

Package ‘MuData’

April 10, 2023

Title Serialization for MultiAssayExperiment Objects

Version 1.2.0

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

Depends Matrix, S4Vectors, rhdf5

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

VignetteBuilder knitr

License GPL-3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Config/testthat/edition 3

biocViews DataImport

git_url <https://git.bioconductor.org/packages/MuData>

git_branch RELEASE_3_16

git_last_commit e790d30

git_last_commit_date 2022-11-01

Date/Publication 2023-04-10

Author Danila Bredikhin [aut, cre] (<<https://orcid.org/0000-0001-8089-6983>>),
Ilia Kats [aut] (<<https://orcid.org/0000-0001-5220-5671>>)

Maintainer Danila Bredikhin <danila.bredikhin@embl.de>

R topics documented:

| | |
|---------------------|----------|
| readH5AD | 2 |
| readH5MU | 3 |
| writeH5AD | 3 |
| writeH5MU | 4 |
| Index | 5 |

| | |
|----------|--|
| readH5AD | <i>Read an .h5ad file and create a SingleCellExperiment.</i> |
|----------|--|

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 | <i>Read an .h5mu file and create a MultiAssayExperiment.</i> |
|----------|--|

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 | <i>Save an experiment to an .h5ad file.</i> |
|-----------|---|

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")
```

Index

MultiAssayExperiment, [3](#), [4](#)

readH5AD, [2](#)

readH5MU, [3](#)

SingleCellExperiment, [2](#)

writeH5AD, [3](#)

writeH5MU, [4](#)