

Package ‘alabaster.sce’

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Title Load and Save SingleCellExperiment from File

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Description Save SingleCellExperiment into file artifacts, and load them back into memory.

This is a more portable alternative to serialization of such objects into RDS files.

Each artifact is associated with metadata for further interpretation;

downstream applications can enrich this metadata with context-specific properties.

Depends SingleCellExperiment, alabaster.base

Imports methods, alabaster.se, jsonlite

Suggests knitr, testthat, BiocStyle, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews DataImport, DataRepresentation

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Author Aaron Lun [aut, cre]

Maintainer Aaron Lun <infinite.monkeys.with.keyboards@gmail.com>

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```
readSingleCellExperiment
```

Read a SingleCellExperiment from disk

Description

Read a [SingleCellExperiment](#) object from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readSingleCellExperiment(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created using the saveObject method for SingleCellExperiment objects.
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments passed to readRangedSummarizedExperiment and internal altReadObject calls.

Value

A [SingleCellExperiment](#) object.

Author(s)

Aaron Lun

See Also

["saveObject, SingleCellExperiment-method"](#), to save the [SingleCellExperiment](#) to disk.

Examples

```
# Mocking up an SCE:
mat <- matrix(rpois(10000, 10), ncol=10)
colnames(mat) <- letters[1:10]
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))

se <- SingleCellExperiment(list(counts=mat))
se$stuff <- LETTERS[1:10]
se$blah <- runif(10)
reducedDims(se) <- list(
  PCA=matrix(rnorm(ncol(se)*10), ncol=10),
  TSNE=matrix(rnorm(ncol(se)*2), ncol=2)
)
altExps(se) <- list(spikes=SummarizedExperiment(list(counts=mat[1:2,])))

# Staging it:
tmp <- tempfile()
saveObject(se, tmp)
readObject(tmp)
```

`saveSingleCellExperiment`*Save a SingleCellExperiment to disk*

Description

Save a [SingleCellExperiment](#) to its on-disk representation.

Usage

```
## S4 method for signature 'SingleCellExperiment'  
saveObject(x, path, ...)
```

Arguments

<code>x</code>	A SingleCellExperiment object or one of its subclasses.
<code>path</code>	String containing the path to a directory in which to save <code>x</code> .
<code>...</code>	Further arguments to pass to the <code>RangedSummarizedExperiment</code> method.

Value

`x` is saved into `path` and `NULL` is invisibly returned.

Author(s)

Aaron Lun

See Also

[readSingleCellExperiment](#), to read the `SingleCellExperiment` back into the R session.

Examples

```
# Mocking up an SCE:  
mat <- matrix(rpois(10000, 10), ncol=10)  
colnames(mat) <- letters[1:10]  
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))  
  
se <- SingleCellExperiment(list(counts=mat))  
se$stuff <- LETTERS[1:10]  
se$blah <- runif(10)  
reducedDims(se) <- list(  
  PCA=matrix(rnorm(ncol(se)*10), ncol=10),  
  TSNE=matrix(rnorm(ncol(se)*2), ncol=2)  
)  
altExps(se) <- list(spikes=SummarizedExperiment(list(counts=mat[1:2,])))  
  
# Staging it:  
tmp <- tempfile()  
saveObject(se, tmp)  
list.files(tmp, recursive=TRUE)
```

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