

Package ‘MuData’

January 30, 2026

Title Serialization for MultiAssayExperiment Objects

Version 1.14.0

Description Save MultiAssayExperiments to h5mu files supported by muon and mudata.

Muon is a Python framework for multimodal omics data analysis. It uses an HDF5-based format for data storage.

URL <https://github.com/ilia-kats/MuData>

BugReports <https://github.com/ilia-kats/MuData/issues>

Imports methods, stats, MultiAssayExperiment, SingleCellExperiment,
SummarizedExperiment, DelayedArray, S4Vectors

Depends Matrix, S4Vectors, rhdf5 (>= 2.45)

Suggests HDF5Array, rmarkdown, knitr, fs, testthat, BiocStyle, covr,
SingleCellMultiModal, CiteFuse, scater

VignetteBuilder knitr

License GPL-3

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readH5AD

Read an .h5ad file and create a [SingleCellExperiment](#).

Description

In file-backed mode, the main X matrix is not read into memory, but references the HDF5 file and its required parts are read on demand. This requires the `HDF5Array` package to be installed.

Usage

```
readH5AD(file, backed = FALSE)
```

Arguments

file	Path to the .h5ad file.
backed	Whether to use file-backed mode.

Value

A [SingleCellExperiment](#).

Examples

```
data(miniACC, package="MultiAssayExperiment")
writeH5AD(miniACC[[1]], "miniacc.h5ad")
sce <- readH5AD("miniacc.h5ad")
```

readH5MU

Read an .h5mu file and create a [MultiAssayExperiment](#).

Description

In file-backed mode, the main X matrices are not read into memory, but reference the HDF5 file and their required parts are read on demand. This requires the `HDF5Array` package to be installed.

Usage

```
readH5MU(file, backed = FALSE)
```

Arguments

file	Path to the .h5mu file.
backed	Whether to use file-backed mode.

Value

A [MultiAssayExperiment](#)

Examples

```
data(miniACC, package="MultiAssayExperiment")
writeH5MU(miniACC, "miniacc.h5mu")
mae <- readH5MU("miniacc.h5mu")
```

writeH5AD

Save an experiment to an .h5ad file.

Description

Note that NA values are not supported by HDF5, and therefore by h5ad. The behavior of this function if NAs are present is undefined.

Usage

```
writeH5AD(object, file, overwrite)
```

Arguments

object	The object to save.
file	Name of the file to save to.
overwrite	Currently unused.

Value

NULL, invisibly

Examples

```
data(miniACC, package="MultiAssayExperiment")
writeH5AD(miniACC[[1]], "miniacc.h5ad")
```

`writeH5MU`

Save a MultiAssayExperiment to an .h5mu file.

Description

Note that NA values are not supported by HDF5, and therefore by h5mu. The behavior of this function if NAs are present is undefined.

Usage

```
writeH5MU(object, file, overwrite)
```

Arguments

object	A MultiAssayExperiment .
file	Name of the file to save to.
overwrite	Currently unused.

Value

NULL, invisibly

Examples

```
data(miniACC, package="MultiAssayExperiment")
writeH5MU(miniACC, "miniacc.h5mu")
```

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