# Package 'omicRexposome'

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**Title** Exposome and omic data associatin and integration analysis

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**Description** omicRexposome systematizes the association evaluation between exposures and omic data, taking advantage of MultiDataSet for coordinated data management, rexposome for exposome data definition and limma for association testing. Also to perform data integration mixing exposome and omic data using multi co-inherent analysis (omicade4) and multi-canonical correlation analysis (PMA).

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---

`add_cls` *Method to add an ExposomeClust to a MultiDataSet*

---

## Description

This method allows to insert an object of class ExposomeClust as an independent dataset into an object of class MultiDataSet.

## Usage

```
add_cls(object, clsSet, ...)

## S4 method for signature 'MultiDataSet,ExposomeClust'
add_cls(object, clsSet, ...)
```

## Arguments

| | |
|---|---|
| `object` | An object of class MultiDataSet. |
| `clsSet` | An object of class ExposomeClust. |
| `...` | Arguments given to add_eset from MultiDataSet. |

## Value

A MultiDataSet with the ExpressionSet added as an independent dataset.

## Examples

```
data("eclust", package = "rexposome")
library(MultiDataSet)
md <- new("MultiDataSet")
names(md)
md <- add_cls(md, expo_c)
names(md)
```

---

add_exp *Method to add an ExposomeSet to a MultiDataSet*

---

## Description

This method allows to insert an object of class ExposomeSet as an independent dataset into an object of class MultiDataSet.

## Usage

```
add_exp(object, expoSet, warnings = TRUE, ...)

## S4 method for signature 'MultiDataSet,ExposomeSet'
add_exp(object, expoSet, warnings = TRUE,
  ...)
```

## Arguments

| | |
|---|---|
| object | An object of class MultiDataSet. |
| expoSet | An object of class ExposomeSet. |
| warnings | (default TRUE) If set to FALSE warnings will not be displayed. |
| ... | Arguments given to add_eset from MultiDataSet. |

## Value

A MultiDataSet with the ExpressionSet added as an independent dataset.

## Examples

```
data("exposome", package = "rexposome")
library(MultiDataSet)
md <- new("MultiDataSet")
names(md)
md <- add_exp(md, expo)
names(md)
```

## asr — ResultSet *for testing and illustration purpouses*

### Description

ResultSet created using association method, testing proteome association to exposome ("mds"), adjusted by sex and age.

### Usage

```
data("asr")
```

### Format

An object of class ResultSet of length 15.

### Value

A ResultSet object.

### Examples

```
data("asr", package = "omicRexposome")
asr
```

## association — # ——— *Method to perform an association study between transcriptome and exposom*

### Description

This function allows to perform an association study between gene expression from microarray and the exposome. An ExpresionSet is the object storing the gene expresion and an ExposomeSet the one storing the exposome. Both of them needs to be encapsulated in a MultiDataSet. The association study is perform through standard limma pipeline. The function allows to perform multiple tests using the argument exposures.

### Usage

```
association(object, formula, expset, omicset, set = "exposures",
  method = "ls", ..., baselevels, sva = "none", vfilter = NULL,
  verbose = FALSE, warnings = TRUE)

## S4 method for signature 'MultiDataSet'
association(object, formula, expset, omicset,
  set = "exposures", method = "ls", ..., baselevels, sva = "none",
  vfilter = NULL, verbose = FALSE, warnings = TRUE)
```

## Arguments

| | |
|---|---|
| object | A MultiDataSet object containing at last one omic data-sets like ExpressionSet, MethylationSet... and, at last, one ExposomeSet. |
| formula | formula to be evaluated by each exposure (or phenotype, see set argument). It should not contain any exposures (or phenotype), it will be added automatically when evaluated. |
| expset | Name of the ExposomeSet in object. |
| omicset | Name of the omic data-set in object. |
| set | (default "exposures") Can take value "exposures" to test the association of the exposures in the ExposomeSet vs. the features in the omic data-set. If takes "phenotypes" all phenotypes in ExposomeSet are tested. |
| method | (default "lm") Check limma help pages. |
| ... | Arguments passed to limma's lmFit. |
| baselevels | (optional) If set, must be a labeled vector with the default base level for categorical exposures. |
| sva | (default "none"). This argument can take value "none" to do not apply SVA. Value "fast" will run SVA using isva and SmartSVA. Value "slow" will run SVA using sva. |
| vfilter | (default NULL). Only used when sva = "slow". Numeric number of probes used in sva. Recomended ~10% of real probes. |
| verbose | (default FALSE) If set to TRUE, a series of messages descriving the process are shown. |
| warnings | (default TRUE) If set to TRUE, a series of warnings are shown when required user atention. |

## Value

An object of class ResultSet.

