

Package ‘anndataR’

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Title AnnData interoperability in R

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Description Bring the power and flexibility of AnnData to the R ecosystem, allowing you to effortlessly manipulate and analyse your single-cell data. This package lets you work with backed h5ad and zarr files, directly access various slots (e.g. X, obs, var), or convert the data into SingleCellExperiment and Seurat objects.

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Description

Bring the power and flexibility of AnnData to the R ecosystem, allowing you to effortlessly manipulate and analyse your single-cell data. This package lets you work with backed h5ad and zarr files, directly access various slots (e.g. X, obs, var), or convert the data into SingleCellExperiment and Seurat objects.

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See Also

Useful links:

- <https://anndatar.data-intuitive.com>
- <https://github.com/scverse/anndataR>
- Report bugs at <https://github.com/scverse/anndataR/issues>

AbstractAnnData	<i>Abstract AnnData class</i>
-----------------	-------------------------------

Description

This class is an abstract representation of an AnnData object. It is intended to be used as a base class for concrete implementations of AnnData objects, such as [InMemoryAnnData](#) or [HDF5AnnData](#).

See [AnnData-usage](#) for details on creating and using AnnData objects.

Value

An AbstractAnnData object

Active bindings

X See [AnnData-usage](#)

layers See [AnnData-usage](#)

obs See [AnnData-usage](#)

var See [AnnData-usage](#)

obs_names See [AnnData-usage](#)

var_names See [AnnData-usage](#)

obsm See [AnnData-usage](#)

varm See [AnnData-usage](#)

obsp See [AnnData-usage](#)

varp See [AnnData-usage](#)

uns See [AnnData-usage](#)

Methods

Public methods:

- [AbstractAnnData#print\(\)](#)
- [AbstractAnnData\\$shape\(\)](#)
- [AbstractAnnData\\$n_obs\(\)](#)
- [AbstractAnnData\\$n_vars\(\)](#)
- [AbstractAnnData\\$obs_keys\(\)](#)
- [AbstractAnnData\\$var_keys\(\)](#)
- [AbstractAnnData\\$layers_keys\(\)](#)
- [AbstractAnnData\\$obsm_keys\(\)](#)
- [AbstractAnnData\\$varm_keys\(\)](#)
- [AbstractAnnData\\$obsp_keys\(\)](#)
- [AbstractAnnData\\$varp_keys\(\)](#)
- [AbstractAnnData\\$uns_keys\(\)](#)
- [AbstractAnnData\\$as_SingleCellExperiment\(\)](#)
- [AbstractAnnData\\$as_Seurat\(\)](#)
- [AbstractAnnData\\$as_InMemoryAnnData\(\)](#)

- [AbstractAnnData\\$as_ReticulateAnnData\(\)](#)
- [AbstractAnnData\\$as_HDF5AnnData\(\)](#)
- [AbstractAnnData\\$write_h5ad\(\)](#)
- [AbstractAnnData\\$clone\(\)](#)

Method `print()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$print(...)`

Arguments:

... Optional arguments to print method

Method `shape()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$shape()`

Method `n_obs()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$n_obs()`

Method `n_vars()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$n_vars()`

Method `obs_keys()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$obs_keys()`

Method `var_keys()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$var_keys()`

Method `layers_keys()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$layers_keys()`

Method `obsm_keys()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$obsm_keys()`

Method `varm_keys()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$varm_keys()`

Method `obsp_keys()`: See [AnnData-usage](#)

Usage:

`AbstractAnnData$obsp_keys()`

Method `varp_keys()`: See [AnnData-usage](#)

Usage:

AbstractAnnData\$varp_keys()

Method uns_keys(): See [AnnData-usage](#)

Usage:

AbstractAnnData\$uns_keys()

Method as_SingleCellExperiment(): Convert to SingleCellExperiment

See [as_SingleCellExperiment\(\)](#) for more details on the conversion

Usage:

```
AbstractAnnData$as_SingleCellExperiment(  
  x_mapping = NULL,  
  assays_mapping = TRUE,  
  colData_mapping = TRUE,  
  rowData_mapping = TRUE,  
  reducedDims_mapping = TRUE,  
  colPairs_mapping = TRUE,  
  rowPairs_mapping = TRUE,  
  metadata_mapping = TRUE  
)
```

Arguments:

x_mapping See [as_SingleCellExperiment\(\)](#)
assays_mapping See [as_SingleCellExperiment\(\)](#)
colData_mapping See [as_SingleCellExperiment\(\)](#)
rowData_mapping See [as_SingleCellExperiment\(\)](#)
reducedDims_mapping See [as_SingleCellExperiment\(\)](#)
colPairs_mapping See [as_SingleCellExperiment\(\)](#)
rowPairs_mapping See [as_SingleCellExperiment\(\)](#)
metadata_mapping See [as_SingleCellExperiment\(\)](#)

Returns: A SingleCellExperiment object

Method as_Seurat(): Convert to Seurat

See [as_Seurat\(\)](#) for more details on the conversion

Usage:

```
AbstractAnnData$as_Seurat(  
  assay_name = "RNA",  
  x_mapping = NULL,  
  layers_mapping = TRUE,  
  object_metadata_mapping = TRUE,  
  assay_metadata_mapping = TRUE,  
  reduction_mapping = TRUE,  
  graph_mapping = TRUE,  
  misc_mapping = TRUE  
)
```

Arguments:

assay_name See [as_Seurat\(\)](#)
x_mapping See [as_Seurat\(\)](#)
layers_mapping See [as_Seurat\(\)](#)
object_metadata_mapping See [as_Seurat\(\)](#)

assay_metadata_mapping See [as_Seurat\(\)](#)

reduction_mapping See [as_Seurat\(\)](#)

graph_mapping See [as_Seurat\(\)](#)

misc_mapping See [as_Seurat\(\)](#)

Returns: A Seurat object

Method [as_InMemoryAnnData\(\)](#): Convert to an [InMemoryAnnData](#)
See [as_InMemoryAnnData\(\)](#) for more details on the conversion

Usage:

```
AbstractAnnData$as_InMemoryAnnData()
```

Returns: An [InMemoryAnnData](#) object

Method [as_ReticulateAnnData\(\)](#): Convert to a [ReticulateAnnData](#)
See [as_ReticulateAnnData\(\)](#) for more details on the conversion

Usage:

```
AbstractAnnData$as_ReticulateAnnData()
```

Returns: A [ReticulateAnnData](#) object

Method [as_HDF5AnnData\(\)](#): Convert to an [HDF5AnnData](#)
See [as_HDF5AnnData\(\)](#) for more details on the conversion

Usage:

```
AbstractAnnData$as_HDF5AnnData(  
  file,  
  compression = c("none", "gzip", "lzf"),  
  mode = c("w-", "r", "r+", "a", "w", "x")  
)
```

Arguments:

file See [as_HDF5AnnData\(\)](#)

compression See [as_HDF5AnnData\(\)](#)

mode See [as_HDF5AnnData\(\)](#)

Returns: An [HDF5AnnData](#) object

Method [write_h5ad\(\)](#): Write the AnnData object to an H5AD file
See [write_h5ad\(\)](#) for details

Usage:

```
AbstractAnnData$write_h5ad(  
  path,  
  compression = c("none", "gzip", "lzf"),  
  mode = c("w-", "r", "r+", "a", "w", "x")  
)
```

Arguments:

path See [write_h5ad\(\)](#)

compression See [write_h5ad\(\)](#)

mode See [write_h5ad\(\)](#)

Returns: path invisibly

Method [clone\(\)](#): The objects of this class are cloneable with this method.

