

Package ‘alabaster.mae’

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Title Load and Save MultiAssayExperiments

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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 7.3.2

biocViews DataImport, DataRepresentation

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`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

<code>path</code>	String containing a path to a directory, itself created using the stageObject method for MultiAssayExperiment objects.
<code>metadata</code>	Named list of metadata for this object, see readObjectFile for details.
<code>...</code>	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.
...	Additional named 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)
```

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