

Package ‘sechm’

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Type Package

Title sechm: Complex Heatmaps from a SummarizedExperiment

Version 1.0.0

Depends R (>= 4.1)

Description sechm provides a simple interface between SummarizedExperiment objects and the ComplexHeatmap package.

It enables plotting annotated heatmaps from SE objects, with easy access to rowData and colData columns,

and implements a number of features to make the generation of heatmaps easier and more flexible. These functionalities used to be part of the SEtools package.

Imports S4Vectors, SummarizedExperiment, seriation, ComplexHeatmap, circlize, methods, randomcoloR, stats, grid, grDevices

Suggests BiocStyle, knitr, rmarkdown

biocViews GeneExpression, Visualization

VignetteBuilder knitr

License GPL-3

Encoding UTF-8

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BugReports <https://github.com/plger/sechm>

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R topics documented:

crossHm	2
data	4
getBreaks	4
qualitativeColors	5
resetAllSechmOptions	5
scale2	6
sechm	6
setSechmOption	9
sortRows	9

Index	11
--------------	-----------

crossHm	<i>crossHm</i>
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Description

Plot a multi-panel heatmap from a list of [SummarizedExperiment-class](#).

Usage

```
crossHm(
  ses,
  genes,
  do.scale = TRUE,
  uniqueScale = FALSE,
  assayName = .getDef("assayName"),
  sortBy = seq_along(ses),
  only.common = TRUE,
  cluster_cols = FALSE,
  cluster_rows = is.null(sortBy),
  toporder = NULL,
  hmcols = NULL,
  breaks = .getDef("breaks"),
  gaps_at = .getDef("gaps_at"),
  gaps_row = NULL,
  name = NULL,
  top_annotation = .getDef("anno_columns"),
  anno_columns = NULL,
  left_annotation = .getDef("anno_rows"),
  anno_rows = NULL,
  anno_colors = list(),
  show_rownames = NULL,
  merge_legends = FALSE,
  show_colnames = FALSE,
  rel.width = NULL,
```

```
    ...
  )
```

Arguments

ses	A (named) list of SummarizedExperiment-class objects.
genes	A vector of genes/row.names to plot.
do.scale	Logical; whether to scale rows in each SE (default TRUE).
uniqueScale	Logical; whether to force the same colorscale for each heatmap.
assayName	The name of the assay to use; if multiple names are given, the first available will be used. Defaults to "logcpm", "lognorm".
sortBy	Names or indexes of 'ses' to use for sorting rows (default all)
only.common	Logical; whether to plot only rows common to all SEs (default TRUE).
cluster_cols	Logical; whether to cluster columns (default FALSE).
cluster_rows	Logical; whether to cluster rows (default TRUE if 'do.sortRows=FALSE', FALSE otherwise).
toporder	Optional vector of categories on which to supra-order when sorting rows, or name of a 'rowData' column to use for this purpose.
hmcpls	Colors for the heatmap.
breaks	Breaks for the heatmap colors. Alternatively, symmetrical breaks can be generated automatically by setting 'breaks' to a numerical value between 0 and 1. The value is passed as the 'split.prop' argument to the getBreaks function, and indicates the proportion of the points to map to a linear scale, while the more extreme values will be plotted on a quantile scale. 'breaks=FALSE' will disable symmetrical scale and quantile capping, while retaining automatic breaks. 'breaks=1' will produce a symmetrical scale without quantile capping.
gaps_at	Columns of 'colData' to use to establish gaps between columns.
gaps_row	A named vector according to which rows will be split.
name	The title of the heatmap key.
top_annotation	Columns of 'colData' to use for top annotation.
anno_columns	Deprecated. Use 'top_annotation' instead.
left_annotation	Columns of 'rowData' to use for left annotation.
anno_rows	Deprecated. Use 'left_annotation' instead.
anno_colors	List of colors to use for annotation.
show_rownames	Whether to show row names (default TRUE if 50 rows or less).
merge_legends	Logical; passed to draw-HeatmapList-method
show_colnames	Whether to show column names (default FALSE).
rel.width	Relative width of the heatmaps
...	Any other parameter passed to each call of Heatmap .

Value

A Heatmap list.

Examples

```
data("Chen2017", package="sechm")
se1 <- Chen2017[,1:6]
se2 <- Chen2017[,7:15]
se3 <- crossHm(list(se1=se1, se2=se2), row.names(se1)[1:10] )
```

data	<i>Example dataset</i>
------	------------------------

Description

A [SummarizedExperiment-class](#) containing (a subset of) hippocampus RNAseq of mice treated with Forskolin.

Value

a [SummarizedExperiment-class](#).

References

Chen et al. 2017. Mapping Gene Expression in Excitatory Neurons during Hippocampal Late-Phase Long-Term Potentiation *Frontiers in Molecular Neuroscience*. DOI: 10.3389/fnmol.2017.00039

getBreaks	<i>getBreaks</i>
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Description

Produces symmetrical breaks for a color scale, with the scale steps increasing for large values, which is useful to avoid outliers influencing too much the color scale.