Usage:

```
AbstractAnnData$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

[AnnData-usage](#) for details on creating and using AnnData objects

Other AnnData classes: [AnnDataView](#), [HDF5AnnData](#), [InMemoryAnnData](#), [ReticulateAnnData](#)

AbstractAnnData-s3methods

S3 Methods for AbstractAnnData Objects

Description

These S3 methods provide standard R interfaces for AbstractAnnData objects, making them behave like native R objects with familiar syntax.

Usage

```
## S3 method for class 'AbstractAnnData'
dim(x)

## S3 method for class 'AbstractAnnData'
nrow(x)

## S3 method for class 'AbstractAnnData'
ncol(x)

## S3 method for class 'AbstractAnnData'
dimnames(x)

## S3 replacement method for class 'AbstractAnnData'
dimnames(x) <- value

## S3 method for class 'AbstractAnnData'
x[i, j, drop = TRUE, ...]
```

Arguments

<code>x</code>	An AbstractAnnData object
<code>value</code>	For <code>dimnames<=</code> : A list of two character vectors (<code>obs_names</code> , <code>var_names</code>)
<code>i</code>	Row indices (observations). Can be numeric, logical, or character.
<code>j</code>	Column indices (variables). Can be numeric, logical, or character.
<code>drop</code>	Ignored (for compatibility with generic)
<code>...</code>	Additional arguments passed to methods

Details

Subsetting behaviour: The `[]` method supports logical, integer, and character subsetting for both observations (rows) and variables (columns). However, unlike standard R behaviour:

- Logical vectors are **not recycled** and must have the exact same length as the dimension being subset

- **Negative indices are not supported** (R's "exclude these" syntax)

These design choices ensure clear and predictable subsetting behaviour for biological data matrices, avoiding potential confusion from accidental recycling or exclusion patterns.

The following S3 methods are available:

- `dim(x)`: Get dimensions (`n_obs`, `n_vars`), equivalent to `x$shape()`
- `nrow(x)`: Get number of observations, equivalent to `x$n_obs()`
- `ncol(x)`: Get number of variables, equivalent to `x$n_vars()`
- `dimnames(x)`: Get dimension names, (`obs_names`, `var_names`)
- `rownames(x)`: Get observation names, equivalent to `x$obs_names()`
- `colnames(x)`: Get variable names, equivalent to `x$var_names()`
- `dimnames(x) <- value`: Set dimension names
- `rownames(x) <- value`: Set observation names, equivalent to `x$obs_names() <- ...`
- `colnames(x) <- value`: Set variable names, equivalent to `x$var_names() <- ...`
- `x[i, j]`: Subset observations and/or variables

Value

- `dim`: Numeric vector of length 2 (`n_obs`, `n_vars`)
- `nrow`, `ncol`: Integer count
- `dimnames`: List with `obs_names` and `var_names`
- `rownames`, `colnames`: Character vector
- `dimnames<-`, `rownames<-`, `colnames<-`: The modified object (invisibly)
- `[:]`: A `AnnDataView` object with the specified subset

Examples

```
# Create example data
ad <- generate_dataset(n_obs = 100, n_vars = 50, format = "AnnData")

# Standard R methods work
dim(ad)
nrow(ad)
ncol(ad)
dimnames(ad)
rownames(ad)
colnames(ad)

# Set names using dimnames
dimnames(ad) <- list(
  paste0("cell_", 1:nrow(ad)),
  paste0("gene_", 1:ncol(ad))
)

# Or set names individually (uses dimnames<- internally)
rownames(ad) <- paste0("cell_", 1:nrow(ad))
colnames(ad) <- paste0("gene_", 1:ncol(ad))

# Subsetting creates AnnDataView
subset_ad <- ad[1:10, 1:5]
subset_ad <- ad[rep(c(TRUE, FALSE), length.out = nrow(ad)), ] # logical subsetting (no recycling)
subset_ad <- ad[c("cell_1", "cell_2"), c("gene_1", "gene_2")] # name subsetting
```

AnnData

*Create an in-memory AnnData object.***Description**

For more information on the functionality of an AnnData object, see [AnnData-usage](#)

Usage

```
AnnData(
    X = NULL,
    obs = NULL,
    var = NULL,
    layers = NULL,
    obsm = NULL,
    varm = NULL,
    obsp = NULL,
    varp = NULL,
    uns = NULL,
    shape = NULL
)
```

Arguments

X	See the X slot in AnnData-usage
obs	See the obs slot in AnnData-usage
var	See the var slot in AnnData-usage
layers	See the layers slot in AnnData-usage
obsm	See the obsm slot in AnnData-usage
varm	See the varm slot in AnnData-usage
obsp	See the obsp slot in AnnData-usage
varp	See the varp slot in AnnData-usage
uns	See the uns slot in AnnData-usage
shape	Shape tuple (e.g. <code>c(n_obs, n_vars)</code>). Can be provided if both X or obs and var are not provided.

Value

An [InMemoryAnnData](#) object

See Also

[AnnData-usage](#) for details of AnnData structure and usage

Other AnnData creators: [as_AnnData\(\)](#), [read_h5ad\(\)](#)

Examples

```
adata <- AnnData(
  X = matrix(1:12, nrow = 3, ncol = 4),
  obs = data.frame(
    row.names = paste0("obs", 1:3),
    n_counts = c(1, 2, 3),
    n_cells = c(1, 2, 3)
  ),
  var = data.frame(
    row.names = paste0("var", 1:4),
    n_cells = c(1, 2, 3, 4)
  )
)

