Package: alabaster.sce (via r-universe)

June 21, 2024

Title Load and Save SingleCellExperiment from File

Version 1.5.1

Date 2024-05-20

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

Repository https://bioc.r-universe.dev

RemoteUrl https://github.com/bioc/alabaster.sce

RemoteRef HEAD

RemoteSha 131edf5cc621202bf6ad4700bde87124ede2fb4e

Contents

`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

x	A SingleCellExperiment object or one of its subclasses.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to the RangedSummarizedExperiment 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)
```

Index