

Package: MuData (via r-universe)

July 2, 2024

Title Serialization for MultiAssayExperiment Objects

Version 1.9.0

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

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

RemoteUrl <https://github.com/bioc/MuData>

RemoteRef HEAD

RemoteSha 9ec354a6ca9897a101791dd8c6eed3e1867e88b6

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

<code>object</code>	A <code>MultiAssayExperiment</code> .
<code>file</code>	Name of the file to save to.
<code>overwrite</code>	Currently unused.

Value

NULL, invisibly

Examples

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

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