adata
```

AnnData-usage

AnnData structure and usage

Description

The AnnData object stores a data matrix `X` together with annotations of observations `obs` (`obsm`, `obsp`) and variables `var` (`varm`, `varp`). Additional layers of data can be stored in `layers` and unstructured annotations in `uns`.

Back ends:

There are different back ends for AnnData objects that inherit from the abstract [AbstractAnnData](#) class and store and access data in different ways:

- [InMemoryAnnData](#) stores data in memory
- [HDF5AnnData](#) provides an interface to a H5AD file
- [ReticulateAnnData](#) wraps a Python AnnData object via **reticulate**

See the class documentation for details.

Usage:

The items listed as "**Slots**" are elements of the AnnData object that contain data and can be accessed or set. "**Fields**" return information about the AnnData object but cannot be set directly. Both, as well as methods, can be accessed using the `$` operator

For example:

- `adata$X` returns the `X` matrix
- `adata$X <- x` sets the `X` matrix
- `adata$method()` calls a method

Value

An AnnData object inheriting from [AbstractAnnData](#)

Fields

`shape` Dimensions (observations x variables) of the AnnData object
`n_obs` Number of observations
`n_vars` Number of variables
`obs_keys` Keys (column names) of `obs`
`var_keys` Keys (column names) of `var`
`layers_keys` Keys (element names) of `layers`
`obsm_keys` Keys (element names) of `obsm`
`varm_keys` Keys (element names) of `varm`
`obsp_keys` Keys (element names) of `obsp`
`varp_keys` Keys (element names) of `varp`
`uns_keys` Keys (element names) of `uns`

Slots

`X` The main data matrix. Either NULL or an observation x variable matrix (without dimnames) with dimensions consistent with `n_obs` and `n_vars`.
`layers` Additional data layers. Must be NULL or a named list of matrices having dimensions consistent with `n_obs` and `n_vars`.
`obs` Observation annotations. A `data.frame` with columns containing information about observations. The number of rows of `obs` defines the observation dimension of the AnnData object (`n_obs`). If NULL, an `n_obs × 0 data.frame` will automatically be generated.
`var` Variable annotations. A `data.frame` with columns containing information about variables. The number of rows of `var` defines the variable dimension of the AnnData object (`n_vars`). If NULL, an `n_vars × 0 data.frame` will automatically be generated.
`obs_names` Observation names. Either NULL or a vector of unique identifiers used to identify each row of `obs` and to act as an index into the observation dimension of the AnnData object. For compatibility with *R* representations, `obs_names` should be a unique character vector.
`var_names` Variable names. Either NULL or a vector of unique identifiers used to identify each row of `var` and to act as an index into the variable dimension of the AnnData object. For compatibility with *R* representations, `var_names` should be a unique character vector.
`obsm` Multi-dimensional observation annotation. Must be NULL or a named list of array-like elements with number of rows equal to `n_obs`.
`varm` Multi-dimensional variable annotations. Must be NULL or a named list of array-like elements with number of rows equal to `n_vars`.
`obsp` Observation pairs. Must be NULL or a named list of array-like elements with number of rows and columns equal to `n_obs`.
`varp` Variable pairs. Must be NULL or a named list of array-like elements with number of rows and columns equal to `n_vars`.
`uns` Unstructured annotations. Must be NULL or a named list.

Methods

Conversion methods::

`as_SingleCellExperiment()` Convert to `SingleCellExperiment::SingleCellExperiment`, see `as_SingleCellExperiment()`

[as_Seurat\(\)](#) Convert to [SeuratObject::Seurat](#), see [as_Seurat\(\)](#)
[as_InMemoryAnnData\(\)](#) Convert to [InMemoryAnnData](#), as [as_InMemoryAnnData\(\)](#)
[as_HDF5AnnData\(\)](#) Convert to [HDF5AnnData](#), see [as_HDF5AnnData\(\)](#)
[as_ReticulateAnnData\(\)](#) Convert to [ReticulateAnnData](#), see [as_ReticulateAnnData\(\)](#)

Output methods::

[write_h5ad\(\)](#) Write the AnnData object to an HDF5 file, see [write_h5ad\(\)](#)

General methods::

[print\(\)](#) Print a summary of the AnnData object

Functions that can be used to create AnnData objects

[AnnData\(\)](#) Create an [InMemoryAnnData](#) object
[read_h5ad\(\)](#) Read an AnnData from a H5AD file
[as_AnnData\(\)](#) Convert other objects to an AnnData object

See Also

The documentation for the Python anndata package <https://anndata.readthedocs.io/en/stable/>

[AbstractAnnData](#) for the abstract class that all AnnData objects inherit from

[InMemoryAnnData](#) for the in-memory implementation of AnnData

[HDF5AnnData](#) for the HDF5-backed implementation of AnnData

[ReticulateAnnData](#) for the reticulate-based implementation that wraps Python AnnData objects

AnnDataView

A View of an AnnData Object

Description

A lazy view of an AnnData object that allows applying subsetting operations without immediately executing them. Subsetting is applied when converting to a concrete AnnData implementation (InMemoryAnnData, HDF5AnnData) or other formats (SingleCellExperiment, Seurat).

Value

A AnnDataView object

Super class

[anndataR::AbstractAnnData](#) -> AnnDataView

Active bindings

X See [AnnData-usage](#)
layers See [AnnData-usage](#)
obs See [AnnData-usage](#)
var See [AnnData-usage](#)
obs_names See [AnnData-usage](#)
var_names See [AnnData-usage](#)
obsm See [AnnData-usage](#)
varm See [AnnData-usage](#)
obsp See [AnnData-usage](#)
varp See [AnnData-usage](#)
uns See [AnnData-usage](#)

Methods

Public methods:

- [AnnDataView\\$new\(\)](#)
- [AnnDataView\\$subset\(\)](#)
- [AnnDataView\\$clone\(\)](#)

Method `new()`: Create a new AnnDataView object

Usage:

```
AnnDataView$new(base_adata, i, j)
```

Arguments:

`base_adata` An existing AnnData object to create a view of
`i` Optional initial obs subset (logical, integer, or character vector)
`j` Optional initial var subset (logical, integer, or character vector)

Returns: A new AnnDataView object Subset the AnnDataView

Method `subset()`:

Usage:

```
AnnDataView$subset(i, j)
```

Arguments:

`i` Row indices (observations). Can be numeric, logical, or character.
`j` Column indices (variables). Can be numeric, logical, or character.

Returns: A new AnnDataView object

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
AnnDataView$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

See Also

[AnnData-usage](#) for details on creating and using AnnData objects

Other AnnData classes: [AbstractAnnData](#), [HDF5AnnData](#), [InMemoryAnnData](#), [ReticulateAnnData](#)

Examples

```
# Create a base AnnData object
ad <- AnnData(
  X = matrix(1:15, 3L, 5L),
  obs = data.frame(row.names = LETTERS[1:3], cell_type = c("A", "B", "A")),
  var = data.frame(row.names = letters[1:5], gene_type = c("X", "Y", "X", "Y", "Z"))
)

# Create a view with lazy subsetting using S3 [ method
view <- ad[ad$obs$cell_type == "A", ad$var$gene_type %in% c("X", "Y")]

# Apply subsetting by converting to a concrete implementation
result <- view$as_InMemoryAnnData()
```

as_AnnData

*Convert to an AnnData object***Description**

Convert other objects to an AnnData object. See the sections below for details on how slots are mapped between objects. For more information on the functionality of an AnnData object, see [AnnData-usage](#).

Usage

```
as_AnnData(
  x,
  x_mapping = NULL,
  layers_mapping = TRUE,
  obs_mapping = TRUE,
  var_mapping = TRUE,
  obsm_mapping = TRUE,
  varm_mapping = TRUE,
  obsp_mapping = TRUE,
  varp_mapping = TRUE,
  uns_mapping = TRUE,
  assay_name = NULL,
  output_class = c("InMemory", "HDF5AnnData", "ReticulateAnnData"),
  ...
)

## S3 method for class 'SingleCellExperiment'
as_AnnData(
  x,
  x_mapping = NULL,
```

```

    layers_mapping = TRUE,
    obs_mapping = TRUE,
    var_mapping = TRUE,
    obsm_mapping = TRUE,
    varm_mapping = TRUE,
    obsp_mapping = TRUE,
    varp_mapping = TRUE,
    uns_mapping = TRUE,
    assay_name = TRUE,
    output_class = c("InMemory", "HDF5AnnData", "ReticulateAnnData"),
    ...
)

