

# Package ‘MuData’

December 5, 2025

**Title** Serialization for MultiAssayExperiment Objects

**Version** 1.15.0

**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** 186e639

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

**Date/Publication** 2025-12-04

**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 . . . . .	2
readH5MU . . . . .	3
writeH5AD . . . . .	3
writeH5MU . . . . .	4
<b>Index</b>	<b>5</b>

---

readH5AD	<i>Read an .h5ad file and create a <a href="#">SingleCellExperiment</a>.</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	Read an .h5mu file and create a <a href="#">MultiAssayExperiment</a> .
----------	--

---

### 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 <a href="#">MultiAssayExperiment</a> .
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](#)