

Package ‘SPADEVizR’

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Type Package

Title Visualization and analysis of SPADE clustering results.

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Description The Spanning tree Progression of Density normalized Events (SPADE) algorithm is powerful for mining flow and mass cytometry data. SPADE xxx. SPADEVizR is an R package dedicated to post-clustering analysis based on the . SPADEVizR is able to identify abundant clusters (AC), differentially enriched clusters (DEC), and cluster correlating with phenotypical variables (CC). Moreover, SPADEVizR provides a large panel of visual representations such as parallel coordinates, phenotypical heatmap, stream graph representation, volcano plot representations. Through all these methods SPADEVizR constitutes a powerful pipeline for the analysis of cell clustering results provided by SPADE.

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Imports data.table,
flowCore,
ggdendro,
ggnetwork,
ggplot2,
gridExtra,
gtools,
igraph,
MASS,
plyr,
reshape2

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abundantClustersViewer

abundantClustersViewer

Description

Generate a barplot representation to compare cluster abundances

Usage

```
abundantClustersViewer(AC, cluster.size = TRUE, all.label = FALSE)
```

Arguments

AC	the AC object
cluster.size	a logical specifying if points size are related to cell count or not (TRUE by default)
all.label	a logical specifying if all cluster label must be show or just significant cluster

Details

By default, only abundant clusters are labeled, set parameter ‘all.label = TRUE’ to visualize all labels.

Value

a ggplot object

AC-class

Abundant Clusters (AC) class definition

Description

The AC object is a S4 object containing the identified of abundant cluster. It contains all informations about statistical parameters used to performs this test.

Details

A cluster is considered as a significant abundant cluster if the 2 thresholds (mean and p-value) are reached. The AC object is returned by the computeAC() fonction. The AC object owns methods to summaries main informations using print and show methods Moreover this object could be exported as a tab separated file using the export method

Slots

`sample.names` a character vector containing the samples used to compute the abundant clusters

`cluster.size` a numeric vector containing the number of cells (– sum of all samples –) for each cluster

`use.percentages` a logical specifying if computation was performed on percentage of cell abundance

`method` a character containing the name of the statistical test used to identify the abundant clusters

`method.adjust` a character containing the name of the multiple correction method used (if any)

`th.mean` a numeric value specifying the mean threshold

`th.pvalue` a numeric value specifying the p-value threshold

`result` a data.frame containing for each cluster (first column): the mean (second column) and the standard deviation (third column) of the biological condition, the associated p-value (fourth column) and a logical (fifth column) specifying if the cluster is significantly abundant.

boxplotViewer

boxplotViewer

Description

Generate a boxplot representation to compare the cell enrichment of biological conditions for each cluster

Usage

```
boxplotViewer(Results, conditions, clusters = NULL, use.percentages = TRUE,
  label = FALSE, violin = TRUE)
```

Arguments

<code>Results</code>	a SPADEResults or Results object
<code>conditions</code>	conditions a named vector providing the correspondence between a sample name (in rownames) and the condition of this sample : NA to exclude a sample from tests
<code>clusters</code>	a numerical vector containing the clusters to use in the representation
<code>use.percentages</code>	a logical specifying if the visualisation should be performed on percentage
<code>label</code>	a logical to show sample label or not (FALSE by default)
<code>violin</code>	xxx

Details

xxx

Value

a ggplot object

CC-class

Correlated Clusters (CC) class definition

Description

CC is a S4 object containing the result of computeCC function.

Details

CC is a printable and a plotable object calling the correlatedClustersViewer() fonction

Slots

cluster.size a numeric vector containing number of cells (sum of all samples) for each cluster

variable a numeric vector containing the expression values of the variable

use.percentages a logical specifying if computations was performed on percentage of cell abundance

method a character containing the name of the statistical test used to identify the CC

method.adjust a character containing the name of the multiple correction method used

th.pvalue a numeric vector with pvalue threshold

th.correlation a numeric vector with correlation threshold (r)

result a three colmuns dataframe with clusters in row. The first column contains the coefficient of correlation (r), the second contains the associated pvalue and the third a logical (significance) specifying if the two thresholds was reached or not.

classifyEnrichmentProfiles

classifyEnrichmentProfiles xxx

Description

xxx

Usage

```
classifyEnrichmentProfiles(Results, method = "hierarchical_h",
  class.number = NULL, eigencell.correlation.th = 0.8,
  clique.correlation.th = 0.7, hierarchical.correlation.th = 0.8)
```