## S3 method for class 'Seurat'
as_AnnData(
  x,
  x_mapping = NULL,
  layers_mapping = TRUE,
  obs_mapping = TRUE,
  var_mapping = TRUE,
  obsm_mapping = TRUE,
  varm_mapping = TRUE,
  obsp_mapping = TRUE,
  varp_mapping = TRUE,
  uns_mapping = TRUE,
  assay_name = NULL,
  output_class = c("InMemory", "HDF5AnnData", "ReticulateAnnData"),
  ...
)

```

Arguments

x	The object to convert
x_mapping	A string specifying the data to map to the X slot. If NULL, no data will be copied to the X slot. See below for details.
layers_mapping	A named character vector where the names are keys of layers in the new AnnData object and values are the names of items in the corresponding slot of x. See below for details.
obs_mapping	A named character vector where the names are names of obs columns in the new AnnData object and values are the names of columns in the corresponding slot of x. See below for details.
var_mapping	A named character vector where the names are names of var columns in the new AnnData object and values are the names of columns in the corresponding slot of x. See below for details.
obsm_mapping	A named character vector where the names are keys of obsm in the new AnnData object and values are the names of items in the corresponding slot of x. See below for details.
varm_mapping	A named character vector where the names are keys of varm in the new AnnData object and values are the names of items in the corresponding slot of x. See below for details.

obsp_mapping	A named character vector where the names are keys of obsp in the new AnnData object and values are the names of items in the corresponding slot of x. See below for details.
varp_mapping	A named character vector where the names are keys of varp in the new AnnData object and values are the names of items in the corresponding slot of x. See below for details.
uns_mapping	A named character vector where the names are keys of uns in the new AnnData object and values are the names of items in the corresponding slot of x. See below for details.
assay_name	For <code>SeuratObject::Seurat</code> objects, the name of the assay to be converted. If NULL, the default assay will be used (<code>SeuratObject::DefaultAssay()</code>). This is ignored for other objects.
output_class	The AnnData class to convert to. Must be one of "HDF5AnnData" or "InMemoryAnnData".
...	Additional arguments passed to the generator function for output_class

Value

An AnnData object of the class requested by output_class containing the data specified in the mapping arguments.

Details of mapping arguments

All mapping arguments except for x_mapping expect a named character vector where names are the keys of the slot in the AnnData object and values are the names of items in the corresponding slot of x. If TRUE, the conversion function will guess which items to copy as described in the conversion tables for each object type. In most cases, the default is to copy all items using the same names except where the correspondence between objects is unclear. To avoid copying anything to a slot, set the mapping argument to FALSE. Empty mapping arguments (NULL, c(), list()) will be treated as FALSE with a warning. If an unnamed vector is provided, the values will be used as names.

- TRUE will guess which items to copy as described in the conversion tables for each object type
- `c(adata_item = "x_item")` will copy x_item from the slot in x to adata_item in the corresponding slot of new AnnData object
- FALSE will avoid copying anything to the slot
- `c("x_item")` is equivalent to `c(x_item = "x_item")`

Converting from a SingleCellExperiment object

This table describes how slots in a `SingleCellExperiment::SingleCellExperiment` object to the new AnnData object.

From SingleCellExperiment	To AnnData	Example mapping argument
assays(x)	adata\$X	x_mapping = "counts"
assays(x)	adata\$layers	layers_mapping = c(counts = "counts")
colData(x)	adata\$obs	obs_mapping = c(n_counts = "n_counts", cell_type = "C")
rowData(x)	adata\$var	var_mapping = c(n_cells = "n_cells", pct_zero = "PctZ")
reducedDims(x)	adata\$obsm	obsm_mapping = c(X_pca = "pca")
featureLoadings(reducedDims(x))	adata\$varm	varm_mapping = c(PCs = "pca")
colPairs(x)	adata\$obsp	obsp_mapping = c(connectivities = "RNA_nn")
rowPairs(x)	adata\$varp	varp_mapping = c(similarities = "gene_overlaps")
metadata(x)	adata\$uns	uns_mapping = c(metadata = "project_metadata")

Converting from a Seurat object

Only one assay can be converted from a `SeuratObject::Seurat` object to an `AnnData` object at a time. This can be controlled using the `assay_name` argument. By default, the current default assay will be used.

This table describes how slots in a `SeuratObject::Seurat` object to the new `AnnData` object.

From Seurat	To AnnData	Example mapping argument
<code>Layers(x)</code>	<code>adata\$X</code>	<code>x_mapping = "counts"</code>
<code>Layers(x)</code>	<code>adata\$layers</code>	<code>layers_mapping = c(counts = "counts")</code>
<code>x[[[]]]</code>	<code>adata\$obs</code>	<code>obs_mapping = c(n_counts = "n_counts", cell_type = "CellType")</code>
<code>x[[assay_name]][[[]]]</code>	<code>adata\$var</code>	<code>var_mapping = c(n_cells = "n_cells", pct_zero = "PctZero")</code>
<code>Reductions(x)</code>	<code>adata\$obsm</code>	<code>obsm_mapping = c(X_pca = "pca")</code>
<code>Loadings(x)</code>	<code>adata\$varm</code>	<code>varm_mapping = c(PCs = "pca")</code>
<code>Graphs(x)</code>	<code>adata\$obsp</code>	<code>obsp_mapping = c(connectivities = "RNA_nn")</code>
<code>Misc(x)</code>	<code>adata\$varp</code>	<code>varp_mapping = c(similarities = "gene_overlaps")</code>
<code>Misc(x)</code>	<code>adata\$uns</code>	<code>uns_mapping = c(metadata = "project_metadata")</code>

Graph conversion:

By default, all graphs in a `SeuratObject::Seurat` object that match the assay being converted are copied to the `obsp` slot of the new `AnnData` object. If a graph does not have an associated assay:

- If `assay_name` is the default assay, they will be *converted* with a warning
- if `assay_name` is not the default assay, they will be *skipped* with a warning

To override this behavior, provide a custom mapping using the `obsp_mapping` argument.

Unexpected dimensions:

A `SeuratObject::Seurat` is more flexible in terms of the dimensions of items that can be stored in various slots. For example, a `Layer` does not have to match the dimensions of the whole object. If an item has unexpected dimensions, it will be skipped with a warning.

See Also

Other `AnnData` creators: `AnnData()`, `read_h5ad()`

Other object converters: `as_HDF5AnnData()`, `as_InMemoryAnnData()`, `as_ReticulateAnnData()`, `as_Seurat()`, `as_SingleCellExperiment()`, `reticulate-helpers`

Examples

```
# Convert a Seurat object to an AnnData object
library(Seurat)

counts <- matrix(rbinom(20000, 1000, .001), nrow = 100)
obj <- CreateSeuratObject(counts = counts)
obj <- NormalizeData(obj)
obj <- FindVariableFeatures(obj)
obj <- ScaleData(obj)
obj <- RunPCA(obj, npcs = 10L)
obj <- FindNeighbors(obj)
```

```

obj <- RunUMAP(obj, dims = 1:10)

as_AnnData(obj)

# Convert a SingleCellExperiment object to an AnnData object
library(SingleCellExperiment)

sce <- SingleCellExperiment(
  assays = list(counts = matrix(1:5, 5L, 3L)),
  colData = DataFrame(cell = 1:3, row.names = paste0("Cell", 1:3)),
  rowData = DataFrame(gene = 1:5, row.names = paste0("Gene", 1:5))
)

as_AnnData(sce)

```

as_HDF5AnnData

*Convert an AnnData to an HDF5AnnData***Description**

Convert another AnnData object to an [HDF5AnnData](#) object

Usage

```

as_HDF5AnnData(
  adata,
  file,
  compression = c("none", "gzip", "lzf"),
  mode = c("w-", "r", "r+", "a", "w", "x")
)

```

Arguments

adata	An AnnData object to be converted to HDF5AnnData
file	The file name (character) of the .h5ad file
compression	The compression algorithm to use when writing the HDF5 file. Can be one of "none", "gzip" or "lzf". Defaults to "none".
mode	The mode to open the HDF5 file: • a creates a new file or opens an existing one for read/write • r opens an existing file for reading • r+ opens an existing file for read/write • w creates a file, truncating any existing ones • w-/x are synonyms, creating a file and failing if it already exists

Value

An [HDF5AnnData](#) object with the same data as the input AnnData object.

See Also

Other object converters: [as_AnnData\(\)](#), [as_InMemoryAnnData\(\)](#), [as_ReticulateAnnData\(\)](#), [as_Seurat\(\)](#), [as_SingleCellExperiment\(\)](#), [reticulate-helpers](#)

as_InMemoryAnnData	<i>Convert an AnnData to an InMemoryAnnData</i>
--------------------	---

Description

Convert another AnnData object to an [InMemoryAnnData](#) object

Usage

