

Package ‘SEtools’

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Type Package

Title SEtools: tools for working with SummarizedExperiment

Version 1.14.0

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	<i>aggSE</i>
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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`*castSE*

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

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

*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"
)
```

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

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.
mergeBy	The 'rowData' column to merge with. If NULL, row.names are used.
aggFun	The aggregation function to use when multiple rows have the same 'mergeBy' value. If merging multiple assays, a different function per assay can be passed as a named list (see aggSE). If NULL (default), entries will be reused to have each combination.
addDatasetPrefix	Logical; whether the name of the dataset should be appended to the sample names (default TRUE).
defValues	An optional named list of default 'colData' values when some columns are missing from some SEs.

keepRowData Logical, whether to keep the rowData (default TRUE).
BPPARAM 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
<i>resetAllSEtoolsOptions</i>

Description

Resets all global options relative to SEtools.

Usage

```
resetAllSEtoolsOptions()
```

Value

None

Examples

```
resetAllSEtoolsOptions()
```

se2xls	<i>se2xlsx</i>
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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	<i>sehm</i>
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Description

Deprecated pheatmap wrapper for [SummarizedExperiment-class](#). ****This function has been replaced by the [sechm](#) function from the ‘sechm’ 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’.
<code>toporder</code>	Optional vector of categories on which to supra-order when sorting rows, or name of a ‘rowData’ column to use for this purpose.
<code>hmcsls</code>	Colors for the heatmap.
<code>breaks</code>	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.
<code>gaps_at</code>	Columns of ‘colData’ to use to establish gaps between columns.
<code>gaps_row</code>	Passed to the heatmap function; if missing, will be set automatically according to toporder.
<code>anno_rows</code>	Columns of ‘rowData’ to use for left annotation.
<code>anno_columns</code>	Columns of ‘colData’ to use for top annotation.
<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>...</code>	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 ‘useVST=TRUE’; otherwise (e.g. proteomics) a log-normalized assay is recommended.

Usage

```
svacor(
  SE,
  form,
  form0 = ~1,
  assayName = NULL,
  regressOutNull = TRUE,
  useVST = TRUE,
  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’.
useVST	Logical; whether to use DESeq2’s variance-stabilizing transformation; (for count data!)
n.sv	The number of surrogate variables (if omitted, sva will attempt to estimate it)
...	Any other argument passed to the sva command.

Value

Returns the ‘SummarizedExperiment’ with a ‘corrected’ assay and the surrogate variables in ‘col-Data’.

Examples

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

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