## Examples

```
library(MultiDataSet)
data(brge_prot, package = "brgedata")
data(brge_expo, package = "brgedata")
mds <- createMultiDataSet()
mds <- add_eset(mds, brge_prot, dataset.type = "proteines")
mds <- add_eset(mds, brge_expo, dataset.type = "exposures", GRanges = NA)

asr <- association(mds, formula = Asthma ~ Sex + Age,
  expset = "exposures", omicset = "proteines")
asr
```

crossomics *Function to perform a Transcriptome-Wide Association Study*

## Description

This function allows to perform a Transcriptome-Wide Association Study by using an ExposmeSet and an ExpressionSet. It allows to perform an adjustment using Surrogate Variable Analysis (from R package sva).

## Usage

```
crossomics(object, method = "mcca", ncomponents = 2, ..., na.rm = FALSE,
  permute = c(100, 3), verbose = FALSE, warnings = TRUE)

## S4 method for signature 'MultiDataSet'
crossomics(object, method = "mcca",
  ncomponents = 2, ..., na.rm = FALSE, permute = c(100, 3),
  verbose = FALSE, warnings = TRUE)
```

## Arguments

| | |
|---|---|
| object | A MultiDataSet object containing at last two data-sets like ExposomeSet, ExpressionSet, MethylationSet... |
| method | (default "mcca") It can takes values "mcca" for Multiple Canonical Correlation Analysis or "mcia" for Multiple Co-Inertia Analysis. |
| ncomponents | (default 2) Number of components to be estimated. |
| ... | Other arguments given to mcia (from omicade4) or to MultiCCA (from PMA). |
| na.rm | (default FALSE) If method was set to "mcca" and na.rm was set to TRUE, features containing missing values are removed. |
| permute | (default c(100, 3)). If method="mcca" and this agument is set to NULL no permutation test to tune-up the parameters for MultiCCA. When filles, permute[1] corresponds to the number permutations (default in MultiCCa.permute is 25) and permute[2] the number of iterations (default in MultiCCA.permute is 3). |
| verbose | (default FALSE) If set to TRUE, a series of messages descriving the process are shown. |
| warnings | (default TRUE) If set to TRUE, a series of warnings are shown when required user atention. |

## Value

An object of class ResultSet.

## Examples

```
library(MultiDataSet)
library(rexposome)
data(brge_prot, package = "brgedata")
data(brge_expo, package = "brgedata")
mds <- createMultiDataSet()
mds <- add_eset(mds, brge_prot, dataset.type = "proteines")
```

```
mds <- add_eset(mds, imputation(brge_expo),
    dataset.type = "exposures", GRanges = NA)

crs <- crossomics(mds, method = "mcia")
crs
```

---

`crs` `ResultSet` *for testing and illustration purpouses*

---

## Description

`ResultSet` created using `crossomics` method, selecting `"mcia"` method. Result from the integration of proteome and exposome data (`"mds"`).

## Usage

```
data("crs")
```

## Format

An object of class `ResultSet` of length 1.

## Value

A `ResultSet` object.

## Examples

```
data("crs", package = "omicRexposome")
crs
```

---

`getIntegration` *Method to extrat integration-feature result from a ResultSet*

---

## Description

Homologous methods from `MultiDataSet` (`getAssociation`) but for `ResultsSet` created by `crossomics`. It Resturns a `data.frame` with the result from `mcia` (`omicade4`) or from `MultiCCA` (`PMA`).