Arguments

Results a Results or SPADEResults object

method a character specifying the clustering method among one of those : 'hierarchical', 'kmeans', 'eigencell', 'clique'

class.number a numeric specifying the number of classes needed when the method parameter choosen is either 'hierarchical_k' or 'kmeans'

eigencell.correlation.th
 a numeric (ignored if method is not 'eigencell') specifying the correlation threshold (in [0,1], 0.8 by default) in case of eigencell clustering

clique.correlation.th
 a numeric (ignored if method is not 'clique') specifying the correlation threshold (in [0,1], 0.7 by default) in case of clique clustering

hierarchical.correlation.th
 a numeric (ignored if method is not 'hierarchical_h') in [0,1]) specifying the threshold of correlation (in [0,1], 0.8 by default) use to cut the hirerchical tree

Details

xxx

Value

a EnrichmentProfiles object

classifyPhenoProfiles *classifyPhenoProfiles* xxx

Description

xxx

Usage

```
classifyPhenoProfiles(Results, method = "hierarchical_h",
  class.number = NULL, eigencell.correlation.th = 0.8,
  clique.correlation.th = 0.7, hierarchical.correlation.th = 0.8)
```

Arguments

Results	a Results or SPADEResults object
method	a character specifying the clustering method among one of those : 'hierarchical', 'kmeans', 'eigencell', 'clique'
class.number	a numeric specifying the number of classes needed when the method parameter choosen is either 'hierarchical_k' or 'kmeans'
eigencell.correlation.th	a numeric (ignored if method is not 'eigencell') specifying the correlation threshold (in [0,1], 0.8 by default) in case of eigencell clustering
clique.correlation.th	a numeric (ignored if method is not 'clique') specifying the correlation threshold (in [0,1], 0.7 by default) in case of clique clustering
hierarchical.correlation.th	a numeric (ignored if method is not 'hierarchical_h') in [0,1]) specifying the threshold of correlation (in [0,1], 0.8 by default) use to cut the hirerchical tree

Details

xxx

Value

a PhenoProfiles object

clusterViewer

ClusterViewer

Description

Cluster viewer

Usage

```
clusterViewer(Results, samples = NULL, clusters = NULL, markers = NULL,
  show.mean = "both")
```

Arguments

Results	a SPADEResults or Result object (without quantiles bounds if a Results object is provided)
samples	a named vector providing the correspondence between samples name (in row-name) and the logical value TRUE to use these samples (all samples by default)
clusters	a character vector containing the clusters to use for the representation
markers	a pattern describing markers to observe
show.mean	a character : "none" "both" "only", "both" by default

Details

xxx

Value

a list of ggplot objects

computeAC

Compute the Abundant Clusters

Description

Abundant Clusters are clusters wich have an enrichment significatvely different of zeor

Usage

```
computeAC(Results, condition, use.percentages = TRUE, method = "t.test",
  method.adjust = NULL, th.pvalue = 0.05, th.mean = 0)
```

Arguments

Results	a Results or SPADEResults object
condition	a named vector providing the correspondence between a sample name (in row-name) and the logical value TRUE to test abundance for this sample or FALSE otherwise
use.percentages	a logical specifying if the computations should be performed on percentage
method	a character containing the statistical method to use for the ACs detection. The parameter can take the values "t.test" or "wilcox.test"
method.adjust	a character specifying if the pvalues should be corrected using the argument "method" available for function p.adjust, among : "holm", "hochberg", "hom-mel", "bonferroni", "BH", "BY", "fdr"
th.pvalue	a numeric specifying the pvalue threshold (0.05 by default)
th.mean	a numeric specifying the mean threshold (0 by default)

Details

xxx

Value

a AC object

computeCC

*Compute the correlation of SPADE cluster with a cynetics phenotype***Description**

Correlated Clusters are clusters with count or

Usage

```
computeCC(Results, variable, use.percentages = TRUE, method = "pearson",
  method.adjust = NULL, th.pvalue = 0.05, th.correlation = 0.5)
```

Arguments

Results	a Results or SPADEResults object
variable	a numerical named vector providing the correspondence between a sample name (in rowname) and the specific phenotype or NA to ignore a sample
use.percentages	a logical specifying if the computations should be performed on percentage
method	a character indicating the correlation method to use : "pearson", "spearman"
method.adjust	a character specifying if the pvalues should be corrected using the argument "method" available for function p.adjust, among : "holm", "hochberg", "hom-mel", "bonferroni", "BH", "BY", "fdr"
th.pvalue	a numeric specifying the pvalue threshold (0.05 by default)
th.correlation	a numeric specifying the r two sided threshold (0.5 by default) in [0,1]

Details

xxx

Value

a CC object

computeClique	<i>Internal - computeClique</i>
---------------	---------------------------------

Description

xxx

Usage

```
computeClique(data, clique.correlation.th = 0.7)
```

Arguments

data a matrix with all clusters in rownames
eigencell.correlation.th

Details

xxx

Value

a dataframe containing the cluster ID, the classe of this cluster and a clustering score.

computeDEC	<i>Compute the Differentially Enriched Clusters</i>
------------	---

Description

Differentially Enriched Clusters are clusters for which the means of cell number are significantly different between two conditions.

