Package 'alabaster.sce'

February 23, 2024

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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Author Aaron Lun [aut, cre]

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

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loadSingleCellExperiment *Load a SingleCellExperiment*

Description

Load a SingleCellExperiment object from file, using the metadata generated by the corresponding `stageObject` method.

Usage

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

Arguments

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

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)
```

`stageObject,SingleCellExperiment-method`
Stage an experiment

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 SingleCellExperiment 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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