")
# Only samples space but coloured by phenotype
plotPCA(epca, set = "samples", phenotype = "sex") +
ggplot2::theme(legend.position = "bottom")
```

`plotPHE` *Plot association score between phentoypes and PCA*

Description

Function used to plot the association between the phentoypes in an ExposomePCA and the values for each component of the PCA in the same ExposomePCA

Usage

```
plotPHE(object, phenotype, exp2fac = 5)
```

Arguments

`object`	An object oc class ExposomePCA
`phenotype`	(optional) to select a set of phenotypes to be ploted. If not given all are used.
`exp2fac`	(default, 5) Threshold to considere a phentoype categorical (less or equal to) or continuous (more than).

Value

An object of class `ggplot`.

See Also

pca to compute PCA on an ExposomeSet, plotEXP to plot the correlation between exposures ans PCA, ExposomePCA as main class

Examples

```
data("exposome")
epca <- pca(expo[3:7, 1:100])
plotPHE(epca)
```

`plotVolcano` *Function to draw a plot of the pvalues stored in an `ExWAS` object*

Description

This function draws a sort of manhattan plots using the p-value of the association of the exposures with phenotypes of an `ExWAS` object.

Usage

```
plotVolcano(x, p.value = -log10(0.001), labels, show.effect = FALSE)
```

Arguments

`x`	An `ExWAS` object which effect will be ploted.
`p.value`	(default `"-log10(0.001)"`) Threshold for P-Value.
`labels`	(optional) Character vector with the labels for each exposure. It must be labeled vector.
`show.effect`	(default `FALSE`) Applyes an exponential transformation on the effects of the exposures.

Value

An object of class `ggplot`.

See Also

`exwas` as a constructor for `ExWAS` objects, `extract` to obtain a table with the result of the ExWAS, `plotEffect` to see or compare effects of one or two models.

`readExposome` *Creation of an ExposomeSet from files*

Description

Given the files that defines the exposome (measures of exposome, exposome description and individuals phentype) it loads them and creates an object of type ExposomeSet.

Usage

```
readExposome(
  exposures,
  description,
  phenotype,
  sep = ",",
  na.strings = c("NA", "-", "?", " ", ""),
  exposures.samCol = "sample",
  description.expCol = "exposure",
  description.famCol = "family",
```

```
    phenotype.samCol = "sample",
    exposures.asFactor = 5,
    warnings = TRUE
  )
```

Arguments

`exposures`	String with the path to the file with the matrix of exposures.
`description`	String with the path to the file with the description of the exposures (relation between exposures and exposure-family).
`phenotype`	String with the path to the file with the phenotypes of interest.
`sep`	(default `","`) Separator used by `read.table` to load the files "exposures", "description" and "phenotype".
`na.strings`	(default `c("NA", "-", "?", " ", "")`) Character defining the `NA` values in expsome's files.
`exposures.samCol`	(default `"sample"`) Index where the samples' name are found in file "exposures". It can be both charatcer or numeric.
`description.expCol`	(default `"exposure"`) Index where the exposures' name are found in file "description". It can be both numeric or character.
`description.famCol`	(default `"family"`) Index where the family's name (per exposures) if found in file "description". It can be both numeric or character.
`phenotype.samCol`	(default `"sample"`) Index where the sample's name are found in file "phenotype". It can be both numeric or character.
`exposures.asFactor`	(default `5`) The exposures with more than this number of unique items will be considered as "continuous" while the exposures with less or equal number of items will be considered as "factor".
`warnings`	(default `TRUE`) If `TRUE` shows useful information/warnings from the process of loading the exposome.

Details

The rows of the exposure's file, that corresponds to samples' names, must be the same than the phenotype's file. In the same way, the columns in exposure's file must be the same found as rows in description file.

Value

An object of class ExposomeSet.

Note

ExposomeSet's `fData` will contain some inner columns called `.std`, `.trn`, `.fct` and `.type` in order to trace the transformations an exposure suffers and to know, at eny moment, if an exposure is categorical or continuous. The "description" file can contains a column called `type` with values `"factor"` and `"numeric"` to speficy how an exposure needs to be understood. If given, this column will be renamed to `.type`. If not given, it will be created using `exposures.asFactor` value.

See Also

ExposomeSet for class description, loadExposome for constructor from loaded `data.frames`

Examples

```
## Locate the data-files
path <- file.path(path.package("rexposome"), "extdata")
description <- file.path(path, "description.csv")
phenotype <- file.path(path, "phenotypes.csv")
exposures <- file.path(path, "exposures.csv")