```
as_InMemoryAnnData(adata)
```

Arguments

adata An AnnData object to be converted to [InMemoryAnnData](#)

Value

An [InMemoryAnnData](#) object with the same data as the input AnnData object

See Also

Other object converters: [as_AnnData\(\)](#), [as_HDF5AnnData\(\)](#), [as_ReticulateAnnData\(\)](#), [as_Seurat\(\)](#), [as_SingleCellExperiment\(\)](#), [reticulate-helpers](#)

Examples

```
ad <- AnnData(
  X = matrix(1:5, 3L, 5L),
  layers = list(
    A = matrix(5:1, 3L, 5L),
    B = matrix(letters[1:5], 3L, 5L)
  ),
  obs = data.frame(row.names = LETTERS[1:3], cell = 1:3),
  var = data.frame(row.names = letters[1:5], gene = 1:5)
)
ad$as_InMemoryAnnData()
```

as_ReticulateAnnData *Convert an AnnData to a ReticulateAnnData*

Description

Convert another AnnData object to a [ReticulateAnnData](#) object

Usage

```
as_ReticulateAnnData(adata)
```

Arguments

adata An AnnData object to be converted to [ReticulateAnnData](#)

Value

A [ReticulateAnnData](#) object with the same data as the input AnnData object

See Also

Other object converters: [as_AnnData\(\)](#), [as_HDF5AnnData\(\)](#), [as_InMemoryAnnData\(\)](#), [as_Seurat\(\)](#), [as_SingleCellExperiment\(\)](#), [reticulate-helpers](#)

Examples

```
# Requires Python anndata to be installed
if (requireNamespace("reticulate", quietly = TRUE) &&
    reticulate::py_module_available("anndata")) {
  ad <- AnnData(
    X = matrix(1:5, 3L, 5L),
    layers = list(
      A = matrix(5:1, 3L, 5L),
      B = matrix(letters[1:5], 3L, 5L)
    ),
    obs = data.frame(row.names = LETTERS[1:3], cell = 1:3),
    var = data.frame(row.names = letters[1:5], gene = 1:5)
  )
  ad$as_ReticulateAnnData()
}
```

as_Seurat *Convert an AnnData to a Seurat*

Description

Convert an AnnData object to a Seurat object

Usage

```
as_Seurat(
  adata,
  assay_name = "RNA",
  x_mapping = NULL,
  layers_mapping = TRUE,
  object_metadata_mapping = TRUE,
  assay_metadata_mapping = TRUE,
  reduction_mapping = TRUE,
  graph_mapping = TRUE,
  misc_mapping = TRUE
)
```

Arguments

<code>adata</code>	The AnnData object to convert.
<code>assay_name</code>	Name of the assay to be created in the new Seurat object
<code>x_mapping</code>	A string specifying the name of the layer in the resulting Seurat object where the data in the X slot of adata will be mapped to
<code>layers_mapping</code>	A named vector where names are names of Layers in the resulting Seurat object and values are keys of layers in adata. See below for details.
<code>object_metadata_mapping</code>	A named vector where names are cell metadata columns in the resulting Seurat object and values are columns of obs in adata. See below for details.
<code>assay_metadata_mapping</code>	A named vector where names are variable metadata columns in the assay of the resulting Seurat object and values are columns of var in adata. See below for details.
<code>reduction_mapping</code>	A named vector where names are names of Embeddings in the resulting Seurat object and values are keys of obsm in adata. Alternatively, a named list where names are names of Embeddings in the resulting Seurat object and values are vectors with the items "key", "embeddings" and (optionally) "loadings". See below for details.
<code>graph_mapping</code>	A named vector where names are names of Graphs in the resulting Seurat object and values are keys of obsp in adata. See below for details.
<code>misc_mapping</code>	A named vector where names are names of Misc in the resulting Seurat object and values are keys of uns in adata. See below for details.

Details**Mapping arguments:**

All mapping arguments expect a named character vector where names are the names of the slot in the Seurat object and values are the keys of the corresponding slot of adata. If TRUE, the conversion function will guess which items to copy as described in the conversion table below. In most cases, the default is to copy all items using the same names except where the correspondence between objects is unclear. The `reduction_mapping` argument can also accept a more complex list format, see below for details. To avoid copying anything to a slot, set the mapping argument to FALSE. Empty mapping arguments (NULL, `c()`, `list()`) will be treated as FALSE with a warning. If an unnamed vector is provided, the values will be used as names.

Examples::

- TRUE will guess which items to copy as described in the conversion table
- `c(seurat_item = "adata_item")` will copy `adata_item` from the slot in `adata` to `seurat_item` in the corresponding slot of the new Seurat object
- FALSE will avoid copying anything to the slot
- `c("adata_item")` is equivalent to `c(adata_item = "adata_item")`

Conversion table:

From AnnData	To Seurat	Example mapping argument
<code>adata\$X</code>	<code>Layers(seurat)</code>	<code>x_mapping = "counts" OR layers_mapping = c(counts = NA)</code>
<code>adata\$layers</code>	<code>Layers(seurat)</code>	<code>layers_mapping = c(counts = "counts")</code>
<code>adata\$obs</code>	<code>seurat[[[]]</code>	<code>object_metadata_mapping = c(n_counts = "n_counts", cell_type = "cell_type")</code>
<code>adata\$var</code>	<code>seurat[[assay_name]][[]]</code>	<code>assay_metadata_mapping = c(n_cells = "n_cells", pct_zero = "pct_zero")</code>
<code>adata\$obsm</code>	<code>Reductions(seurat)</code>	<code>reduction_mapping = c(pca = "X_pca") OR reduction_mapping = c(reduction = "PCA")</code>
<code>adata\$obsp</code>	<code>Graphs(seurat)</code>	<code>graph_mapping = c(nn = "connectivities")</code>
<code>adata\$varp</code>	NA	NA
<code>adata\$uns</code>	<code>Misc(seurat)</code>	<code>misc_mapping = c(project_metadata = "metadata")</code>

The reduction_mapping argument:

For the simpler named vector format, the names should be the names of Embeddings in the resulting Seurat object, and the values should be the keys of obsm in `adata`. A key will be created from the obsm key.

For more advanced mapping, use the list format where each item is a vector with the following names defining arguments to `SeuratObject::CreateDimReducObject()`:

- key: the key of the resulting `SeuratObject::DimReduc` object, passed to the key argument after processing with `SeuratObject::Key()`
- embeddings: a key of the obsm slot in `adata`, `adata$obsm[[embeddings]]` is passed to the embeddings argument
- loadings: a key of the varm slot in `adata` (optional), `adata$varm[[loadings]]` is passed to the loadings argument

The x_mapping and layers_mapping arguments:

In order to specify where the data in `adata$X` will be stored in the `Layers(seurat)` slot of the resulting object, you can use either the `x_mapping` argument or the `layers_mapping` argument. If you use `x_mapping`, it should be a string specifying the name of the layer in `Layers(seurat)` where the data in `adata$X` will be stored. If you use `layers_mapping`, it should be a named vector where names are names of `Layers(seurat)` and values are keys of layers in `adata`. In order to indicate the `adata$X` slot, you use NA as the value in the vector. The name you provide for `x_mapping` may not be a name in `layers_mapping`.

Value

A Seurat object containing the requested data from `adata`

See Also

Other object converters: `as_AnnData()`, `as_HDF5AnnData()`, `as_InMemoryAnnData()`, `as_ReticulateAnnData()`, `as_SingleCellExperiment()`, `reticulate-helpers`

Examples

```
ad <- AnnData(
  X = matrix(1:5, 3L, 5L),
  obs = data.frame(row.names = LETTERS[1:3], cell = 1:3),
  var = data.frame(row.names = letters[1:5], gene = 1:5)
)