## Usage

```
getIntegration(object, ...)

## S4 method for signature 'ResultSet'
getIntegration(object, ...)
```

## Arguments

| | |
|---|---|
| `object` | An object of class ResultSet obtained from |
| `...` | NOT USED |

## Value

A `data.frame`

## Examples

```
data("crs", package = "omicRexposome")
class(getIntegration(crs))
```

---

`mds` `MultiDataSet` *for testing and illustration purpouses*

---

## Description

`MultiDataSet` containing both proteome data-set and exposome data-set.

## Usage

```
data("mds")
```

## Format

An object of class `MultiDataSet` of length 2.

## Value

A `MultiDataSet` object.

## Examples

```
data("mds", package = "omicRexposome")
mds
```

---

`omicRexposome` *omicRexposome: Package for exposome and omic data associatin and integration*

---

## Description

omicRexposome: Package for exposome and omic data associatin and integration

### exposome-omic data association study

The packages offers the function `association` that allows to perform an association study using transcriptome, methylome, etc. as dependent variable and exposome data as independent variable. The function relies on `limma` pipeline and generates an object of class `ResultSet`, that can be ploted using `plotAssociation`.

### exposome-omic data integration study

The packages offers the function `crossomics` that allows to perform two types of integration study: Multi Canonical Correlation Analysis and Multi Co-Inertia Analysis. The function allos to use any type and number of datasets (aka. exposome transcriptome, methylome, etc.). The function generates an object of class `ResultSet`, that can be ploted using `plotIntegration`.

plotAssociation *Function to draw de result of an association study*

## Description

This function draws two type of plots for the ResultSet from association functions

## Usage

```
plotAssociation(object, rid = 1, coef = 2, contrast = 1,
  type = c("manhattan", "qq", "volcano"), tPV = NULL, tFC = NULL,
  show.effect = FALSE)

## S4 method for signature 'ResultSet'
plotAssociation(object, rid = 1, coef = 2,
  contrast = NULL, type = c("manhattan", "qq", "volcano"), tPV = NULL,
  tFC = NULL, show.effect = FALSE)
```

## Arguments

| | |
|---|---|
| object | An object of class ResultSet obtained from assoc_* functions. |
| rid | (default 1) Index or name of the test to be plotted. |
| coef | (default 2) Index of the coefficient to be extracted. |
| contrast | (default 1) When code corresponds to a multicategorical variable, contasr selects the comparison. |
| type | Can take "volcano", "qq", "manhattan" and "protein". "protein" lot is a type of Manhattan plot designed for protein association analysis. |
| tPV | (optional) Threshold for P.Value when type="volcano". |
| tFC | (optional) Threshold for Fold Change or Effect when type="volcano". |
| show.effect | (default FALSE) If set to TRUE, when type="volcano" the X-axis will show 2^logFC instead of logFC. |

## Value

A ggplot2 object

## See Also

plotIntegration for plotting integration results. association to create a ResultSet to be passed to this function.

## Examples

```
data("asr", package = "omicRexposome")
plotAssociation(asr, type = "qq")
plotAssociation(asr, type = "volcano")
```

## plotHits *Plot number of hits per result in ResultSet*

### Description

This method draws a barplot with the number of hits in each result stored in the given ResultSet.

### Usage

```
plotHits(object, th = 0.05, width = 0.75)

## S4 method for signature 'ResultSet'
plotHits(object, th = 0.05, width = 0.75)
```

### Arguments

| | |
|---|---|
| object | An object of class ResultSet |
| th | (default 0.05) Threshold (p-value) to considere a result as a hit. |
| width | (default 0.70) width of the bar |

### Value

A ggplot2 object

### See Also

plotLambda for a graphical representation of the lambda score per analysys, tableLambda for the lambda score per analysys, tableHits for the hists per analysys

### Examples

```
data(asr, package = "omicRexposome")
plotHits(asr)
```

## plotIntegration *Function to draw de result of an integration study*

### Description

This function draws a plots for the ResultSet from integration function

### Usage

```
plotIntegration(object, cmpX = 1, cmpY = 2, lb.th = 0.2,
  legend.show = TRUE, colors, ...)

## S4 method for signature 'ResultSet'
plotIntegration(object, cmpX = 1, cmpY = 2,
  lb.th = 0.2, legend.show = TRUE, colors, ...)
```