Usage

```
computeDEC(Results, conditions, use.percentages = TRUE, method = "t.test",  
          method.adjust = NULL, method.paired = FALSE, th.pvalue = 0.05,  
          th.fc = 1)
```

Arguments

conditions	a named vector providing the correspondence between a sample name (in row-names) and the condition of this sample : NA to exclude a sample from tests, 1 or 2 to attribute this sample, respectively to the first or second condition
use.percentages	a logical specifying if the computations should be performed on percentage
method	a character specifying the name of the statistical test to use "t.test" or "wilcox.test"
method.adjust	a character specifying if the pvalues should be corrected using the argument "method" available for function p.adjust, among : "holm", "hochberg", "hom-mel", "bonferroni", "BH", "BY", "fdr"
method.paired	a logical indicating whether data measurement are paired (by default FALSE)
th.pvalue	a numeric specifying the pvalue threshold (0.05 by default)
th.fc	a numeric specifying the foldchange threshold (1 by default)
result	a Results or SPADEResults object

Details

xxx

Value

a DEC object

computeEigenCellClusters
*Internal - computeEigenCellClusters***Description**

xxx

Usage

```
computeEigenCellClusters(data, eigencell.correlation.th = 0.8)
```

Arguments

data	a matrix with all clusters in rownames
eigencell.correlation.th	

Details

xxx

Value

a dataframe containing the cluster ID, the classe of this cluster and a clustering score.

`computeHierarchicalClustering`*Internal - computeHierarchicalClustering*

Description

xxx

Usage

```
computeHierarchicalClustering(data, class.number = NULL,  
  hierarchical.correlation.th = 0.8)
```

Arguments

<code>data</code>	a matrix with all clusters in rownames
<code>class.number</code>	the number of classe to cluster, if class.number is NULL numer of classe will be determined base on hierarchical correlation threshold
<code>hierarchical.correlation.th</code>	

Details

xxx

Value

a dataframe containing the cluster ID, the classe of this cluster and a clustering score.

`computeKMeans`*Internal - computeKMeans*

Description

xxx

Usage

```
computeKMeans(data, k)
```

Arguments

<code>data</code>	a matrix with all clusters in rownames
<code>k</code>	number of classes

Details

xxx

Value

a dataframe containing the cluster ID, the classe of this cluster and a clustering score.

computePhenoTable	<i>Internal - computePhenoTable</i>
-------------------	-------------------------------------

Description

computePhenoTable

Usage

```
computePhenoTable(SPADEResults, num = 5)
```

Arguments

SPADEResults	a SPADEResults object
num	a numeric indicating the number of "phenotype"

Details

xxx

Value

xxx

computeQuantile	<i>Internal - Compute quantile with FCS flowset marker by marker</i>
-----------------	--

Description

This function is used internally

Usage

```
computeQuantile(flowset, probs = c(0.05, 0.95))
```

Arguments

flowset	a flowCore flowset
probs	a vector of probabilities with 2 values in [0,1] to compute quantiles

Details

xxx

Value

a numeric matrix with bounds

computeQuantile.heuristic

Internal - Compute quantile with FCS flowset sample by sample

Description

This function is used internally, it provide the mean of quantiles from each sample to seed up computation

Usage

```
computeQuantile.heuristic(flowset, probs = c(0.05, 0.95))
```

Arguments

flowset	a flowCore flowset
probs	a vector of probabilities with 2 values in [0,1] to compute quantiles

Value

a numeric matrix with bounds

correlatedClustersViewer

correlatedClustersViewer

Description

Generate a representation to compare cluster abundances

Usage

```
correlatedClustersViewer(CC, cluster.size = TRUE, all.label = FALSE)
```

Arguments

CC	the CC object
cluster.size	a logical specifying if points size are related to cell count or not (TRUE by default)
all.label	a logical specifying if all cluster label must be show or just significant cluster

