

# Package ‘sechm’

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**Type** Package

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

**Version** 1.17.1

**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.

**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

**Encoding** UTF-8

**RoxygenNote** 7.2.3

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

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|         |                |
|---------|----------------|
| crossHm | <i>crossHm</i> |
|---------|----------------|

---

## 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),
  toporder = 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 <a href="#">SummarizedExperiment-class</a> 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 <a href="#">getBreaks</a> 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 <a href="#">draw-HeatmapList-method</a>                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| show_colnames   | Whether to show column names (default FALSE).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| rel.width       | Relative width of the heatmaps                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| ...             | Any other parameter passed to each call of <a href="#">Heatmap</a> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

## 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> |
|-----------|------------------|

---

**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)
```

---

getDEA

getDEA

---

**Description**

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

**Usage**

```
getDEA(se, dea = NULL, homogenize = FALSE, sort = TRUE)
```

**Arguments**

|            |                                                                                                                                            |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------|
| se         | A <a href="#">SummarizedExperiment-class</a> , 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                                                                                                     |
| sort       | Logical; whether to return the table sorted by significance                                                                                |

**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:
getDEA(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

*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

*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
)
```

**Arguments**

|                          |                                                                                                                                                                                                                |
|--------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>           | A numeric matrix, or a ‘SummarizedExperiment’ object                                                                                                                                                           |
| <code>fromAssay</code>   | The assay to use if ‘x’ is a ‘SummarizedExperiment’                                                                                                                                                            |
| <code>controls</code>    | A vector of which samples should be used as controls for foldchange calculations.                                                                                                                              |
| <code>by</code>          | An optional vector indicating groups/batches by which the controls will be averaged to calculate per-group foldchanges.                                                                                        |
| <code>isLog</code>       | Logical; whether the data is log-transformed. If NULL, will attempt to figure it out from the data and/or assay name                                                                                           |
| <code>agFun</code>       | Aggregation function for the baseline (default rowMeans)                                                                                                                                                       |
| <code>toAssay</code>     | 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. |
| <code>pseudocount</code> | 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.                         |
| <code>ndigits</code>     | 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

*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**

|                             |                                                                                                                                                       |
|-----------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>x</code>              | An object of class <a href="#">SummarizedExperiment-class</a>                                                                                         |
| <code>features</code>       | A vector of features (i.e. <code>row.names</code> ) to include. Use <code>'features=NULL'</code> to include all.                                      |
| <code>assayName</code>      | The name(s) of the assay(s) to use. If <code>NULL</code> and the assays are named, all of them will be included.                                      |
| <code>colDat.columns</code> | The colData columns to include (defaults includes all). Use <code>'colDat.columns=NA'</code> in order not to include any.                             |
| <code>rowDat.columns</code> | The rowData columns to include (default all). Use <code>'rowData=NA'</code> to not include any.                                                       |
| <code>flatten</code>        | Logical, whether to flatten nested data.frames.                                                                                                       |
| <code>baseDF</code>         | 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"))
```

---

|                   |                          |
|-------------------|--------------------------|
| qualitativeColors | <i>qualitativeColors</i> |
|-------------------|--------------------------|

---

**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> |
|----------------------|-----------------------------|

---

**Description**

Resets all package options

**Usage**

```
resetAllSechmOptions()
```

**Value**

None

**Examples**

```
resetAllSechmOptions()
```

---

|           |                  |
|-----------|------------------|
| safescale | <i>safescale</i> |
|-----------|------------------|

---

**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)
```

---

|       |              |
|-------|--------------|
| sechm | <i>sechm</i> |
|-------|--------------|

---

**Description**

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

**Usage**

```
sechm(
  se,
  features,
  do.scale = FALSE,
  assayName = NULL,
  name = NULL,
  sortRowsOn = NULL,
  cluster_cols = FALSE,
  cluster_rows = NULL,
  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 <a href="#">SummarizedExperiment-class</a> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| 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.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 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 <a href="#">getBreaks</a> 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.                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| left_annotation  | Columns of 'rowData' to use for left annotation. Alternatively, an 'HeatmapAnnotation' object.                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| right_annotation | Columns of 'rowData' to use for left 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                                                                                                                                                |
| annorow_title_side     | Side (top or bottom) of row annotation names                                                                                                                      |
| 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 <a href="#">sortRows</a> )                                                                                                                |
| ...                    | 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 | <i>Set rowData attribute of given rows</i> |
|------------|--------------------------------------------|

---

**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 | <i>setSechmOption</i> |
|----------------|-----------------------|

---

**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("hmcsls", value=c("blue","black","yellow"))
```

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.                                    |
| 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)
```

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