Package 'SEtools'

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Type Package

Title SEtools: tools for working with SummarizedExperiment

Version 1.0.0

Depends R (>= 3.6)

Description This includes a set of tools for working with the SummarizedExperiment class, including handy merging and plotting functions.

Imports SummarizedExperiment, data.table, pheatmap, seriation, ComplexHeatmap, circlize, methods

Suggests BiocStyle, knitr, rmarkdown, ggplot2

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VignetteBuilder knitr

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R topics documented:

crossHm *crossHm*

Description

Plot a multi-panel heatmap from a list of SummarizedExperiment-class

Usage

```
crossHm(ses, genes, do.scale = TRUE, uniqueColorScale = FALSE,
  assayName = .getDef("assayName"), do.sortRows = TRUE,
  only.common = TRUE, anno_columns = .getDef("anno_columns"),
  spreadAnnotation = FALSE, hmcols = NULL, cluster_columns = FALSE,
  cluster_rows = !do.sortRows, show_rownames = ifelse(length(genes) <
  80, "once", FALSE), show_colnames = FALSE,
  anno_colors = .getDef("anno_colors"), ...)
```

Arguments

ses	A (named) list of SummarizedExperiment-class.
genes	A vector of genes/row.names to plot.
do.scale	Logical; whether to scale rows in each SE (default TRUE).
uniqueColorScale	Logical; whether to force the same colorscale for each heatmap (default FALSE; applicable only when what!='asis').
assayName	The name of the assay to use; if multiple names are given, the first available will be used. Defaults to "logcpm", "lognorm".
do.sortRows	Logical; whether to sort rows according to MDS (default TRUE).
only.common	Logical; whether to plot only rows common to all SEs (default TRUE).
anno_columns	A vector of colData columns to use (if available) for annotation, default "Condition" and "TimePoint".
spreadAnnotation	Logical; whether to spread annotation to all SEs (not yet supported)
hmcols	An optional color palette, such as produced by the 'colorRampPalette' function.
cluster_columns	Logical; whether to cluster columns (default FALSE).
cluster_rows	Logical; whether to cluster rows (default TRUE if 'do.sortRows=FALSE', FALSE otherwise).
show_rownames	Logical; whether to show row names (default TRUE if 'length(genes)<80', FALSE otherwise).
show_colnames	Logical; whether to show column names (default FALSE)
anno_colors	A vector of color for annotations.
...	Any other parameter passed to each call of Heatmap.

Value

A Heatmap-class object.

Examples

```
data("SE", package="SEtools")
crossHm(list(se1=SE[,1:10], se2=SE[,11:20]), head(row.names(SE)))
```

`data` *Example dataset*

Description

A `SummarizedExperiment-class` containing (a subset of) whole-hippocampus RNAseq of mice after different stressors.

Value

a `SummarizedExperiment-class`.

References

Floriou-Servou et al. (2018). Distinct Proteomic, Transcriptomic, and Epigenetic Stress Responses in Dorsal and Ventral Hippocampus. *Biological Psychiatry*, **84**(7): 531-541. DOI: 10.1016/j.biopsych.2018.02.003.

`log2FC` *log2FC*

Description

Generates log2(foldchange) matrix/assay

Usage

```
log2FC(x, fromAssay = NULL, controls, by = NULL, isLog = NULL)
```

Arguments

`x`	A numeric matrix, or a 'SummarizedExperiment' object
`fromAssay`	The assay to use if 'x' is a 'SummarizedExperiment'
`controls`	A vector of which samples should be used as controls for foldchange calculations.
`by`	An optional vector indicating groups/batches by which the controls will be averaged to calculate per-group foldchanges.
`isLog`	Logical; whether the data is log-transformed. If NULL, will attempt to figure it out from the data and/or assay name

Value

An object of same class as 'x'; if a 'SummarizedExperiment', will have the additional assay 'log2FC'.

Examples

```
log2FC( matrix(rnorm(40), ncol=4), controls=1:2 )
```

`meltSE` *meltSE*

Description

Melts a SE object into a ggplot-ready long data.frame.

Usage

```
meltSE(x, genes, assayName = NULL, colDat.columns = NULL,
  rowDat.columns = NA)
```

Arguments

`x`	An object of class SummarizedExperiment-class
`genes`	A vector of genes to include. Use 'genes=NULL' to include all.
`assayName`	The name(s) of the assay(s) to use. If NULL and the assays are named, all of them will be included (if they are not named, the first one will be used).
`colDat.columns`	The colData columns to include (defaults includes all). Use 'colDat.columns=NA' in order not to include any.
`rowDat.columns`	The rowData columns to include (none included by default). Use 'rowData=NULL' to include all.