Details

xxx

Value

a ggplot object

CountViewer	<i>CountViewer</i>
Description <p>Generate a two dimensional vizualisation showing the number of cells (sum of selected samples) of each cluster.</p>	
Usage <pre>CountViewer(Results, samples = NULL, clusters = NULL, min.cells = 0, sort = TRUE, show.samples = TRUE)</pre>	
Arguments	
Results	a SPADEResults or Results object
samples	a named vector providing the correspondence between samples name (in row-name) and the logical value TRUE to use these samples (all samples by default)
clusters	a character vector containing the clusters to use for the representation
min.cells	a numeric specifying the minimun number of cell (sum of all selected samples) to display a cluster
sort	a logical specifying if clusters will be to be sorted (descending) based on the sum of all selected samples for each cluster.
show.samples	a logical specifying if the number of cells for all selected samples will be displayed.
Details <p>xxx</p>	
Value <p>a ggplot object</p>	
DEC-class	<i>Differentially Enriched Clusters (DEC) class definition</i>

Description

The DEC object is a S4 object containing the identified differentially enriched clusters beetween the selected conditions. It contains all informations about statistical parameters used to performs this test.

Details

A cluster is considered as a significant differentially enriched cluster if the 2 thresholds (foldchange and p-value) are reached. The DEC object is returned by the computeDEC() fonction. The AC object owns methods to summuries main informations using print and show methods Moreover this object could be exported as a tab separated file using the export method

Slots

`sample.cond1` a character specifying the names of the samples corresponding the first condition
`sample.cond2` a character specifying the names of the samples corresponding the second condition
`cluster.size` a numeric vector containing number of cells (sum of all samples) for each cluster
`use.percentages` a logical specifying if computations was performed on percentage of cell abundance
`method` a character containing the name of the statistical test used to identify the DEC
`method.adjust` a character containing the name of the multiple correction method used
`method.paired` a logical indicating if the test has been performed in a paired manner
`th.pvalue` a numeric vector with pvalue threshold
`th.fc` a numeric vector with foldchange threshold
`result` a dataframe with clusters in row. The first and second column contain the mean and the standard deviation for the first condition, the third and fourth the mean and standard deviation for the second condition, the sixth the fold-change and the seventh the pvalue and finally the significance according to pvalue threshold and fold change threshold

dendro

title Internal - Build a dendrograms plot

Description

xxx

Usage

```
dendro(ddata, row = !col, col = !row)
```

Arguments

<code>ddata</code>	xxx
<code>row</code>	xxx
<code>col</code>	xxx

Details

xxx

Value

a dendroplot

distogramViewer

biplotViewer

Description

Generates a biplot representation with two markers

Generates a biplot representation with two markers

Generates a biplot representation with two markers

Generate a distogram representation showing the marker co-expression.

Usage

```
distogramViewer(Results)
```

Arguments

Results	a SPADEResults or Results object
SPADEResults	a SPADEResults object (Results object is not accepted)
x.marker1	a character indicating the marker name of the first dimension
y.marker2	a character indicating the marker name of the second dimension
samples	xxx
clusters	xxx
default.min	a numeric value indicating the lower bound of the biplot representation
SPADEResults	a SPADEResults object (Results object is not accepted)
x.marker1	a character indicating the marker name of the first dimension
y.marker2	a character indicating the marker name of the second dimension
samples	xxx
clusters	xxx
default.min	a numeric value indicating the lower bound of the biplot representation
return.gg	a logical indicating if the function should return a list of ggplot objects
SPADEResults	a SPADEResults object (Results object is not accepted)
x.marker1	a character indicating the marker name of the first dimension
y.marker2	a character indicating the marker name of the second dimension
samples	xxx
clusters	xxx
default.min	a numeric value indicating the lower bound of the biplot representation
sample.merge	xxx
resample.ratio	xxx

Details

In such representation, each dot corresponds to a cell profile and dot are plotted in a 2-dimentional space corresponding to the marker expressions.

In such representation, each dot corresponds to a cell profile and dot are plotted in a 2-dimentional space corresponding to the marker expressions.

In such representation, each dot corresponds to a cell profile and dot are plotted in a 2-dimentional space corresponding to the marker expressions.

xxx

Value

if return.gg is TRUE, the function returns a list of ggplot objects

if return.gg is TRUE, the function returns a list of ggplot objects

if return.gg is TRUE, the function returns a list of ggplot objects

a list of ggplot objects

EnrichmentProfiles-class

EnrichmentProfiles class definition

Description

EnrichmentProfiles is a S4 object containing the result of classifyEnrichmentProfiles() function. It classify clusters by their cells enrichment properties across the samples.

