

Package ‘SEtools’

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Type Package

Title SEtools: tools for working with SummarizedExperiment

Version 1.25.0

Depends R (>= 4.0), SummarizedExperiment, sechm

Description This includes a set of convenience functions for working with the SummarizedExperiment class. Note that plotting functions historically in this package have been moved to the sechm package (see vignette for details).

Imports BiocParallel, Matrix, DESeq2, S4Vectors, data.table, edgeR, openxlsx, pheatmap, stats, circlize, methods, sva

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 aggSE

aggSE

Description

Aggregates the rows of a ‘SummarizedExperiment’.

Usage

```
aggSE(x, by, assayFun = NULL, rowDatFuns = list())
```

Arguments

x	An object of class ‘SummarizedExperiment’
by	Vector by which to aggregate, or column of ‘rowData(x)’
assayFun	Function by which to aggregate, or a list of such functions (or vector of function names) of the same length as there are assays. If NULL will attempt to use an appropriate function (and notify the functions used), typically the mean.
rowDatFuns	A named list providing functions by which to aggregate each rowData columns. If a given column has no specified function, the default will be used, i.e. logical are transformed into a proportion, numerics are aggregated by median, and unique factors/characters are pasted together. Use ‘rowDataFuns=NULL’ to discard rowData.

Value

An object of class ‘SummarizedExperiment’

Examples

```
library(SummarizedExperiment)
data("SE", package="SEtools")
# arbitrary IDs for example aggregation:
rowData(SE)$otherID <- rep(LETTERS[1:10],each=10)
SE <- aggSE(SE, "otherID")
```

castSE	<i>castSE</i>
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Description

Casts a data.frame as a [SummarizedExperiment-class](#)

Usage

```
castSE(  
  x,  
  rowNames = NULL,  
  colNames = NULL,  
  assayNames = NULL,  
  colData = NULL,  
  rowData = NULL,  
  sparse = FALSE  
)
```

Arguments

x	A data.frame
rowNames	Column of 'x' containing the row.names (if omitted, will build from 'rowData')
colNames	Column of 'x' containing the column names (if omitted, will build from 'colData')
assayNames	Columns of 'x' to turn into assays
colData	Columns of 'x' to use as colData
rowData	Columns of 'x' to use as rowData
sparse	Local, whether to keep the assays sparse.

Value

A [SummarizedExperiment-class](#)

Examples

```
d <- data.frame(transcript=rep(LETTERS[1:10],each=2), gene=rep(LETTERS[1:5],each=4),  
               count=rpois(20, 10), sample=letters[1:2])  
head(d)  
castSE(d, rowData=c("transcript","gene"), colNames="sample")
```

data	<i>Example dataset</i>
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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.

flattenPB	<i>flattenPB</i>
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Description

Flattens a pseudo-bulk `SummarizedExperiment` as produced by `'muscat::aggregateData'` so that all cell types are represented in a single assay. Optionally normalizes the data and calculates per-sample logFCs.

Usage

```
flattenPB(pb, norm = TRUE, lfc_group = NULL)
```

Arguments

pb	a pseudo-bulk <code>SummarizedExperiment</code> as produced by <code>'muscat::aggregateData'</code> , with different celltypes/clusters are assays.
norm	Logical; whether to calculate logcpm (TMM normalization).
lfc_group	the colData column to use to calculate foldchange. If NULL (default), no fold-change assay will be computed.

Value

A `SummarizedExperiment`

log2FC	<i>log2FC</i>
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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"
)
```

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.

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 )
```

mergeSEs

*mergeSEs***Description**

Merges a list of `SummarizedExperiment-class`, either by `row.names` or through specified `rowData` fields. In cases of many-to-many (or one-to-many) mappings, `'aggFun'` determines whether the records are aggregated by linking ID (if an aggregation method is given) or all combinations are returned (if `'aggFun=NULL'` - default).

Usage

```
mergeSEs(
  ll,
  use.assays = NULL,
  do.scale = TRUE,
  commonOnly = TRUE,
  colColumns = NULL,
  mergeBy = NULL,
  aggFun = NULL,
  addDatasetPrefix = TRUE,
  defValues = list(),
  keepRowData = TRUE,
  BPPARAM = SerialParam()
)
```

