

# Package ‘rexposome’

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---

<code>classification</code>	<i>Method to get the classification of the samples from an <code>ExposomeClust</code>.</i>
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---

### 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 directly 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](#), [plot-Classification](#) to plot the groups

**Examples**

```

data("exosome")

# 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: Clustering with flexmix
library(flexmix)
# First we create 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 $classification

# 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 <i>for testing purposes</i>
------	---

---

**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 <i>ExposomeSet</i> .
-------	---

---

### 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 <i>ExposomeClust</i>
---------------	----------------------------

---

### 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 <a href="#">ExposomeClust</a>
type	(default "heatmap") Type of plot.

**Value**

An object of class ExposomeClust

**Methods (by generic)**

- plot: Wrapper for plotClassification method.
- classification: Return classe assigned to each sample
- plotClassification: Draws a heatmap for the samples' classification.
- sampleNames: 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 continuous 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 <a href="#">ExposomeCorr</a>
y	NOT USED
...	Arguments passed to corplot when type="matrix".
object	An <a href="#">ExposomeCorr</a> object.
sort	NOT USED
type	To choose between "circos" and "matrix".

**Value**

An object of class `ExposomeCorr`

**Methods (by generic)**

- `plot`: Wrapper for `plotClassification` method.
- `dim`: Return the dimension of the internat matrix of correlation.
- `extract`: Return the raw correlation matrix
- `plotCorrelation`: 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 containing 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 <a href="#">ExposomePCA</a> 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: Wrapper for plotPCA method.
- exposureNames: Getter to obtain the exposures's names.
- extract: Method to extract the raw results of the PCA.
- ndim: Number of principal components in an ExposomePCA.

- phenotypeNames: Getter to obtain the phenotype's names.
- plot3PCA: Method to draw a 3D plot for PCA
- plotEXP: Plot correlation between exposures and PCA
- plotPCA: Method to draw a 2D plot for PCA
- plotPHE: Plot association score between phenotypes 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
)

## 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 <a href="#">ExposomeSet</a> object.
y	NOT USED
...	Arguments to be passed to <code>imputeFAMD</code>
object	An <a href="#">ExposomeSet</a> object.
method	Method to be used.
cmethod	Function implementing a systems to retrieve classification from clustering output
warnings	If set to TRUE it prints the warning messages.
formula	Formula, not including exposures, to be tested. No need to provide response (left term)
filter	Expression to be used to filter <a href="#">ExposomeSet</a>
family	Family describing 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 it returns the family which each exposure belongs
ngroups	Number of intervals to be used
intervals	If "standard" all levels are kept, if "extreme" intermediate levels are set to NA.
select	Vector selecting the exposures 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 <code>mice</code> 's function will be displayed.
phenotype	Health outcome to be used as dependent variable.
exposure	Vector of exposures to be used.
th	Threshold of P-Value used to consider normality
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 density plot is drawn 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	Can take values "exposures" or "phenotypes".
output	Can take values "n" (count) or "p" (percentage)
fun	Function to be used in the transformation process

**Value**

An object of class `ExposomeSet`

**Methods (by generic)**

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



- **Summary:** Summary of both continuous and categorical exposures
- **tableLOD:** Returns a vector with the number of under-LOD values per exposure.
- **tableMissings:** Returns a vector with the number of missing values per exposure.
- **trans:** 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	<i>Getter to obtain the exposures's names of an ExposomeSet or ExposomePCA</i>
---------------	--

---

### 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 <i>for testing purposes</i>
--------	---

---

**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	<i>Raw data from ExWAS, ExposomeClust and ExposomeCorr.</i>
---------	---

---

**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'
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 <a href="#">ExWAS</a> object
y	An <a href="#">ExWAS</a> object
...	NOT USED
object	An object of class <code>ExWAS</code> , <code>mExWAS</code> or <code>n1ExWAS</code> .
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 <code>ExWAS</code> .
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 $-\log_{10}(0.001)$ ) Is the threshold from where the exposures can be taken as significant.
show.effect	(default false) Apply exp to obtained beta.

**Value**

An object of class `ExWAS`

**Methods (by generic)**

- `plot`: Wrapper for `plotExwas` method.
- `extract`: Method to obtain the matrix of association scores
- `names`: Method to obtain the Threshold for effective tests (TEF)
- `plotEffect`: Draws a plot with the confidence interval of each exposure. Allows to compare two `ExWAS` instances.
- `plotExwas`: Method to plot a manhatan plot for association between exposures and phenotypes
- `plotVolcano`: Method to plot a volcano plot for association between exposures and phenotypes
- `tef`: 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	<i>Testing the association between an exposure and a phenotype of an ExposomeSet</i>
-------	--

---

**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
)
```

**Arguments**

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

---

**Description**

imExposomeSet created from the raw data included in the package. The creation process is illustrated 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	<i>Getter to obtain the exposures's names of an ExposomeSet.</i>
-------------	--

