

# Package ‘alabaster.sce’

October 1, 2025

**Title** Load and Save SingleCellExperiment from File  
**Version** 1.9.0  
**Date** 2024-10-16  
**License** MIT + file LICENSE  
**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  
**git\_url** <https://git.bioconductor.org/packages/alabaster.sce>  
**git\_branch** devel  
**git\_last\_commit** 03a65cc  
**git\_last\_commit\_date** 2025-04-15  
**Repository** Bioconductor 3.22  
**Date/Publication** 2025-10-01  
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readSingleCellExperiment

*Read a SingleCellExperiment from disk*


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## 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 <a href="#">saveObject</a> method for <a href="#">SingleCellExperiment</a> objects. |
| metadata | Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.                                                               |
| ...      | Further arguments passed to <a href="#">readRangedSummarizedExperiment</a> and internal <a href="#">altReadObject</a> 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)
```

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`saveSingleCellExperiment`*Save a SingleCellExperiment to disk*

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**Description**

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

**Usage**

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

**Arguments**

|                   |                                                                                  |
|-------------------|----------------------------------------------------------------------------------|
| <code>x</code>    | A <a href="#">SingleCellExperiment</a> 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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