Details

EnrichmentProfiles is a printable and a plotable object calling the profileViewer() fonction

Slots

method a character specifying the method used to classify cluster

method.parameter a list of parameters used by the selected method

cluster.size a numeric vector with the number of cell in each cluster (sum of all samples)

cluster.number a numeric providing the number of cluster

class.number a numeric providing the number of classes

classes a two column dataframe with the cluster in first column and corresponding classe in the second column

exclude.markers	<i>Internal - Removing of cell markers to exclude from a matrix</i>
-----------------	---

Description

This function is used internally to remove one or several cell markers.

Usage

```
exclude.markers(data, exclude, colnames.FCS = NULL)
```

Arguments

data	a numeric matrix or flowset
exclude	a character vector containing the cell markers to be excluded
colnames.FCS	a character vector containing colnames if data is a FCS flowset

Details

xxx

Value

a numeric matrix without the cell markers to exclude

export	<i>Exportation of SPADEVizR objects</i>
--------	---

Description

Exports an object into a TAB delimited file with parameters in header (begining with a sharp '#')

Usage

```
export(object, filename)

## S4 method for signature 'Results'
export(object, filename = "Results.txt")

## S4 method for signature 'AC'
export(object, filename = "AC.txt")

## S4 method for signature 'DEC'
export(object, filename = "DEC.txt")

## S4 method for signature 'CC'
export(object, filename = "CC.txt")

## S4 method for signature 'PhenoProfiles'
```

```

export(object, filename = "PhenoProfiles.txt")

## S4 method for signature 'EnrichmentProfiles'
export(object,
  filename = "EnrichmentProfiles.txt")

```

Arguments

object	a SPADEVizR object
filename	a character indicating the location of output file

Value

none

filter.medians	<i>Internal - filter medians to exclude from a matrix</i>
----------------	---

Description

This function is used internally to remove raw or transform medians from SPADE matrix. CVS medians are always remove

Usage

```
filter.medians(data, use.raw.medians = FALSE)
```

Arguments

data	a SPADE matrix
use.raw.medians	a logical specifying if "transformed" or "raw" medians will be use (FALSE by default)

Details

xxx

Value

a numeric matrix without the cell markers to exclude

generateReport	<i>Generate report and plot.</i>
----------------	----------------------------------

Description

Generate a report based on the SPADE result object.

Usage

```
generateReport(Results, PDFfile, reports = c("pheno", "kinetic", "cluster",
      "kinetic_cluster", "tree", "disto", "stream", "MDS"), clusters = NULL,
      markers = NULL, assignments = NULL, stat.objects = list(),
      profile.objects = list(), width = 29.7, height = 21)
```

Arguments

Results	a SPADEResults or Result object
PDFfile	a character specifying the output path
reports	a vector of the plot names to add in the report (following the vector order). Plot names are : "pheno", "MDS", "cluster", "tree", "disto", "stream". By default all plots will be add
clusters	a character vector of ID cluster to be reported
markers	a character vector of markers to be reported
stat.objects	a list of stat.object (object of type DEC, AC or CC)
profile.objects	a list of profile.objects (object of type PhenoProfiles or EnrichmentProfiles)
width	a numeric specifying the plot width
height	a numeric specifying the plot height

ggheatmap	<i>title Internal - Create a list of elements allowing to build a heatmap</i>
-----------	---

Description

Use the function ggheatmap.plot to display this heatmap

Usage

```
ggheatmap(mat, dendrogram.type = "rectangle", num = 5,
      clustering.markers = NULL)
```

Arguments

mat	a matrix
dendrogram.type	a character specifying the look of dendrograms ("rectangle" or "triangle", "rectangle" by default)
num	xxx
clustering.markers	a character vector of clustering markers

Value

a list of 3 plots (top dendrogram, right dendrogram, heatmap)

ggheatmap.plot	<i>title Internal - ggheatmap.plot</i>
----------------	--

Description

ggheatmap.plot display the heatmap build by ggheatmap

Usage

```
ggheatmap.plot(L, col.width = 0.15, row.width = 0.15)
```

Arguments

L	the list of ggplot object provided by ggheatmap
col.width	size of horizontal dendrogram
row.width	size of vertical dendrogram

Details

xxx

Value

a ggplot2 axis

g_axis	<i>title Internal - g_axis</i>
--------	--------------------------------

Description

Extract axis from a plot

Usage

```
g_axis(a.gplot, x = !y, y = !x)
```

Arguments

a.gplot	a ggplot2 plot
x	a logical, TRUE to extract x axis
y	a logical, TRUE to extract y axis

Details

x and y are mutuality excluded (both can't be TRUE) with priority to x

Value

a ggplot2 axis

g_legend	<i>title Internal - g_legend</i>
----------	----------------------------------

Description

Extract legend from a plot

Usage

```
g_legend(a.gplot)
```

Arguments

a.gplot	a ggplot2 plot
---------	----------------

Details

xxx

Value

a ggplot2 legend

importResults	<i>importSPADEResults</i>
---------------	---------------------------

Description

Import the SPADE results from a specified path to a SPADEResult object.

