Package ‘sechm’

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**Type**  Package

**Title**  sechm: Complex Heatmaps from a SummarizedExperiment

**Version**  1.11.0

**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.

**Depends**  R (>= 4.0), SummarizedExperiment, ComplexHeatmap

**Imports**  S4Vectors, seriation, circlize, methods, randomcoloR, stats, grid, grDevices, matrixStats

**Suggests**  BiocStyle, knitr, rmarkdown

**biocViews**  GeneExpression, Visualization

**VignetteBuilder**  knitr

**License**  GPL-3

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Description

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

Usage

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

Arguments

ses A (named) list of \texttt{SummarizedExperiment-class} objects, with some matching row.names between them.

features A vector of features (i.e. 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.

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 \texttt{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.

left_annotation Columns of ‘rowData’ to use for left annotation.

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 \texttt{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 \texttt{Heatmap}.
getBreaks

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] )

---

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

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getBreaks

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)
getDEA

Value

A vector of breaks of length = 'n'

Examples

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

Description

Extracts (standardized) DEA results from the rowData of an SE object.

Usage

g DEA(se, dea = NULL, homogenize = FALSE)

Arguments

se A SummarizedExperiment-class, with DEAs each saved as a rowData column of 'se', with the column name prefixed with "DEA."
dea The optional name of the DEA to extract
homogenize Logical; whether to homogenize the DEA

Value

The DEA data.frame if 'dea' is given, otherwise a named list of data.frames.

Examples

# loading example SE
data("Chen2017", package="sechm")
# this ones doesn't have saved DEAs in the standard format:
g DEA(Chen2017)
getDEGs

Get DEGs from a SE or list of DEA results

Description

Get DEGs from a SE or list of DEA results

Usage

getDEGs(
  x,
  dea = NULL,
  lfc.th = log2(1.3),
  fdr.th = 0.05,
  direction = 0,
  merge = TRUE
)

Arguments

x A ‘SummarizedExperiment’ object with DEA results in rowData, or a list of DEA result data.frames.
dea Which DEA(s) to use (default all). Used only if ‘x’ is a ‘SummarizedExperiment’.
lfc.th Absolute log-foldchange threshold.
fdr.th FDR threshold.
direction If !=0, specifies whether to fetch only upregulated or downregulated features
merge Logical; whether to take the union of DEGs from the different DEAs (when more than one).

Value

A character vector with the significant features, or a list of such vectors.

Examples

# loading example SE
data("Chen2017", package="sechm")
# this ones doesn't have saved DEAs in the standard format:
getDEGs(Chen2017)
homogenizeDEA

Description
Standardizes the outputs of differential expression methods (to an edgeR-like style)

Usage
homogenizeDEA(x)

Arguments
x A data.frame containing the results of a differential expression analysis

Value
A standardized data.frame.

log2FC

Description
Generates log2(foldchange) matrix/assay, eventually on a per-batch fashion.

Usage
log2FC(
x, 
fromAssay = NULL, 
controls, 
by = NULL, 
isLog = NULL, 
agFun = rowMeans, 
toAssay = "log2FC", 
pseudocount = 1L, 
ndigits = 2
)

meltSE

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
agFun Aggregation function for the baseline (default rowMeans)
toAssay The name of the assay in which to save the output. If left to the default value, both a log2FC assay as well as a scaled log2FC assay (scaled by unit-variance, but not centered) will be saved in the object.
pseudocount If the origin assay is not log-transformed, ‘pseudocount’ will be added to the values before calculating a log-transformation. This prevents infinite fold-changes and moderates them.
ndigits Number of digits after the decimal of the log2FC (and scaledLFC).

Value

An object of same class as ‘x’; if a ‘SummarizedExperiment’, will have the additional assay named from ‘toAssay’.

Examples

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

meltSE

Description

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

Usage

meltSE(
x, features, assayName = NULL, colDat.columns = NULL, rowDat.columns = NULL, flatten = TRUE, baseDF = TRUE
)
Arguments

x An object of class `SummarizedExperiment-class`
features A vector of features (i.e. row.names) to include. Use ‘features=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.
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 (default all). Use ‘rowData=NA‘ to not include any.
flatten Logical, whether to flatten nested data.frames.
baseDF Logical, whether to return a base data.frame (removing columns containing other objects such as atomic lists). Filtering is applied after flattening.

