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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Author Aaron Lun [aut, cre]

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

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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

`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.
...	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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