Generate a SPADEResults object based on SPADE results.

The tables are loaded, the SPADE tree is loaded as well as the layout

Usage

```
importResults(marker.expressions, cells.count)
```

Arguments

marker.expressions	a numerical dataframe containing median expression values for each marker of each sample, in additions of markers, the 2 two first columns are "cluster" and "sample"
cells.count	a matrix of cells abundances with clusters in row and samples in column

Details

We advice to use quantile.heuristic = TRUE because it is faster and much more efficient in term of memory with a low impact on precision.

Value

Results a result object

importSPADEResults	<i>importSPADEResults</i>
--------------------	---------------------------

Description

Import the SPADE results from a specified path to a SPADEResult object.

Generate a SPADEResults object based on SPADE results.

The tables are loaded, the SPADE tree is loaded as well as the layout

Usage

```
importSPADEResults(path, dict = data.frame(), exclude.markers = NULL,
  probs = c(0.05, 0.95), use.raw.medians = FALSE,
  quantile.heuristic = FALSE)
```

Arguments

path	the a character specify the path of SPADE results folder
dict	a two column data.frame providing the correspondance between the original marker names (first column) and the new marker names (second column)
exclude.markers	a vector of markers to exclude
probs	a vector of probabilities with 2 values in [0,1] to compute quantiles. First is the lower bound and second is the lower bound.
use.raw.medians	a logical specifying if "transformed" or "raw" medians will be use (FALSE by default)
quantile.heuristic	a logical specifying if quantile are compute for with all cells (FALSE), or is the means of the quantile of each samples (TRUE)

Details

We advice to use quantile.heuristic = TRUE because it is faster and much more efficient in term of memory with a low impact on precision.

Value

SPADEResults a SPADE result object

kineticsViewer	<i>Kinetic Viewer</i>
----------------	-----------------------

Description

Kinetic viewer aim to represent the kinetics of xxx

Usage

```
kineticsViewer(Results, assignments, clusters = NULL,
               use.percentages = TRUE)
```

Arguments

Results	a SPADEResults or Results object
assignments	a 2 column data.frame with the samples names in rownames providing firstly the timepoints (numeric) and secondly the individuals (character) of the experiment
clusters	a numerical vector containing the clusters to use in the representation, by default all clusters will be use
use.percentages	a logical specifying if the visualisation should be performed on percentage

Details

xxx

Value

a ggplot object

MDSViewer	<i>MDS viewer.</i>
-----------	--------------------

Description

Generate a MDS representation based on the SPADE result object.

Usage

```
MDSViewer(Results, use.percentages = TRUE, assignments, clusters = NULL,
          space = "clusters", dist.method = "euclidean")
```

Arguments

Results	a SPADEResults or Results object
use.percentages	a logical specifying if the visualisation should be performed on percentage
assignments	a 2 column data.frame with the samples names in rownames providing firstly the timepoints (numeric) and secondly the individuals (character) of the experiment
clusters	specify the set of clusters to use
space	a character specifying the space ("clusters" or "samples", cluster by default)
dist.method	a character string containing the name of the distance measure to use

Details

xxx

Value

a list of ggplot objects

names	<i>Results object's name</i>
-------	------------------------------

Description

- Named a Results object.
- Named a SPADEResults object.
- Named a AC object.
- Named a DEC object.
- Named a CC object.
- Named a PhenoProfiles object.
- Named a EnrichmentProfiles object.

