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

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

VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews DataImport, DataRepresentation

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loadMultiAssayExperiment *Load a MultiAssayExperiment*

Description

Load a dataset as a MultiAssayExperiment, based on the metadata generated by the corresponding `stageObject` method.

Usage

```
loadMultiAssayExperiment(
  ds.info,
  project,
  experiments = NULL,
  BPPARAM = NULL,
  include.nested = TRUE
)
```

Arguments

`ds.info`	Named list containing the metadata for this object.
`project`	Any argument accepted by the acquisition functions, see `?acquireFile`. By default, this should be a string containing the path to a staging directory.
`experiments`	Character or integer vector specifying the subset of experiments to load. If `NULL`, all experiments are loaded.
`BPPARAM`	A BiocParallelParam object indicating how loading should be parallelized across multiple experiments. If `NULL`, loading is done serially.
`include.nested`	Logical scalar indicating whether to include nested DataFrames in the `colData` of the output.

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)
```

`stageObject,MultiAssayExperiment-method`
Stage a dataset

Description

Save the metadata and annotations of a MultiAssayExperiment in a staging directory.

Usage

```
## S4 method for signature 'MultiAssayExperiment'
stageObject(
  x,
  dir,
  path,
  child = FALSE,
  sm.name = "sample_mapping",
  sd.name = "sample_data",
  meta.name = "dataset.json"
)
```

Arguments

`x`	A MultiAssayExperiment 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.
`sm.name`	String containing the prefix of the sample mapping file.
`sd.name`	String containing the prefix of the sample data file.
`meta.name`	String containing the name of the metadata file.

Details

`meta.name` is only needed to set up the output `path`, for consistency with the `stageObject` contract. Callers should make sure to write the metadata to the same document by using `.writeMetadata` with `meta.only=TRUE`.

Value

A named list containing the metadata for this dataset. The contents of `x` are saved into a `path` subdirectory inside `dir`.

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))

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

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