Value

A data.frame.

Examples

```
data("SE", package="SEtools")
head(meltSE(SE,"Fos"))
```

`mergeSEs` *mergeSEs*

Description

Merges a list of SummarizedExperiment-class.

Usage

```
mergeSEs(ll, use.assays = NULL, do.scale = TRUE, commonOnly = TRUE,
  colColumns = NULL, addDatasetPrefix = TRUE, defValues = list())
```

Arguments

ll	A (named) list of SummarizedExperiment-class
use.assays	Names (or indexes) of the assays to use. By default, all common assays are used.
do.scale	A logical vector indicating (globally or for each assay) whether to perform row unit-variance scaling on each dataset before merging (default TRUE).
commonOnly	Logical; whether to restrict to rows present in all datasets (default TRUE).
colColumns	A character vector specifying 'colData' columns to include (if available in at least one of the datasets). If NULL, everything is kept.
addDatasetPrefix	Logical; whether the name of the dataset should be appended to the sample names (default TRUE).
defValues	A list specifying the default values for 'colColumns' when these are absent.

Value

An object of class SummarizedExperiment-class

Examples

```
data("SE", package="SEtools")
mergeSEs( list( se1=SE[,1:10], se2=SE[,11:20] ) )
```

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resetAllSEtoolsOptions *resetAllSEtoolsOptions*

Description

Resents all global options relative to SEtools.

Usage

```
resetAllSEtoolsOptions()
```

Value

None

Examples

```
resetAllSEtoolsOptions()
```

sehm *sehm*

Description

Heatmap wrapper for SummarizedExperiment-class.

Usage

```
sehm(se, genes = NULL, do.scale = FALSE,
  assayName = .getDef("assayName"), sortRowsOn = seq_len(ncol(se)),
  cluster_cols = FALSE, cluster_rows = is.null(sortRowsOn),
  toporder = NULL, hmcols = NULL, breaks = .getDef("breaks"),
  gaps_at = .getDef("gaps_at"), gaps_row = NULL,
  anno_rows = .getDef("anno_rows"),
  anno_columns = .getDef("anno_columns"),
  anno_colors = .getDef("anno_colors"), show_rownames = NULL,
  show_colnames = FALSE, ...)
```

Arguments

se	A SummarizedExperiment-class.
genes	An optional vector of genes (i.e. row names of 'se')
do.scale	Logical; whether to scale rows (default FALSE).
assayName	An optional vector of assayNames to use. The first available will be used, or the first assay if NULL.
sortRowsOn	Sort rows by MDS polar order using the specified columns (default all)
cluster_cols	Whether to cluster columns (default F)
cluster_rows	Whether to cluster rows; default FALSE if 'do.sortRows=TRUE'.
toporder	Optional verctor of categories on which to supra-order when sorting rows, or name of a 'rowData' column to use for this purpose.
hmcols	Colors for the heatmap.
breaks	Breaks for the heatmap colors. Alternatively, if 'breaks==TRUE', a symmetrical scale with capped ends will be used (appropriate when plotting log2 fold-changes)
gaps_at	Columns of 'colData' to use to establish gaps between columns.
gaps_row	Passed to pheatmap; if missing, will be set automatically according to toporder.
anno_rows	Columns of 'rowData' to use for annotation.
anno_columns	Columns of 'colData' to use for annotation.
anno_colors	List of colors to use for annotation.
show_rownames	Whether to show row names (default TRUE if 50 rows or less).
show_colnames	Whether to show column names (default FALSE).
...	Further arguments passed to 'pheatmap'.

Value

A heatmap (see pheatmap).

Examples

```
data("SE", package="SEtools")
sehm(SE, do.scale=TRUE)
```

---

sortRows *sortRows*

Description

sortRows

Usage

```
sortRows(x, z = FALSE, toporder = NULL, na.rm = FALSE,
  method = "MDS_angle", toporder.meth = "before")
```

Arguments

x	A numeric matrix or data.frame.
z	Whether to scale rows for the purpose of calculating order (default FALSE).
toporder	Optional verctor of categories (length=nrow(x)) on which to supra-order when sorting rows.
na.rm	Wheter to remove missing values and invariant rows (default FALSE).
method	Seriation method; 'MDS_angle' (default) or 'R2E' recommended.
toporder.meth	Whether to perform higher-order sorting 'before' (default) or 'after' the lower-order sorting.

Value

A reordered matrix or data.frame.

Examples

```
# random data
m <- matrix( round(rnorm(100,mean=10, sd=2)), nrow=10,
             dimnames=list(LETTERS[1:10], letters[11:20]) )
m
sortRows(m)
```

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