Package 'MuData'

July 19, 2025

Title Serialization for MultiAssayExperiment Objects

Version 1.13.0

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

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Config/testthat/edition 3

biocViews DataImport

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

git_branch devel

git_last_commit 9b7fe24

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-07-18

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

Maintainer Ilia Kats <i.kats@dkfz-heidelberg.de>

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")
```

Index