Package: MuData (via r-universe)

May 29, 2026

Title Serialization for MultiAssayExperiment Objects

Version 1.16.0

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

Encoding UTF-8

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RoxygenNote 7.2.3

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Config/pak/sysreqs libicu-dev libssl-dev zlib1g-dev

Repository https://bioc-release.r-universe.dev

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

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Contents

`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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