# Default usage
seurat <- ad$as_Seurat(
  assay_name = "RNA",
  x_mapping = "counts",
  layers_mapping = TRUE,
  object_metadata_mapping = TRUE,
  assay_metadata_mapping = TRUE,
  reduction_mapping = TRUE,
  graph_mapping = TRUE,
  misc_mapping = TRUE
)
```

as_SingleCellExperiment

Convert an AnnData to a SingleCellExperiment

Description

Convert an AnnData object to a SingleCellExperiment object

Usage

```
as_SingleCellExperiment(
  adata,
  x_mapping = NULL,
  assays_mapping = TRUE,
  colData_mapping = TRUE,
  rowData_mapping = TRUE,
  reducedDims_mapping = TRUE,
  colPairs_mapping = TRUE,
  rowPairs_mapping = TRUE,
  metadata_mapping = TRUE
)
```

Arguments

adata	The AnnData object to convert
x_mapping	A string specifying the name of the assay in the resulting SingleCellExperiment where the data in the X slot of adata will be mapped to
assays_mapping	A named vector where names are names of assays in the resulting SingleCellExperiment object and values are keys of layers in adata. See below for details.
colData_mapping	A named vector where names are columns of colData in the resulting SingleCellExperiment object and values are columns of obs in adata. See below for details.

rowData_mapping	A named vector where names are columns of rowData in the resulting SingleCellExperiment object and values are columns of var in adata. See below for details.
reducedDims_mapping	A named vector where names are names of reducedDims in the resulting SingleCellExperiment object and values are keys of obsm in adata. Alternatively, a named list where names are names of reducedDims in the resulting SingleCellExperiment object and values are vectors with the items "sampleFactors" and "featureLoadings" and/or "metadata". See below for details.
colPairs_mapping	A named vector where names are names of colPairs in the resulting SingleCellExperiment object and values are keys of obsp in adata. See below for details.
rowPairs_mapping	A named vector where names are names of rowPairs in the resulting SingleCellExperiment object and values are keys of varp in adata. See below for details.
metadata_mapping	A named vector where names are names of metadata in the resulting SingleCellExperiment object and values are keys of uns in adata. See below for details.

Details

Mapping arguments:

All mapping arguments expect a named character vector where names are the names of the slot in the SingleCellExperiment object and values are the keys of the corresponding slot of adata. If TRUE, the conversion function will guess which items to copy as described in the conversion tables below. In most cases, the default is to copy all items using the same names except where the correspondence between objects is unclear. The reducedDims_mapping argument can also accept a more complex list format, see below for details. To avoid copying anything to a slot, set the mapping argument to FALSE. Empty mapping arguments (NULL, c(), list()) will be treated as FALSE with a warning. If an unnamed vector is provided, the values will be used as names.

Examples::

- TRUE will guess which items to copy as described in the conversion table
- c(sce_item = "adata_item") will copy adata_item from the slot in adata to sce_item in the corresponding slot of the new SingleCellExperiment object
- FALSE will avoid copying anything to the slot
- c("adata_item") is equivalent to c(adata_item = "adata_item")

Conversion table:

From AnnData	To SingleCellExperiment	Example mapping argument
adata\$X	assays(sce)	x_mapping = "counts"
adata\$layers	assays(sce)	assays_mapping = c(counts = "counts")
adata\$obs	colData(sce)	colData_mapping = c(n_counts = "n_counts", cell_type = "CellType")
adata\$var	rowData(sce)	rowData_mapping = c(n_cells = "n_cells", pct_zero = "PctZero")
adata\$obsm	reducedDims(sce)	reducedDims_mapping = c(pca = "X_pca") OR reducedDims_mapping = c(list(pca = "X_pca"))
adata\$obsp	colPairs(sce)	colPairs_mapping = c(nn = "connectivities")
adata\$varp	rowPairs(sce)	rowPairs_mapping = c(gene_overlaps = "similarities")
adata\$uns	metadata(sce)	uns_mapping = c(project_metadata = "metadata")

The reducedDims_mapping argument:

For the simpler named vector format, the names should be the names of reducedDims in the resulting SingleCellExperiment object, and the values should be the keys of obsm in adata.

For more advanced mapping, use the list format where each item is a vector with the following names used to create a [SingleCellExperiment::LinearEmbeddingMatrix](#) (if featureLoadings or metadata is provided):

- sampleFactors: a key of the obsm slot in adata, adata\$obsm[[sampleFactors]] is passed to the sampleFactors argument
- featureLoadings: a key of the varm slot in adata (optional), adata\$varm[[featureLoadings]] is passed to the featureLoadings argument
- metadata: a key of the uns slot in adata (optional), adata\$uns[[metadata]] is passed to the metadata argument

The x_mapping and assays_mapping arguments:

In order to specify where the data in adata\$X will be stored in the assays(sce) slot of the resulting object, you can use either the x_mapping argument or the assays_mapping argument. If you use x_mapping, it should be a string specifying the name of the layer in assays(sce) where the data in adata\$X will be stored. If you use assays_mapping, it should be a named vector where names are names of assays(sce) and values are keys of layers in adata. In order to indicate the adata\$X slot, you use NA as the value in the vector. The name you provide for x_mapping may not be a name in assays_mapping.

Value

A SingleCellExperiment object containing the requested data from adata

See Also

Other object converters: [as_AnnData\(\)](#), [as_HDF5AnnData\(\)](#), [as_InMemoryAnnData\(\)](#), [as_ReticulateAnnData\(\)](#), [as_Seurat\(\)](#), [reticulate-helpers](#)

Examples

```
ad <- AnnData(
  X = matrix(1:5, 3L, 5L),
  layers = list(A = matrix(5:1, 3L, 5L), B = matrix(letters[1:5], 3L, 5L)),
  obs = data.frame(row.names = LETTERS[1:3], cell = 1:3),
  var = data.frame(row.names = letters[1:5], gene = 1:5)
)

# Default usage
sce <- ad$as_SingleCellExperiment(
  assays_mapping = TRUE,
  colData_mapping = TRUE,
  rowData_mapping = TRUE,
  reducedDims_mapping = TRUE,
  colPairs_mapping = TRUE,
  rowPairs_mapping = TRUE,
  metadata_mapping = TRUE
)
```

generate_dataset	<i>Generate a mock dataset</i>
------------------	--------------------------------

Description

Generate a mock synthetic dataset with different types of columns and layers. This is primarily designed for use in tests, examples, vignettes and other documentation but is also provided to users for creating reproducible examples.

Use `get_generator_types()` to get the available types for each slot.

Usage