---

### 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)
```

---

highAndLow	<i>Function to convert continuous exposures to categorical exposures</i>
------------	--

---

### 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 extremes (aka. lowes and highest) are discarded and their values set to NA.

**Usage**

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

**Arguments**

object	An object of class <code>ExposomeSet</code> .
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 <code>ExposomeSet</code> . 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 phenotypes
#      104      1200          4
dim(expo)
# exposures  samples phenotypes
#      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

<code>object</code>	ExposomeSet which exposures will be imputed.
<code>seed</code>	(default 1234) Seed to make the imputation reproducible.
<code>lod.col</code>	(default "LOD") Name of the column in <code>fData</code> with the threshold of the LOD.
<code>pNA</code>	(default 0.2) Maximum percentage allowed of values under LOD
<code>tLog</code>	(default FALSE) If set to TRUE it transforms all the exposures to lod before the imputation.
<code>method</code>	(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").
<code>warnings</code>	(default TRUE) If set to FALSE warnings will not be displayed.
<code>...</code>	Arguments passed to <code>impute.QRILC</code> or <code>impute.MinProb</code> from <code>imputeLCMD</code> .

### 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 particularity 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
)

## 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 <a href="#">imExposomeSet</a> object.
y	NOT USED
...	Other used arguments
object	An object of class <a href="#">imExposomeSet</a>
rid	Number of the imputation to be extracted
formula	Formula, not including exposures, to be tested.
filter	Expression to be used to filter <a href="#">ExposomeSet</a>
family	Family describing 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 progression.
by.exposure	If set to TRUE it 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 corresponding 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`: Wrapper for `plotFamily` method.
- `dim`: Returns the number of exsures, samples and phenotypes.
- `expos`: Returns a `data.frame` with exposures.
- `exposureNames`: Method to obtain samples' names
- `extract`: Method to extract exposures for a single imputation
- `exwas`: Performs an EXposome-Wide Association Study
- `familyNames`: Getter to obtain the families's names of the family of each exposure.
- `phenotypeNames`: Getter to obtain the families's names of the family of each exposure.
- `plotFamily`: Draws a boxplot or accumulated-bar plot for each exposure in the all imputed sets.
- `sampleNames`: Method to obtain samples' names
- `[[]`: Get an `ExposomeSet` with the selected imputation
- `[`: Subset an `imExposomeSet`
- `toES`: 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	<i>Function to impute missing values from an ExposomeSet</i>
------------	--

---

### 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

<code>object</code>	ExposomeSet which exposures will be imputed.
<code>select</code>	Exposures to be imputed. If missing, all exposes will be imputed.
<code>...</code>	Argument given to function <code>mice</code> of package <code>mice</code> ( <code>printFlag</code> is set from <code>messages</code> ).
<code>messages</code>	(default FALSE) If set to TRUE messages from <code>mice</code> '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

<code>x</code>	data.frame containing the exposures as columns and the samples as rows.
<code>lod</code>	vector containing the
<code>description</code>	1 means values under LOD while 2 means quantifiable value, 3
<code>pNA</code>	(default: 0.2) maximum percentage of allowed missing data
<code>pLOD</code>	(default: 0) minimum percentave of values under LOD
<code>log</code>	(default: NA) log transformation to normalize data
<code>seed</code>	(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	<i>Testing the association between an exposure and a phenotype of an ExposomeSet (modelling the exposures as response)</i>
----------	--

---

## 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 threshold 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	<i>Creation of an ExposomeSet from data.frames</i>
--------------	--

---

### Description

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

### Usage

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

### Arguments

<code>exposures</code>	<code>data.frame</code> of exposures.
<code>description</code>	<code>data.frame</code> with the description of the exposures (relation between exposures and exposure-family).
<code>phenotype</code>	<code>data.frame</code> with the phenotypes of interest.
<code>description.famCol</code>	(default "family") Index where the family's name (per exposures) is found in file "description". It can be both numeric or character.
<code>exposures.asFactor</code>	(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".
<code>warnings</code>	(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 any moment, if an exposure is categorical or continuous. The "description" file can contains a column called `type` with values "factor" and "numeric" to specify 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 <code>read.table</code> 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: <code>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"))</code> . 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	<i>Creation of an imExposomeSet from data.frames</i>
-------------	--

---

### 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

<code>data</code>	The <code>data.frame</code> of both exposures and phenotypes obtained from mice.
<code>description</code>	<code>data.frame</code> with the description of the exposures (relation between exposures and exposure-family).
<code>description.famCol</code>	(default "family") Index where the family's name (per exposures) if found in file "description". It can be both numeric or character.
<code>description.expCol</code>	(default "exposures") Index where the exposure's name if found in file "description". It can be both numeric or character.
<code>exposures.asFactor</code>	(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".
<code>warnings</code>	(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 phenotypes.

### Value

An object of class `imExposomeSet`.

**See Also**

[imExposomeSet](#) for class description

**Examples**

```
data("me") # me is an imputed matrix of exposure and phenotypes
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	<i>data.frame for testing purposes</i>
----	--

---

**Description**

data.frame created with mice used to test and illustrate 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	<i>Class mExWAS</i>
--------	---------------------

---

### 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

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

**Value**

An object of class `mExWAS`

**Methods (by generic)**

- `plot`: Wrapper for `plotExwas` method.
- `extract`: Method to obtain the generated model
- `plotExwas`: Method to plot a heap-map with the coefficient of each exposure

**Slots**

`result` klist with the fitted model and result.