### Arguments

| | |
|---|---|
| object | An object of class ResultSet obtained from crossomics. |
| cmpX | (default 1) Value of the X-axis when ploting rsults from mcia. |
| cmpY | (default 2) Value of the Y-axis when ploting rsults from mcia. |
| lb.th | (default 0.20) Threshold to place labels on radar chart drawn when ploting results from MultiCCA. |
| legend.show | (default TRUE) If set to FALSE, right legend of radar plot is hidden when ploting results from MultiCCA. |
| colors | (optional) Names vector with the colors sued to draw each dataset. Used when ploting results from MultiCCA. If missing, random colores are chosen. |
| ... | Optional arguments are given to plot from omicade4 pacage (argument axes is filled with values from cmpX and cmpY). |

### Value

A ggplot2 object

### See Also

plotAssociation for plotting association results. crossomics to create a ResultSet to be passed to this function.

### Examples

```
data("crs", package = "omicRexposome")
plotIntegration(crs)
```

---

## plotLambda *Plot lambda score for all results in a ResultSet*

---

### Description

This method draws a baplor with the lambda score of each result in the given ResultSet.

### Usage

```
plotLambda(object, width = 0.75)

## S4 method for signature 'ResultSet'
plotLambda(object, width = 0.75)
```

### Arguments

| | |
|---|---|
| object | An object of class ResultSet |
| width | (default 0.70) width of the bar |

### Value

A ggplot2 object

## See Also

plotHits for a graphical representation of the hits per analysys, tableLambda for the lambda score per analysys, tableHits for the hists per analysys

## Examples

```
data("asr", package = "omicRexposome")
plotLambda(asr)
```

---

snpToContinuous *Transforms the discrete genotype from a* snpSet *to a* matrix *of a continuous variable.*

---

## Description

The function converts the categorical variable of SNPs to a continuous variable by normalizing each SNP as described in Abraham G. and Inouye M. 2014 (DOI: 10.1371/journal.pone.0093766).

## Usage

```
snpToContinuous(snpSet, verbose = FALSE)
```

## Arguments

| | |
|---|---|
| snpSet | An object of class snpSet with set calls slot . |
| verbose | If set to TRUE, messages will be shown. |

## Value

An matrix of the calls of the SNPs converted to a continuous variable.

## See Also

crossomics use this function

---

tableHits *Counts the number of hits on the results stored in a ResultSet*

---

## Description

Given a threshold it counts the number of hits in each result in the given ResultSet.

## Usage

```
tableHits(object, th = 0.05)

## S4 method for signature 'ResultSet'
tableHits(object, th = 0.05)
```

### Arguments

| | |
|---|---|
| object | An object of class ResultSet |
| th | (default 0.05) Threshold (p-value) to considere a result as a hit. |

### Value

A labeled numeric vector with the exposures and the number of hits.

### See Also

tableLambda for the lambda score per analysys, plotLambda for a graphical representation of the lambda score per analysys, plotHits for a graphical representation of the hists per analysys

### Examples

```
data("asr", package = "omicRexposome")
tableHits(asr)
```

---

## tableLambda *Compute a lambda score on the results stored in a ResultSet*

---

### Description

Compute lambda score on each result in the given ResultSet by using lambdaClayton.

### Usage

```
tableLambda(object, trim = 0.5)

## S4 method for signature 'ResultSet'
tableLambda(object, trim = 0.5)
```

### Arguments

| | |
|---|---|
| object | An object of class ResultSet |
| trim | (default 0.5) percentage of right omited values for lambdaClayton. |

### Value

Returns a data.frame having the exposures and the computed lambda score.

A labeled numeric vector with the lambda score for each exposure.

### See Also

tableHits for the number of hits per analysys, plotHits for a graphical representation of the hists per analysys, plotLambda for a graphical representation of the lambda score per analysys

### Examples

```
data("asr", package = "omicRexposome")
tableLambda(asr)
```

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