Usage

```
## S4 method for signature 'Results'
names(x)

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

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

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

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

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

## S4 method for signature 'EnrichmentProfiles'
names(x)
```

Arguments

- x a Results object
- x a SPADEResults object
- x a AC object

x	a DEC object
x	a CC object
x	a PhenoProfiles object
x	a EnrichmentProfiles object

Value

none
 none
 none
 none
 none
 none
 none

PhenoProfiles-class *PhenoProfiles class definition*

Description

PhenoProfiles is a S4 object containing the result of classifyPhenoProfiles() function. It classify clusters by their markers properties provided by the fonction computePhenoTable()

Details

PhenoProfiles is a printable and a plotable object calling the xxx() fonction

Slots

method a character specifying the method used to classify cluster
 method.parameter a list of parameters used by the selected method
 cluster.size a numeric vector with the number of cell in each cluster (sum of all samples)
 cluster.number a numeric providing the number of cluster
 class.number a numeric providing the number of classes
 classes a two column dataframe with the cluster in first column and corresponding classe in the second column

phenoViewer

Pheno Viewer

Description

Heatmap Viewer aims to xxx

Usage

```
phenoViewer(SPADEResults, pheno.table = NULL, num = 5)
```

Arguments

SPADEResults	a SPADEResults object (Results object is not accepted)
pheno.table	a result of the function computePhenoTable
num	a numeric indicating the precision of computed expression scores

Details

xxx

Value

a list of ggplot objects

plot

xxx

Description

xxx

Usage

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

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

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

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

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

Arguments

xxx

Details

xxx

Value

xxx

print	<i>Textual preview for Results objects</i>
-------	--

Description

- Prints a preview for a Results object.
- Prints a preview for a SPADEResults object.
- Prints a preview for a Abundant Clusters (AC) object.
- Prints a preview for a Differentially Enriched Clusters (DEC) object.
- Prints a preview for a Correlated Clusters (CC) object.
- Prints a preview for a PhenoProfiles object.
- Prints a preview for a EnrichmentProfiles object.

Usage

```
## S4 method for signature 'Results'
print(x)

## S4 method for signature 'SPADEResults'
print(x)

## S4 method for signature 'AC'
print(x)

## S4 method for signature 'DEC'
print(x)

## S4 method for signature 'CC'
print(x)

## S4 method for signature 'PhenoProfiles'
print(x)

## S4 method for signature 'EnrichmentProfiles'
print(x)
```

Arguments

x	a Results object
x	a SPADEResults object
x	a Abundant Clusters (AC) object
x	a Differentially Enriched Clusters (DEC) object
x	a Correlated Clusters (CC) object
x	a PhenoProfiles object
x	a EnrichmentProfiles object

Value

none
 none
 none
 none
 none
 none
 none

profilesViewer	<i>profilesViewer</i>
----------------	-----------------------

Description

Generate a graph representation of PhenoProfiles classes
 Generate a graph representation of PhenoProfiles classes

Usage

```
profilesViewer(profile.object, cluster.size = TRUE)
```

Arguments

profile.object	a PhenoProfiles object or an EnrichmentProfiles object
cluster.size	a logical specifying if points size are related to cell count or not (TRUE by default)
show.unclassified	a logical specifying if unclassified clusters must be shown or not (FALSE by default)
profile.object	a PhenoProfiles object or an EnrichmentProfiles object
cluster.size	a logical specifying if points size are related to cell count or not (TRUE by default)

Details

xxx
 xxx

Value

a ggplot object

a ggplot object

rename.markers

Internal - Renaming cell markers

Description

This function is used internally to rename the cell markers based on a dictionary.

Usage

```
rename.markers(header, dictionary)
```

Arguments

header a character vector containing the original maker names

dictionary a character vector containing a correspondence between the original and the new marker names

Details

dictionary is a data.frame used to rename the marker names. The first column must correspond to the original marker names, the second column must correspond to the new marker names.

Value

a character vector containing the renamed marker names

Results-class

Results class definition

Description

The Results object is a S4 object containing results of automatic gating. This object store mainly the count matrix and the cluster phenotypes. It is to note that Results is a super classe of the SPADEResult

Details

The Results object is the core (super classe) of SPADEResults object. This object could store automatic gating results from other algorithms. The importX() function returns a Result Object.

The cells.count dataframe have in the first column the cluster names or numeric ID and some columns with number of cells for each sample (with the sample names in colnames) The marker.expressions dataframe have .. to continue

The Results object owns methods to summaries main informations using print and show methods Moreover this object could be exported as a tab separated file using the export method

Slots

`cells.count` a dataframe containing the number of cells for each cluster of each sample

`marker.expressions` a numerical dataframe containing marker median expressions for each cluster of each sample

`sample.names` a character vector containing the sample names

`marker.names` a character vector containing the markers names

`cluster.number` a numeric specifying the number of cell clusters

show

*Textual preview for Results objects***Description**

Show a preview a Results object.

Show a preview a SPADEResults object.

Show a preview a for Abundant Clusters (AC) object

Show a preview a for Differentially Enriched Clusters (DEC) object

Show a preview a Correlated Clusters (CC) object.

Show a preview a PhenoProfiles object.