Arguments

<code>ll</code>	A (named) list of <code>SummarizedExperiment-class</code>
<code>use.assays</code>	Names (or indexes) of the assays to use. By default, all common assays are used.
<code>do.scale</code>	A logical vector indicating (globally or for each assay) whether to perform row unit-variance scaling on each dataset before merging (default TRUE).
<code>commonOnly</code>	Logical; whether to restrict to rows present in all datasets (default TRUE).
<code>colColumns</code>	A character vector specifying <code>'colData'</code> columns to include (if available in at least one of the datasets). If NULL, everything is kept.
<code>mergeBy</code>	The <code>'rowData'</code> column to merge with. If NULL, <code>row.names</code> are used.
<code>aggFun</code>	The aggregation function to use when multiple rows have the same <code>'mergeBy'</code> value. If merging multiple assays, a different function per assay can be passed as a named list (see <code>aggSE</code>). If NULL (default), entries will be reused to have each combination.
<code>addDatasetPrefix</code>	Logical; whether the name of the dataset should be appended to the sample names (default TRUE).
<code>defValues</code>	An optional named list of default <code>'colData'</code> values when some columns are missing from some SEs.
<code>keepRowData</code>	Logical, whether to keep the <code>rowData</code> (default TRUE).
<code>BPPARAM</code>	For multithreading the aggregation step.

Value

An object of class [SummarizedExperiment-class](#)

Examples

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

```
resetAllSEtoolsOptions
      resetAllSEtoolsOptions
```

Description

Resets all global options relative to SEtools.

Usage

```
resetAllSEtoolsOptions()
```

Value

None

Examples

```
resetAllSEtoolsOptions()
```

```
se2xls          se2xlsx
```

Description

Writes a SummarizedExperiment to an excel/xlsx file. Requires the 'openxlsx' package.

Usage

```
se2xls(se, filename, addSheets = NULL)
```

Arguments

se	The 'SummarizedExperiment'
filename	xlsx file name
addSheets	An optional list of additional tables to save as sheets.

Value

Saves to file.

Examples

```
data("SE", package="SEtools")
# not run
# se2xls(SE, filename="SE.xlsx")
```

sehm

sehm

Description

Deprecated pheatmap wrapper for [SummarizedExperiment-class](#). ****This function has been replaced by the `sehm` function from the ‘sehm’ package and is retained here solely for backward compatibility.****

Usage

```
sehm(
  se,
  genes,
  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 = NULL,
  show_rownames = NULL,
  show_colnames = FALSE,
  ...
)
```

Arguments

<code>se</code>	A SummarizedExperiment-class .
<code>genes</code>	An optional vector of genes (i.e. row names of ‘se’)
<code>do.scale</code>	Logical; whether to scale rows (default FALSE).
<code>assayName</code>	An optional vector of assayNames to use. The first available will be used, or the first assay if NULL.
<code>sortRowsOn</code>	Sort rows by MDS polar order using the specified columns (default all)
<code>cluster_cols</code>	Whether to cluster columns (default F)
<code>cluster_rows</code>	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.
anno_rows	Columns of 'rowData' to use for left annotation.
anno_columns	Columns of 'colData' to use for top annotation.
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).
...	Further arguments passed to 'pheatmap'

Value

A heatmap.

svacor

svacor

Description

A wrapper around SVA-based correction, providing a corrected assay. If this is RNAseq data or similar, use a count assay with 'method' either 'vst' or 'svaseq'; otherwise (e.g. proteomics) a log-normalized assay is recommended with 'method="sva"'. Note that the corrected assay, while useful for visualization, should be interpreted with care, as they omit major variation!

Usage

```
svacor(
  SE,
  form,
  form0 = ~1,
  assayName = NULL,
  regressOutNull = TRUE,
  method = c("vst", "svaseq", "sva"),
  useVST = NULL,
  n.sv = NULL,
  ...
)
```

Arguments

SE	An object of class ‘SummarizedExperiment’.
form	The formula of the differential expression model
form0	An optional formula for the null model
assayName	The name (or index) of the assay to use.
regressOutNull	Logical; whether to regress out the variables of ‘form0’.
method	Either ‘vst’ (uses DESeq2 variance-stabilization before running SVA), ‘svaseq’ (uses sva::svaseq on normalized counts), or ‘sva’ (uses standard sva, not appropriate for count data).
useVST	Deprecated; use the ‘method’ argument instead.
n.sv	The number of surrogate variables (if omitted, sva will attempt to estimate it). Note that automatic determination of the number of SVs will often lead to fairly large number of SVs, use ‘numSVmethod="leek"’ for a more conservative estimate.
...	Any other argument passed to the sva command.

Value

Returns the ‘SummarizedExperiment’ with a ‘corrected’ assay and the surrogate variables in ‘colData’.

Examples

```
data("SE", package="SEtools")
SE <- svacor(SE, ~Condition)
```

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