## Create ExposomeSet from files
exp <- readExposome(
  exposures = exposures,
  description = description,
  phenotype = phenotype,
  exposures.samCol = 1,
  description.expCol = 2,
  description.famCol = 1,
  phenotype.samCol = 1
)
```

`rexposome` *rexposome: Package for exposome exploration and outcome data analysis*

Description

#' @section exposures loading and exposures managment: `rexposome` offers two methods to bring exposome data to R and Bioconductor. `readExposome` allows to read three txt-like files (`.csv`, `.tsv`, ...) while `loadExposome` is sued with `matrix` and `data.frames`. The class obtained is an `ExposomeSet`, a class based in `eSet` for exposome data managment.

exposures processing

The packages offers a wide set of functions to preprocess exposome data. Method `trans` allow to transforms the exposures, method `normalityTest` allows to check for normality in exposome, `standardize` allows to standardize the exposures, among others. Finally, `impute` and `ilod` allow tu use `mice`, `Hmisc` and `imputeLCMD` for exposure missing data and exposure under-lod data imputation.

exposures analyses

the two methods `exwas` and `mexwas` allows to test the association between exposures and health outcomes (phenotpe data).

exposures plotting

The methods `plotFamily` allows to see how the exposures behaves within families. `plotCorrelation` helps to understand how exposures are related between themselves. `plotClassification` allos to visually detect cuslters of samples that share the same pattern of levels of exposures.

`standardize`	*#’ Summary of an ExposomeSet. #’ #’ Given an ExposomeSet is shows a summary for its exposures or #’ its phenotypes. #’ #’ @name Summary #’ @rdname Summary-methods #’ @aliases Summary #’ @param object codeExposomeSet with ’set’ will be summarized. #’ @param set Set to be sumarized (*`"exposures"` *or* `"phenotypes"`*). #’ @param select Subseting of exposures of phenotypes. #’ @return A basic description of the exposures in the* `ExposomeSet` *#’ @examples #’ data("exposome") #’ Summary(expo, set = "exposures") #’ @export Summary setGeneric("Summary", function(object, set=c("exposures", "phenotypes"), select) standardGeneric("Summary")) Standardize of an ExposomeSet.*

Description

Given an ExposomeSet it standardizes the exposures by using mean/sd if method is `"normal"` or by using median/mad if method is `"robust"`.

Usage

```
standardize(object, select, method = "normal", na.rm = TRUE, warnings = TRUE)
```

Arguments

`object`	`ExposomeSet` with exposures to be standardized.
`select`	Subseting of exposures of phenotypes.
`method`	(default `"normal"`) Character selecting the method to be applied (`"normal"` `"iqr"` or `"robust"`).
`na.rm`	(by default `TRUE`) Removes NA data to perform standardization.
`warnings`	(defaulr `TRUE`) If set to `FALSE` warnings are not shown.

Value

An `ExposomeSet` with the selected exposures standardized and keeping the others exposures as the original input object.

See Also

highAndLow to transform the continuous exposures to levelled factors, trans to transform the exposures

Examples

```
data("exposome")
exp.sn <- standardize(expo, method = "normal", select = "lbde100_lip")
exp.rs <- standardize(expo, method = "iqr", select = "lbde100_lip")
exp.rs <- standardize(expo, method = "robust", select = "lbde100_lip")
```

`tableLOD` *It creates a vector with the amount of under-LOD exposures in an ExposomeSet*

Description

This function can be used to obtain a table with the under-LOD data in exposures of an ExposomeSet.

Usage

```
tableLOD(object, output = "n", lod.col = "LOD", sort = TRUE)
```

Arguments

`object`	ExposomeSet which exposome will be plotted.
`output`	(default `"n"`) Can be `"n"` for number of values, and `"p"` for percentage.
`lod.col`	(default `"LOD"`) Name of the column in `fData` containing the LOD thresholds.
`sort`	(default `TRUE`) If `TRUE` the chart will be ordered from the features with less missing data to the ones with more under-LOD values.

Value

A numeric vector with number of udner-LOD values per exposure. The vector is labeled with the exposure's names.

See Also

plotFamily to draw the profile of a family of exposures, plotHistogram to draw the shape of an exposure, plotMissings to draw a plot with the missing data an ExposomeSet, imputation to impute missing data on the exposures of an ExposomeSet

Examples

