

# 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

**Suggests** knitr, testthat, BiocStyle, rmarkdown

**VignetteBuilder** knitr

**RoxygenNote** 7.2.3

**biocViews** DataImport, DataRepresentation

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`loadSingleCellExperiment`*Load a SingleCellExperiment*

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## Description

Load a [SingleCellExperiment](#) object from file, using the metadata generated by the corresponding [stageObject](#) method.

## Usage

```
loadSingleCellExperiment(exp.info, project, ...)
```

## Arguments

<code>exp.info</code>	Named list containing the metadata for this experiment.
<code>project</code>	Any argument accepted by the acquisition functions, see <a href="#">?acquireFile</a> . By default, this should be a string containing the path to a staging directory.
<code>...</code>	Further arguments to pass to <a href="#">loadSummarizedExperiment</a> .

## Value

A [SingleCellExperiment](#) object.

## Author(s)

Aaron Lun

## 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()
dir.create(tmp)
info <- stageObject(se, dir=tmp, "rna-seq")
```

```
# Loading it back into memory:
loadSingleCellExperiment(info, tmp)
```

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```
stageObject,SingleCellExperiment-method
  Stage an experiment
```

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## Description

Save a [SingleCellExperiment](#) to file inside the staging directory.

## Usage

```
## S4 method for signature 'SingleCellExperiment'
stageObject(x, dir, path, child = FALSE, rd.name = "dimreds", ...)
```

## Arguments

x	A <a href="#">SingleCellExperiment</a> object or one of its subclasses.
dir	String containing the path to the staging directory.
path	String containing a prefix of the relative path inside dir where x is to be saved. The actual path used to save x may include additional components, see Details.
child	Logical scalar indicating whether x is a child of a larger object.
rd.name	String containing the prefix of the file to save the reduced dimensions.
...	Further arguments to pass to the RangedSummarizedExperiment method.

## Value

A named list of metadata that follows the `single_cell_experiment` schema. The contents of x are saved into a path subdirectory inside dir.

## Author(s)

Aaron Lun

## 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()  
dir.create(tmp)  
stageObject(se, dir=tmp, "rna-seq")  
list.files(file.path(tmp, "rna-seq"))
```

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