

Package ‘alabaster.mae’

May 24, 2024

Title Load and Save MultiAssayExperiments

Version 1.5.0

Date 2024-01-30

License MIT + file LICENSE

Description Save MultiAssayExperiments 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 MultiAssayExperiment, alabaster.base

Imports methods, alabaster.se, S4Vectors, jsonlite, rhdf5

Suggests testthat, knitr, SummarizedExperiment, BiocParallel,
BiocStyle, rmarkdown

VignetteBuilder knitr

RoxygenNote 7.3.1

biocViews DataImport, DataRepresentation

git_url <https://git.bioconductor.org/packages/alabaster.mae>

git_branch devel

git_last_commit 3ad081d

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-05-24

Author Aaron Lun [aut, cre]

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

Contents

readMultiAssayExperiment	2
saveObject,MultiAssayExperiment-method	3
Index	4

readMultiAssayExperiment

Read a MultiAssayExperiment from disk

Description

Read a [MultiAssayExperiment](#) from its on-disk representation. This is usually not directly called by users, but is instead called by dispatch in [readObject](#).

Usage

```
readMultiAssayExperiment(path, metadata, ...)
```

Arguments

path	String containing a path to a directory, itself created using the stageObject method for MultiAssayExperiment objects.
metadata	Named list of metadata for this object, see readObjectFile for details.
...	Further arguments passed to internal altReadObject calls.

Value

A [MultiAssayExperiment](#) object.

Author(s)

Aaron Lun

Examples

```
library(SummarizedExperiment)

# Mocking up an MAE
mat <- matrix(rnorm(1000), ncol=10)
colnames(mat) <- letters[1:10]
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))
se <- SummarizedExperiment(list(counts=mat))

library(MultiAssayExperiment)
mae <- MultiAssayExperiment(list(gene=se))

# Staging it:
tmp <- tempfile()
dir.create(tmp)
info <- stageObject(mae, tmp, "dataset")

# Loading it back in:
loadMultiAssayExperiment(info, tmp)
```

saveObject,MultiAssayExperiment-method
Save a MultiAssayExperiment

Description

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

Usage

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

Arguments

x	A MultiAssayExperiment object or one of its subclasses.
path	String containing the path to a directory in which to save x.
...	Further arguments to pass to specific methods.

Value

The contents of x are saved into a path, and NULL is invisibly returned.

Author(s)

Aaron Lun

Examples

```
# Mocking up an MAE  
mat <- matrix(rnorm(1000), ncol=10)  
colnames(mat) <- letters[1:10]  
rownames(mat) <- sprintf("GENE_%i", seq_len(nrow(mat)))  
  
library(SummarizedExperiment)  
se <- SummarizedExperiment(list(counts=mat))  
  
library(MultiAssayExperiment)  
mae <- MultiAssayExperiment(list(gene=se))  
  
# Saving it:  
tmp <- tempfile()  
saveObject(mae, tmp)
```

Index

altReadObject, [2](#)

loadMultiAssayExperiment
 (readMultiAssayExperiment), [2](#)

MultiAssayExperiment, [2](#), [3](#)

readMultiAssayExperiment, [2](#)

readObject, [2](#)

readObjectFile, [2](#)

saveObject, MultiAssayExperiment-method,
 [3](#)

stageObject, [2](#)

stageObject, MultiAssayExperiment-method
 (saveObject, MultiAssayExperiment-method),
 [3](#)