```
generate_dataset(
  n_obs = 10L,
  n_vars = 20L,
  x_type = "numeric_matrix",
  layer_types = get_generator_types(slot = "layers"),
  obs_types = get_generator_types(slot = "obs"),
  var_types = get_generator_types(slot = "var"),
  obsm_types = get_generator_types(slot = "obsm"),
  varm_types = get_generator_types(slot = "varm"),
  obsp_types = get_generator_types(slot = "obsp"),
  varp_types = get_generator_types(slot = "varp"),
  uns_types = get_generator_types(slot = "uns"),
  example = FALSE,
  format = c("list", "AnnData", "SingleCellExperiment", "Seurat")
)

get_generator_types(example = FALSE, slot = NULL)
```

Arguments

<code>n_obs</code>	Number of observations to generate
<code>n_vars</code>	Number of variables to generate
<code>x_type</code>	Type of matrix to generate for X
<code>layer_types</code>	Types of matrices to generate for layers
<code>obs_types</code>	Types of vectors to generate for obs
<code>var_types</code>	Types of vectors to generate for var
<code>obsm_types</code>	Types of matrices to generate for obsm
<code>varm_types</code>	Types of matrices to generate for varm
<code>obsp_types</code>	Types of matrices to generate for obsp
<code>varp_types</code>	Types of matrices to generate for varp
<code>uns_types</code>	Types of objects to generate for uns
<code>example</code>	If TRUE, the types will be overridden with a small subset of types. This is useful for documentation.
<code>format</code>	Object type to output, one of "list", "AnnData", "SingleCellExperiment", or "Seurat".
<code>slot</code>	Which slot to return types for, if NULL a named list of all slots is returned

Details

To generate no data for a given slot, set the matching type argument to `NULL` or an empty vector, e.g. `obs_types = c()` will generate an empty obs data frame.

When generating `SingleCellExperiment` or `Seurat` objects, only some of the generated slots will be included in the output object. To generate a more complete object, use `format = "AnnData"` followed by `adata$as_SingleCellExperiment()` or `adata$as_Seurat()`.

Use `get_generator_types()` to get a list of the available types for each slot, or for a specific slot by setting `slot`. If `example = TRUE`, only the example types are returned.

Value

For `generate_dataset()`, an object as defined by output containing the generated dataset

For `get_generator_types()`, a named list of character vectors or a single character vector if `slot` is not `NULL`

Examples

```
# Generate all types as a list
dummy <- generate_dataset()

# Generate the example types
dummy_example <- generate_dataset(example = TRUE)

# Generate an AnnData
dummy_anndata <- generate_dataset(format = "AnnData", example = TRUE)

# Generate a SingleCellExperiment
if (rlang::is_installed("SingleCellExperiment")) {
  dummy_sce <- generate_dataset(format = "SingleCellExperiment", example = TRUE)
}

# Generate a Seurat object
if (rlang::is_installed("SeuratObject")) {
  dummy_seurat <- generate_dataset(format = "Seurat", example = TRUE)
}

# Get all available generator types
get_generator_types()

# Get generator types for a specific slot
get_generator_types(slot = "obs")

# Get generator types used when example = TRUE
get_generator_types(example = TRUE)
```

Description

Implementation of an HDF5-backed AnnData object. This class provides an interface to a H5AD file and minimal data is stored in memory until it is requested by the user. It is primarily designed as an intermediate object when reading/writing H5AD files but can be useful for accessing parts of large files.

See [AnnData-usage](#) for details on creating and using AnnData objects.

Value

An HDF5AnnData object

Super class

`anndataR::AbstractAnnData` -> HDF5AnnData

Active bindings

`X` See [AnnData-usage](#)

`layers` See [AnnData-usage](#)

`obsm` See [AnnData-usage](#)

`varm` See [AnnData-usage](#)

`obsp` See [AnnData-usage](#)

`varp` See [AnnData-usage](#)

`obs` See [AnnData-usage](#)

`var` See [AnnData-usage](#)

`obs_names` See [AnnData-usage](#)

`var_names` See [AnnData-usage](#)

`uns` See [AnnData-usage](#)

Methods**Public methods:**

- `HDF5AnnData$new()`
- `HDF5AnnData$close()`
- `HDF5AnnData$n_obs()`
- `HDF5AnnData$n_vars()`

Method `new()`: Close the HDF5 file when the object is garbage collected

HDF5AnnData constructor

Usage:

```
HDF5AnnData$new(
  file,
  X = NULL,
  obs = NULL,
  var = NULL,
  layers = NULL,
  obsm = NULL,
  varm = NULL,
```

```

    obsp = NULL,
    varp = NULL,
    uns = NULL,
    shape = NULL,
    mode = c("a", "r", "r+", "w", "w-", "x"),
    compression = c("none", "gzip", "lzf")
)

```

Arguments:

file The file name (character) of the .h5ad file. If this file already exists, other arguments must be NULL.

X See the X slot in [AnnData-usage](#)

obs See the obs slot in [AnnData-usage](#)

var See the var slot in [AnnData-usage](#)

layers See the layers slot in [AnnData-usage](#)

obsm See the obsm slot in [AnnData-usage](#)

varm See the varm slot in [AnnData-usage](#)

obsp See the obsp slot in [AnnData-usage](#)

varp See the varp slot in [AnnData-usage](#)

uns See the uns slot in [AnnData-usage](#)

shape Shape tuple (e.g. c(n_obs, n_vars)). Can be provided if both X or obs and var are not provided.

mode The mode to open the HDF5 file. See [as_HDF5AnnData\(\)](#) for details

compression The compression algorithm to use. See [as_HDF5AnnData\(\)](#) for details

Details: The constructor creates a new HDF5 AnnData interface object. This can either be used to either connect to an existing .h5ad file or to create a new one. If any additional slot arguments are set an existing file will be overwritten.

Method `close()`: Close the HDF5 file

Usage:

```
HDF5AnnData$close()
```

Method `n_obs()`: See the n_obs field in [AnnData-usage](#)

Usage:

```
HDF5AnnData$n_obs()
```

Method `n_vars()`: See the n_vars field in [AnnData-usage](#)

Usage:

```
HDF5AnnData$n_vars()
```

See Also

[AnnData-usage](#) for details on creating and using AnnData objects

Other AnnData classes: [AbstractAnnData](#), [AnnDataView](#), [InMemoryAnnData](#), [ReticulateAnnData](#)

InMemoryAnnData	<i>InMemoryAnnData</i>
-----------------	------------------------

Description

Implementation of an in-memory AnnData object where data is stored within the R session. This is the simplest back end and will be most familiar to users. It is what you will want to use in most cases where you want to interact with an AnnData object.

See [AnnData-usage](#) for details on creating and using AnnData objects.

Value

An InMemoryAnnData object

Super class

`anndataR::AbstractAnnData` -> InMemoryAnnData

Active bindings

X See [AnnData-usage](#)

layers See [AnnData-usage](#)

obs See [AnnData-usage](#)

var See [AnnData-usage](#)

obs_names See [AnnData-usage](#)

var_names See [AnnData-usage](#)

obsm See [AnnData-usage](#)

varm See [AnnData-usage](#)

obsp See [AnnData-usage](#)

varp See [AnnData-usage](#)

uns See [AnnData-usage](#)

Methods

Public methods:

- `InMemoryAnnData$new()`
- `InMemoryAnnData$clone()`

Method `new()`: Creates a new instance of an in-memory AnnData object. Inherits from [AbstractAnnData](#).

Usage:

```
InMemoryAnnData$new(
  X = NULL,
  obs = NULL,
  var = NULL,
  layers = NULL,
  obsm = NULL,
```

```

    varm = NULL,
    obsp = NULL,
    varp = NULL,
    uns = NULL,
    shape = NULL
  )

```

Arguments:

X See the X slot in [AnnData-usage](#)

obs See the obs slot in [AnnData-usage](#)

var See the var slot in [AnnData-usage](#)

layers See the layers slot in [AnnData-usage](#)

obsm See the obsm slot in [AnnData-usage](#)

varm See the varm slot in [AnnData-usage](#)

obsp See the obsp slot in [AnnData-usage](#)

varp See the varp slot in [AnnData-usage](#)

uns See the uns slot in [AnnData-usage](#)

shape Shape tuple (e.g. `c(n_obs, n_vars)`). Can be provided if both X or obs and var are not provided.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
InMemoryAnnData$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

See Also

[AnnData-usage](#) for details on creating and using AnnData objects

Other AnnData classes: [AbstractAnnData](#), [AnnDataView](#), [HDF5AnnData](#), [ReticulateAnnData](#)

Examples

