

# Package: alabaster.mae (via r-universe)

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**Title** Load and Save MultiAssayExperiments

**Version** 1.5.0

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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** 7.3.1

**biocViews** DataImport, DataRepresentation

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/alabaster.mae>

**RemoteRef** HEAD

**RemoteSha** 3ad081d0d88a76417f20c6fe3f1865a00c3621f9

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`readMultiAssayExperiment`*Read a MultiAssayExperiment from disk*

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### 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 <a href="#">stageObject</a> method for <a href="#">MultiAssayExperiment</a> objects.
<code>metadata</code>	Named list of metadata for this object, see <a href="#">readObjectFile</a> for details.
<code>...</code>	Further arguments passed to internal <a href="#">altReadObject</a> 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)
```

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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 <a href="#">MultiAssayExperiment</a> 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)
```

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