Package ‘omicRexposome’

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Title Exposome and omic data association and integration analysis
Version 1.26.0
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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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Contents

add_cls ..................................................... 2
add_exp ..................................................... 3
asr ......................................................... 4
association ............................................... 4
crossomics ................................................ 6
crs .......................................................... 7
getIntegration ............................................ 8
mds .......................................................... 8
omicRexposome ......................................... 9
plotAssociation .......................................... 9
plotHits ..................................................... 10
plotIntegration .......................................... 11
plotLambda ................................................ 12
snpToContinuous ........................................ 13
tableHits ................................................... 13
tableLambda ............................................... 14

Index 15

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 'MultiData,ExposomeClust'
add_cls(object, clsSet, ...)

Arguments

  object     An object of class MultiData.
  clsSet     An object of class ExposomeClust.
  ...        Arguments given to add_eset from MultiData.

Value

A MultiData with the ExpressionSet added as an independent dataset.
add_exp

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)
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 = "omicReposome")
asr

```
association  # -------------------------------------------------- Method to perform an association study between transcriptome and exposome
```

Description

This function allows to perform an association study between gene expression from microarray and the exposome. An `ExpressionSet` is the object storing the gene expression 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 describing the process are shown.

warnings (default TRUE) If set to TRUE, a series of warnings are shown when required user attention.

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**

```r
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 least 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 argument is set to NULL no permutation test to tune-up the parameters for MultiCCA. When files, 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 describing the process are shown.
- `warnings` (default TRUE) If set to TRUE, a series of warnings are shown when required user attention.

**Value**

An object of class `ResultSet`. 
Examples

```r
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
```

Description

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

Usage

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

Format

An object of class ResultSet of length 1.

Value

A ResultSet object.

Examples

```r
data("crs", package = "omicReposome")
crs
```
**getIntegration**  
*Method to extract integration-feature result from a ResultSet*

**Description**

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

**Usage**

```r
getIntegration(object, ...)
```

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

**Arguments**

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

**Value**

A data.frame

**Examples**

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

---

**mds** 
*MultiDataSet for testing and illustration purposes*

**Description**

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

**Usage**

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

**Format**

An object of class MultiDataSet of length 2.

**Value**

A MultiDataSet object.
Examples

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

---

### Description

**omicRexposome**: Package for exposome and omic data association 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 plotted 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 allows to use any type and number of datasets (aka. exposome transcriptome, methylome, etc.). The function generates an object of class `ResultSet`, that can be plotted 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**

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

```r
## 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.

coeff: (default 2) Index of the coefficient to be extracted.

contrast: (default 1) When code corresponds to a multicategorical variable, contrast 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 $2^{\log FC}$ instead of $\log FC$. 

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 = "omicReposome")
plotAssociation(asr, type = "qq")
plotAssociation(asr, type = "volcano")
plotIntegration

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An object of class ResultSet obtained from crossomics.</td>
</tr>
<tr>
<td>th</td>
<td>(default 0.05) Threshold (p-value) to consider a result as a hit.</td>
</tr>
<tr>
<td>width</td>
<td>(default 0.70) Width of the bar</td>
</tr>
</tbody>
</table>

Value

A ggplot2 object

See Also

plotLambda for a graphical representation of the lambda score per analysis, tableLambda for the lambda score per analysis, tableHits for the hits per analysis

Examples

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

plotIntegration Function to draw the result of an integration study

Description

This function draws a plot 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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>An object of class ResultSet obtained from crossomics.</td>
</tr>
<tr>
<td>cmpX</td>
<td>(default 1) Value of the X-axis when plotting results from mcia.</td>
</tr>
<tr>
<td>cmpY</td>
<td>(default 2) Value of the Y-axis when plotting results from mcia.</td>
</tr>
<tr>
<td>lb.th</td>
<td>(default 0.20) Threshold to place labels on the radar chart drawn when plotting results from MultiCCA.</td>
</tr>
<tr>
<td>legend.show</td>
<td>(default TRUE) If set to FALSE, right legend of the radar plot is hidden when plotting results from MultiCCA.</td>
</tr>
<tr>
<td>colors</td>
<td>(optional) Names vector with the colors used to draw each dataset. Used when plotting results from MultiCCA. If missing, random colors are chosen.</td>
</tr>
<tr>
<td>...</td>
<td>Optional arguments are given to plot from omicade4 package (argument axes is filled with values from cmpX and cmpY).</td>
</tr>
</tbody>
</table>
plotLambda

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 analysis, plotLambda for a graphical representation of the lambda score per analysis, plotHits for a graphical representation of the hits per analysis.

Examples

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

```

## S4 method for signature 'ResultSet'

## 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 analysis, plotHits for a graphical representation of the hits per analysis, plotLambda for a graphical representation of the lambda score per analysis.

Examples

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

* datasets
  asr, 4
  crs, 7
  mds, 8

  add_cls, 2
  add_cls, MultiDataSet, ExposomeClust-method (add_cls), 2
  add_eset, 2, 3
  add_exp, 3
  add_exp, MultiDataSet, ExposomeSet-method (add_exp), 3

  asr, 4
  association, 4, 4, 9, 10
  association, MultiDataSet-method (association), 4

  crossomics, 6, 7–9, 11–13
  crossomics, MultiDataSet-method (crossomics), 6
  crs, 7

  ExposomeClust, 2
  ExposomeSet, 3
  ExpressionSet, 2, 3

  getIntegration, 8
  getIntegration, ResultSet-method (getIntegration), 8

  lambdaClayton, 14

  mcia, 11
  mds, 8
  MultiCCA, 11
  MultiDataSet, 2, 3

  omicade4, 11
  omicRexposome, 9
  omicRexposome-package (omicRexposome), 9

  plotAssociation, 9, 9, 12
  plotAssociation, ResultSet-method
    (plotAssociation), 9
  plotHits, 10, 12, 14
  plotHits, ResultSet-method (plotHits), 10
  plotIntegration, 9, 10, 11
  plotIntegration, ResultSet-method
    (plotIntegration), 11
  plotLambda, 11, 12, 14
  plotLambda, ResultSet-method
    (plotLambda), 12

  ResultSet, 5, 6, 8, 10–14

  snpToContinuous, 13
  snpToContinuous, SnpSet-method
    (snpToContinuous), 13

  sva, 5

  tableHits, 11, 12, 13, 14
  tableHits, ResultSet-method (tableHits), 13
  tableLambda, 11, 12, 14, 14
  tableLambda, ResultSet-method
    (tableLambda), 14