

# 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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```
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)
```

---

`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 <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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