Usage

```
getBreaks(x, n, split.prop = 0.98, symmetric = TRUE)
```

Arguments

x	A matrix of log2FC (or any numerical values centered around 0)
n	The desired number of breaks.
split.prop	The proportion of the data points to plot on a linear scale; the remaining will be plotted on a scale with regular frequency per step (quantile).
symmetric	Logical; whether breaks should be symmetric around 0 (default TRUE)

Value

A vector of breaks of length = 'n'

Examples

```
dat <- rnorm(100, sd = 10)
getBreaks(dat, 10)
```

qualitativeColors	<i>qualitativeColors</i>
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Description

qualitativeColors

Usage

```
qualitativeColors(names, ...)
```

Arguments

names	The names to which the colors are to be assigned, or an integer indicating the desired number of colors
...	passed to 'randomcoloR::distinctColorPalette'

Value

A vector (eventually named) of colors

resetAllSechmOptions	<i>resetAllSechmOptions</i>
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Description

Resets all package options

Usage

```
resetAllSechmOptions()
```

Value

None

Examples

```
resetAllSechmOptions()
```

scale2	<i>scale2</i>
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Description

A wrapper for non-centered unit-variance scaling

Usage

```
scale2(x)
```

Arguments

`x` A matrix whose rows are to be scaled.

Value

A matrix of dimensions like `x`

Examples

```
scale2(matrix(1:9,nrow=3))
```

sechm	<i>sechm</i>
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Description

ComplexHeatmap wrapper for [SummarizedExperiment-class](#).

Usage

```
sechm(
  se,
  genes,
  do.scale = FALSE,
  assayName = .getDef("assayName"),
  name = NULL,
  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,
```

```

left_annotation = .getDef("anno_rows"),
right_annotation = NULL,
top_annotation = .getDef("anno_columns"),
bottom_annotation = NULL,
anno_rows = NULL,
anno_columns = NULL,
anno_colors = list(),
show_rownames = NULL,
show_colnames = FALSE,
isMult = FALSE,
show_heatmap_legend = !isMult,
show_annotation_legend = TRUE,
mark = NULL,
na_col = "white",
annorow_title_side = ifelse(show_colnames, "bottom", "top"),
includeMissing = FALSE,
sort.method = "MDS_angle",
...
)

```

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.
name	The name of the heatmap, eventually appearing as title of the color scale.
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 vector 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, symmetrical breaks can be generated automatically by setting 'breaks' to a numerical value between 0 and 1. The value is passed as the 'split.prop' argument to the getBreaks function, and indicates the proportion of the points to map to a linear scale, while the more extreme values will be plotted on a quantile scale. 'breaks=FALSE' will disable symmetrical scale and quantile capping, while retaining automatic breaks. 'breaks=1' will produce a symmetrical scale without quantile capping.
gaps_at	Columns of 'colData' to use to establish gaps between columns.
gaps_row	Passed to the heatmap function; if missing, will be set automatically according to toporder.

<code>left_annotation</code>	Columns of 'rowData' to use for left annotation. Alternatively, an 'HeatmapAnnotation' object.
<code>right_annotation</code>	Columns of 'rowData' to use for left annotation. Alternatively, an 'HeatmapAnnotation' object.
<code>top_annotation</code>	Columns of 'colData' to use for top annotation. Alternatively, an 'HeatmapAnnotation' object.
<code>bottom_annotation</code>	Columns of 'colData' to use for bottom annotation. Alternatively, an 'HeatmapAnnotation' object.
<code>anno_rows</code>	Deprecated. Use 'left_annotation' or 'right_annotation' instead.
<code>anno_columns</code>	Deprecated. Use 'top_annotation' or 'bottom_annotation' instead.
<code>anno_colors</code>	List of colors to use for annotation.
<code>show_rownames</code>	Whether to show row names (default TRUE if less than 50 rows to plot).
<code>show_colnames</code>	Whether to show column names (default FALSE).
<code>isMult</code>	Logical; used to silence labels when plotting multiple heatmaps
<code>show_heatmap_legend</code>	Logical; whether to show heatmap legend
<code>show_annotation_legend</code>	Logical; whether to show the annotation legend.
<code>mark</code>	An optional vector of gene names to highlight.
<code>na_col</code>	Color of NA values
<code>annorow_title_side</code>	Side (top or bottom) of row annotation names
<code>includeMissing</code>	Logical; whether to include missing genes (default FALSE)
<code>sort.method</code>	Row sorting method (see sortRows)
<code>...</code>	Further arguments passed to 'Heatmap'

Value

A a [Heatmap-class](#).

Examples

```
data("Chen2017", package="sechm")
sechm(Chen2017, row.names(Chen2017)[1:10], do.scale=TRUE)
```

setSechmOption	<i>setSechmOption</i>
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Description

Sets a package-wide option for 'sechm'

Usage

```
setSechmOption(variable, value)
```

Arguments

variable	The name of the variable to set
value	The parameter value to save

Value

None

Examples

```
setSechmOption("hmcpls", value=c("blue","black","yellow"))
```

sortRows	<i>sortRows</i>
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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.
toporder	Optional vector of categories (length=nrow(x)) on which to supra-order when sorting rows.
na.rm	Whether to remove missing values and invariant rows.
method	Serialization 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)
```

Index

Chen2017 (data), 4
crossHm, 2

data, 4

getBreaks, 3, 4, 7

Heatmap, 3

qualitativeColors, 5

resetAllSechmOptions, 5

scale2, 6

sechm, 6

setSechmOption, 9

sortRows, 8, 9