Show a preview a EnrichmentProfiles object.

Usage

```
## S4 method for signature 'Results'
show(object)

## S4 method for signature 'SPADEResults'
show(object)

## S4 method for signature 'AC'
show(object)

## S4 method for signature 'DEC'
show(object)

## S4 method for signature 'CC'
show(object)

## S4 method for signature 'PhenoProfiles'
show(object)

## S4 method for signature 'EnrichmentProfiles'
show(object)
```

Arguments

x	a Results object
x	a SPADEResults object
x	a Abundant Clusters (AC) object
x	a Differentially Enriched Clusters (DEC) object
x	a Correlated Clusters (CC) object
x	a PhenoProfiles object
x	a EnrichmentProfiles object

Value

none
 none
 none
 none
 none
 none
 none

SPADEResults-class *SPADEResults class definition*

Description

The Results object is a S4 object containing results of SPADE automatic gating. This object inherits from the Result object and consequently store the count matrix and the cluster phenotypes. In addition, SPADEResults object contains the informations about SPADE cell clustering results, such as makers used to identify clusters, FCS files and the SPADE Tree.

Details

SPADEResults object is the central element used by SPADEViR functions, it is returned by the importSPADEResult() function. The SPADEResults object owns methods to summaries main informations using print and show methods Moreover this object could be exported as a tab separated file using the export method

Slots

use.raw.medians a logical specifying if the marker expressions correspond to the raw or transformed data
 dictionary a two column data.frame providing the correspondence between the original marker names (first column) and the real marker names (second column)
 marker.clustering a logical vector specifying marker that have been used during the clustering procedure
 fcs.files a character vector containing the absolute path of the original FCS files
 quantiles a numeric data.frame containing the quantiles for each each markers of cluster
 graph a igraph object containing the SPADE tree
 graph.layout a numeric matrix containing the layout of the SPADE tree

statSteamgraph	<i>title Internal - Transforms data for a steam graph (from by ggTimeSeries : https://github.com/Ather-Energy/ggTimeSeries)</i>
----------------	--

Description

xxx

Usage

statSteamgraph

Arguments

xxx

Format

An object of class statSteamgraph (inherits from Stat, ggproto) of length 4.

Details

xxx

Value

xxx

stat_steamgraph	<i>title Internal - Plot a steamgraph (from by ggTimeSeries : https://github.com/Ather-Energy/ggTimeSeries)</i>
-----------------	--

Description

xxx

Usage

```
stat_steamgraph(mapping = NULL, data = NULL, show.legend = NA,  
  inherit.aes = TRUE, na.rm = TRUE, ...)
```

Arguments

xxx

Details

xxx

Value

xxx

streamgraphViewer	<i>streamgraphViewer</i>
-------------------	--------------------------

Description

Generate a streamgraph representation showing the evolution of cell count in clusters across samples

Usage

```
streamgraphViewer(Results, order = NULL, clusters = NULL)
```

Arguments

Results	a SPADEResults or Results object
order	a named vector a named vector providing the correspondence between a sample name (in rownames) and an integer ordering samples in numeric (NA to exclude this sample)
clusters	a numerical vector containing the clusters to use in the representation, by default all clusters will be use

Details

xxx

Value

a ggplot object

treeViewer	<i>SPADE Tree viewer</i>
------------	--------------------------

Description

xxx

Usage

```
treeViewer(SPADEResults, samples = NULL, stat.object = NULL, vertex_size = c(1, 15))
```

Arguments

SPADEResults	a SPADEResults object (Results object is not accepted)
samples	a named vector providing the correspondence between samples name (in row-name) and the logical value TRUE to use these samples for cell counting (all samples by default)
stat.object	an AC, DEC or CC object to highligh significant clusters in the SPADE tree
vertex_size	a numeric vector of two values indicating the range of

Details

xxx

Value

a list of ggplot objects

volcanoViewer	<i>Volcano Plot Viewer</i>
---------------	----------------------------

Description

Generate a Volcano plot representation based on Differentially Enriched Clusters (DEC) of The SPADE result object.

Usage

```
volcanoViewer(DEC = NULL, fc.log2 = TRUE, cluster.size = TRUE,
  all.label = FALSE)
```

Arguments

DEC	object DEC provided by the function computeDEC
fc.log2	a logical specifying if foldchange or log2(foldchange) is use
cluster.size	a logical specifying if points size are related to cell count or not (TRUE by default)
all.label	a logical specifying if all cluster labels must be show or just significant cluster
SPADEResults	the SPADEViewer result object

Details

xxx

Value

a ggplot object

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