```
data("exposome")
# The included has no missing data
tableLOD(expo, output = "n")
```

`tableMissings` *It creates a vector with the amount of missing in an ExposomeSet*

Description

This function can be used to obtain a table with the missing data in exposures and in phenotypes of an ExposomeSet.

Usage

```
tableMissings(object, set, output = "n", sort = TRUE)
```

Arguments

`object`	ExposomeSet which exposome will be plotted.
`set`	Can be set to `"exposures"` or to `"phenotypes"`.
`output`	(default `"n"`) Can be `"n"` for number of values, and `"p"` for percentage.
`sort`	(default `TRUE`) If `TRUE` the chart will be ordered from the features with less missing data to the ones with more missing data.

Value

A numeric vector with number of missing values per exposure. The vector is labeled with the exposure's names.

See Also

plotFamily to draw the profile of a family of exposures, plotHistogram to draw the shape of an exposure, plotMissings to draw a plot with the missing data an ExposomeSet, imputation to impute missing data on the exposures of an ExposomeSet

Examples

```
data("exposome")
# The included has no missing data
tableMissings(expo, set = "exposures")
tableMissings(expo, set = "phenotypes")
```

`tef` *Function to get the Threshold for effective tests (TEF)*

Description

Function to get the Threshold for effective tests (TEF)

Usage

```
tef(object)
```

Arguments

`object`	An `ExWAS` object

Value

A number indicating the efective threshold.

References

Evaluating the effective numbers of independent tests and significant p-value thresholds in commercial genotyping arrays and public imputation reference datasets. Miao-Xin Li, Juilian M. Y. Yeung, Stacey S. Cherny and Pak C. Sham. May 2012 Hum Genet.

See Also

exwas as a constructor for ExWAS objects

Examples

```
data(exposome)
w1 <- exwas(expo[1:5, ], asthma~1, family = "binomial")
w2 <- exwas(expo[1:5, ], asthma~sex+age, family = "binomial")
tef(w1)
tef(w2)
```

`toES` *Method to convert an imExposomeSet to an ExposomeSet*

Description

This methods allows to select an imputed-set and use it to create an `ExposomeSet` from an `imExposomeSet`.

Usage

```
toES(object, rid = 1)
```

Arguments

`object`	An object of class `imExposomeSet`
`rid`	(default `1`) Number of the imputation to be extracted

Value

An object of class `ExposomeSet`-

Examples

```
data("ex_imp")
toES(ex_imp, rid = 1)
```

`trans` *Function to apply a transformation to the exposures of an ExposomeSet*

Description

The exposures in an ExposomeSet can be transformed using this function. `transform` apples a function `fun` to the selected exposures.

Usage

```
trans(object, fun, select, by.exposure = FALSE, ...)
```

Arguments

`object`	`ExposomeSet` which exposures will be transformed.
`fun`	Function to be applied on the exposures.
`select`	If not set, receive the name of all exposures. It can takes a character vector to select specific exposures.
`by.exposure`	(default `FALSE`) If `TRUE` applies `fun` to each exposure (given as a vector). If `FALSE` the matrix of exposures is fiven to `fun`.
`...`	Argument given to `fun`.

Value

A new `ExposomeSet` with selected exposures transformed with `fun`.

See Also

highAndLow to transform the continuous exposures to levelled factors, standardize to standardize by normal or robust methods the exposures

Examples

```
data("exposome")
exp.t <- trans(expo, fun = log, select = "ldde_lip")
```

`volcano_plot` *Function to draw a Volcano Plot*

Description

Function that takes two numeric vectors (P-Value and fold change) and draws a volcano plot using ggplot2

Usage

```
volcano_plot(
  pval,
  fc,
  names,
  size = 2,
  tFC = 2,
  tPV = -log10(0.001),
  show.effect = FALSE
)
```

Arguments

`pval`	numeric vector of P.Values
`fc`	numeric vector of fold change
`names`	character vector with the feature's names.
`size`	(default 2) Sice of the labels in case they are placed.

`tFC`	(default `2`) fold change threshold. It can be set to `NULL` to do not filter.
`tPV`	(default `-log10(0.001)`) P-Value threshold. It can be set to `NULL` to not filter.
`show.effect`	(default `FALSE`) If set to `TRUE`, the X-axis will should `2^logFC` instead to teh default `logFC`.

Value

A `ggplot` object

Examples

```
data(exposome)
w1 <- extract(exwas(expo[1:20, ], asthma~1, family = "binomial"))
volcano_plot(w1$pvalue, w1$effect, rownames(w1))
```

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