

# Package ‘MuData’

June 5, 2026

**Title** Serialization for MultiAssayExperiment Objects

**Version** 1.17.0

**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

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readH5AD	<i>Read an .h5ad file and create a <a href="#">SingleCellExperiment</a>.</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")
```

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readH5MU	<i>Read an .h5mu file and create a <a href="#">MultiAssayExperiment</a>.</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")
```

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writeH5AD	<i>Save an experiment to an .h5ad file.</i>
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**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")
```

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`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 <a href="#">MultiAssayExperiment</a> .
<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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