Value

A data.frame (or a DataFrame).

Examples

data("Chen2017", package="sechm")
head(meltSE(Chen2017,"Fos"))

data("Chen2017", package="sechm")
head(meltSE(Chen2017,"Fos"))

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

Value

A vector (eventually named) of colors
resetAllSechmOptions

Description
Resets all package options

Usage
resetAllSechmOptions()

Value
None

Examples
resetAllSechmOptions()

safescale

Description
Equivalent to 'base::scale', but handling missing values and null variance a bit more elegantly.

Usage
safescale(x, center = TRUE, byRow = FALSE)

Arguments
- x A matrix.
- center Logical, whether to center values.
- byRow Logical, whether to scale by rows instead of columns.

Value
A scaled matrix.

Examples
m <- matrix(rnorm(100), nrow=10)
m.scaled <- safescale(m)
Description

ComplexHeatmap wrapper for `SummarizedExperiment-class`.

Usage

```r
sechm(
  se,
  features,
  do.scale = FALSE,
  assayName = NULL,
  name = NULL,
  sortRowsOn = seq_len(ncol(se)),
  cluster_cols = FALSE,
  cluster_rows = is.null(sortRowsOn),
  toporder = NULL,
  hmcols = NULL,
  breaks = .getDef("breaks"),
  gaps_at = NULL,
  gaps_row = NULL,
  left_annotation = NULL,
  right_annotation = NULL,
  top_annotation = NULL,
  bottom_annotation = 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"),
  annocol_title_side = "right",
  includeMissing = FALSE,
  sort.method = "MDS_angle",
  ...
)
```

Arguments

- `se`: A `SummarizedExperiment-class`.
- `features`: A vector of features (i.e. row names of `se`). Alternatively, can be a list of feature sets, in which case these will be plotted as different row chunks.
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.
sizeSortRowsOn 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=’ 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.
left_annotation Columns of ‘rowData’ to use for left annotation. Alternatively, an ‘HeatmapAnnotation’ object.
right_annotation Columns of ‘rowData’ to use for right annotation. Alternatively, an ‘HeatmapAnnotation’ object.
top_annotation Columns of ‘colData’ to use for top annotation. Alternatively, an ‘HeatmapAnnotation’ object. To disable (overriding defaults), use ‘top_annotation=character()’.
bottom_annotation Columns of ‘colData’ to use for bottom annotation. Alternatively, an ‘HeatmapAnnotation’ object.
anno_colors List of colors to use for annotation.
show_rownames Whether to show row names (default TRUE if less than 50 rows to plot).
show_colnames Whether to show column names (default FALSE).
isMult Logical; used to silence labels when plotting multiple heatmaps
show_heatmap_legend Logical; whether to show heatmap legend
show_annotation_legend Logical; whether to show the annotation legend.
mark An optional vector of gene names to highlight.
na_col Color of NA values
anntitle_side Side (top or bottom) of row annotation names
setRowAttr

annocol_title_side
   Side (left or right) of column annotation names
includeMissing
   Logical; whether to include missing features (default FALSE)
sort.method
   Row sorting method (see sortRows)
...
   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)

---

setRowAttr

Set rowData attribute of given rows

Description

Set rowData attribute of given rows

Usage

setRowAttr(se, values, name = "cluster", clear = TRUE, other = NA)

Arguments

  se       A ‘SummarizedExperiment’ object
  values   A named vector of values, where the names correspond to rows of ‘se’
  name     The name of the rowData column in which to store the attribute.
  clear    Logical; whether to clear out any pre-existing such column.
  other    The value for unspecified rows (default NA)

Value

The modified ‘se’ object.

Examples

data("Chen2017", package="sechm")
Chen2017 <- setRowAttr(Chen2017, c("Arc"=1,"Junb"=1,"Npas4"=2))
### setSechmOption

**Description**

Sets a package-wide option for 'sechm'

**Usage**

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

**Arguments**

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

**Value**

None

**Examples**

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

---

### sortRows

**Description**

sortRows

**Usage**

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

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: 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

```r
# 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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