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

`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 approach.*

---

**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**

<code>object</code>	ExposomeSet that will be used for the ExWAS.
<code>phenotype</code>	Target phenotype used for the study. If missing all the phenotypes in the <a href="#">ExposomeSet</a> will be used.
<code>family</code>	It must describe the nature of the outcome. Can take values "gaussian", "binomial", "poisson", "multinomial", "cox" or "mgaussian".
<code>warnings</code>	(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	<i>Number of principal components in an ExposomePCA.</i>
------	--

---

**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	<i>It creates a data.frame of boolean indicating if the exposures follows a normal distribution or not.</i>
---------------	---

---

### 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	<a href="#">ExposomeSet</a> 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 returns 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 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

*Plotting PCA in a 3D space*

---

**Description**

Method 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 object 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 phenotype  
 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 compute 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	<i>Draw the profile of the levels exposures after a classification with a clustering method</i>
--------------------	---

---

**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	<i>It draws both circos or matrix plot for the correlation in ExposomeCorr</i>
-----------------	--

---

### 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 <a href="#">corrplot</a> 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	<i>Function to draw a plot of the pvalues stored in an ExWAS object</i>
------------	---

---

### 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 plotted.
y	(optional) Another ExWAS object. If provided its effects will be plotted 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 <a href="#">ExposomePCA</a>
exposure	(optional) to select a set of exposures to be plotted. 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 and 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 "subtitle" 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	<a href="#">ExposomeSet</a> which exposome will be plotted.
family	Name of the family 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	<a href="#">ExposomeSet</a> 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	<i>It draws a chart with the percentage of under-LOD values in an <a href="#">ExposomeSet</a></i>
---------	---

---

### 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	<a href="#">ExposomeSet</a> 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 maximum 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	<i>It draws a chart with the percentage of missing in an ExposomeSet</i>
--------------	--

---

### 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	<a href="#">ExposomeSet</a> which exposome will be plotted.
set	Can be set to "exposures" or to "phenotypes".
x.max	(default 100) Fix the maximum 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	<i>Ploting PCA</i>
---------	--------------------

---

## Description

Method 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 object of class <a href="#">ExposomePCA</a>
set	Group ("all", "samples" or "exposures") that will be plotted.
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 compute 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 phenotypes and PCA*

---

## Description

Function used to plot the association between the phenotypes 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 of class <a href="#">ExposomePCA</a>
phenotype	(optional) to select a set of phenotypes to be plotted. If not given all are used.
exp2fac	(default, 5) Threshold to consider a phenotype 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 and PCA, [ExposomePCA](#) as main class

## Examples

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

---

plotVolcano	<i>Function to draw a plot of the pvalues stored in an ExWAS object</i>
-------------	---

---

### 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 plotted.
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) Applies 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	<i>Creation of an ExposomeSet from files</i>
--------------	--

---

### Description

Given the files that defines the exposome (measures of exposome, exposome description and individuals phenotype) 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 <a href="#">read.table</a> to load the files "exposures", "description" and "phenotype".
na.strings	(default c("NA", "-", "?", " ", "")) Character defining the NA values in exposure'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 any moment, if an exposure is categorical or continuous. The "description" file can contains a column called `type` with values "factor" and "numeric" to specify 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 management: 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 management.

### 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 it
                  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 Subsetting 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

<code>object</code>	ExposomeSet with exposures to be standardized.
<code>select</code>	Subsetting of exposures of phenotypes.
<code>method</code>	(default "normal") Character selecting the method to be applied ("normal" "iqr" or "robust").
<code>na.rm</code>	(by default TRUE) Removes NA data to perform standardization.
<code>warnings</code>	(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	<i>It creates a vector with the amount of under-LOD exposures in an <code>ExposomeSet</code></i>
----------	--

---

**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	<a href="#">ExposomeSet</a> 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 <code>fData</code> 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 under-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	<i>It creates a vector with the amount of missing in an ExposomeSet</i>
---------------	---

---

## 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	<a href="#">ExposomeSet</a> 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	<i>Function to get the Threshold for effective tests (TEF)</i>
-----	--

---

### 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	<i>Method to convert an imExposomeSet to an ExposomeSet</i>
------	---

---

### 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 <code>imExposomeSet</code>
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	<i>Function to apply a transformation to the exposures of an Exposome-Set</i>
-------	---

---

### Description

The exposures in an [ExposomeSet](#) can be transformed using this function. `transform` applies a function `fun` to the selected exposures.

### Usage

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

### Arguments

object	<a href="#">ExposomeSet</a> 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 <code>fun</code> to each exposure (given as a vector ). If FALSE the matrix of exposures is fiven to <code>fun</code> .
...	Argument given to <code>fun</code> .

**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) Size 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 $-\log_{10}(0.001)$ ) 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 $2^{\log_{2}FC}$ instead to the default $\log_{2}FC$ .

**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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