```

## complete example
ad <- AnnData(
  X = matrix(1:15, 3L, 5L),
  layers = list(
    A = matrix(5:1, 3L, 5L),
    B = matrix(letters[1:5], 3L, 5L)
  ),
  obs = data.frame(row.names = LETTERS[1:3], cell = 1:3),
  var = data.frame(row.names = letters[1:5], gene = 1:5)
)
ad

## minimum example
AnnData(
  obs = data.frame(row.names = letters[1:10]),
  var = data.frame(row.names = LETTERS[1:5])
)

```

read_h5ad	<i>Read H5AD</i>
-----------	------------------

Description

Read data from a H5AD file

Usage

```
read_h5ad(
  path,
  as = c("InMemoryAnnData", "HDF5AnnData", "SingleCellExperiment", "Seurat"),
  mode = c("r", "r+", "a", "w", "w-", "x"),
  ...
)
```

Arguments

path	Path to the H5AD file to read
as	The type of object to return. One of: "InMemoryAnnData": Read the H5AD file into memory as an InMemoryAnnData object "HDF5AnnData": Read the H5AD file as an HDF5AnnData object "SingleCellExperiment": Read the H5AD file as a SingleCellExperiment::SingleCellExperiment object "Seurat": Read the H5AD file as a SeuratObject::Seurat object
mode	The mode to open the HDF5 file. - a creates a new file or opens an existing one for read/write. - r opens an existing file for reading. - r+ opens an existing file for read/write. - w creates a file, truncating any existing ones. - w-/x are synonyms, creating a file and failing if it already exists.
...	Extra arguments provided to the as_* conversion function for the object specified by as

Value

The object specified by as

See Also

Other AnnData creators: [AnnData\(\)](#), [as_AnnData\(\)](#)

Examples

```
h5ad_file <- system.file("extdata", "example.h5ad", package = "anndataR")

# Read the H5AD as a SingleCellExperiment object
if (requireNamespace("SingleCellExperiment", quietly = TRUE)) {
  sce <- read_h5ad(h5ad_file, as = "SingleCellExperiment")
}

# Read the H5AD as a Seurat object
if (requireNamespace("SeuratObject", quietly = TRUE)) {
  seurat <- read_h5ad(h5ad_file, as = "Seurat")
}
```

reticulate-helpers *Reticulate Helper Functions for AnnData Conversion*

Description

This file contains helper functions that enable seamless conversion between R and Python AnnData objects using the reticulate package. These functions provide automatic S3 method dispatch for converting AnnData objects across the R-Python boundary.

Usage

```
## S3 method for class 'collections.abc.Mapping'
py_to_r(x)

## S3 method for class 'anndata._core.anndata.AnnData'
py_to_r(x)

## S3 method for class 'AbstractAnnData'
r_to_py(x, convert = TRUE)
```

Arguments

x	An AbstractAnnData object (any anndataR implementation)
convert	Whether to convert the result (passed to reticulate)

Details

The main conversion functions include:

- `py_to_r.anndata._core.anndata.AnnData`: Converts Python AnnData objects to R [ReticulateAnnData](#) objects
- `r_to_py.AbstractAnnData`: Converts R [AbstractAnnData](#) objects to Python AnnData objects
- `py_to_r.collections.abc.Mapping`: Converts Python mapping objects to R lists

These functions are automatically registered as S3 methods and are called when using `reticulate::py_to_r()` and `reticulate::r_to_py()` on compatible objects.

Value

A [ReticulateAnnData](#) object wrapping the Python object

A Python AnnData object

See Also

Other object converters: [as_AnnData\(\)](#), [as_HDF5AnnData\(\)](#), [as_InMemoryAnnData\(\)](#), [as_ReticulateAnnData\(\)](#), [as_Seurat\(\)](#), [as_SingleCellExperiment\(\)](#)

Examples

```
# Requires Python anndata to be installed
if (requireNamespace("reticulate", quietly = TRUE) &&
    reticulate::py_module_available("anndata")) {

  library(reticulate)

  # Create Python AnnData object
  ad_py <- import("anndata", convert = FALSE)
  py_adata <- ad_py$AnnData(X = r_to_py(matrix(1:12, 3, 4)))

  # Automatic conversion to R (uses py_to_r.anndata._core.anndata.AnnData)
  r_adata <- py_to_r(py_adata)

  # Automatic conversion back to Python (uses r_to_py.AbstractAnnData)
  py_adata2 <- r_to_py(r_adata)
}
```

ReticulateAnnData

ReticulateAnnData

Description

Implementation of an AnnData object that wraps a Python **anndata** AnnData object using **reticulate**. This allows direct interaction with Python AnnData objects while maintaining the R interface. It is useful when you already have a Python AnnData or to access functionality that has not yet been implemented in **anndataR**.

See [AnnData-usage](#) for details on creating and using AnnData objects.

Value

A ReticulateAnnData object

Super class

[anndataR::AbstractAnnData](#) -> ReticulateAnnData

Active bindings

X See [AnnData-usage](#)
 layers See [AnnData-usage](#)
 obs See [AnnData-usage](#)
 var See [AnnData-usage](#)
 obs_names See [AnnData-usage](#)
 var_names See [AnnData-usage](#)
 obsm See [AnnData-usage](#)
 varm See [AnnData-usage](#)
 obsp See [AnnData-usage](#)
 varp See [AnnData-usage](#)
 uns See [AnnData-usage](#)

Methods**Public methods:**

- [ReticulateAnnData\\$new\(\)](#)
- [ReticulateAnnData\\$n_obs\(\)](#)
- [ReticulateAnnData\\$n_vars\(\)](#)
- [ReticulateAnnData\\$py_anndata\(\)](#)

Method `new()`: ReticulateAnnData constructor

Usage:

```

ReticulateAnnData$new(
  py_anndata = NULL,
  X = NULL,
  obs = NULL,
  var = NULL,
  layers = NULL,
  obsm = NULL,
  varm = NULL,
  obsp = NULL,
  varp = NULL,
  uns = NULL,
  shape = NULL
)

```

Arguments:

`py_anndata` A Python AnnData object created using reticulate, or NULL to create a new empty Python AnnData object

X See the X slot in [AnnData-usage](#) (only used if `py_anndata` is NULL)

obs See the obs slot in [AnnData-usage](#) (only used if `py_anndata` is NULL)

var See the var slot in [AnnData-usage](#) (only used if `py_anndata` is NULL)

layers See the layers slot in [AnnData-usage](#) (only used if `py_anndata` is NULL)

obsm See the obsm slot in [AnnData-usage](#) (only used if `py_anndata` is NULL)

varm See the varm slot in [AnnData-usage](#) (only used if `py_anndata` is NULL)

obsp See the obsp slot in [AnnData-usage](#) (only used if `py_anndata` is NULL)

varp See the varp slot in [AnnData-usage](#) (only used if py_anndata is NULL)
uns See the uns slot in [AnnData-usage](#) (only used if py_anndata is NULL)
shape Shape tuple (e.g. c(n_obs, n_vars)). Can be provided if both X or obs and var are not provided. (only used if py_anndata is NULL)

Details: The constructor creates a new ReticulateAnnData interface object that wraps a Python AnnData object. If py_anndata is provided, it must be a valid Python AnnData object. If NULL, a new Python AnnData object will be created using the other provided arguments.

Method n_obs(): See the n_obs field in [AnnData-usage](#)

Usage:

```
ReticulateAnnData$n_obs()
```

Method n_vars(): See the n_vars field in [AnnData-usage](#)

Usage:

```
ReticulateAnnData$n_vars()
```

Method py_anndata(): Get the underlying Python AnnData object

Usage:

```
ReticulateAnnData$py_anndata()
```

Returns: The Python AnnData object wrapped by this ReticulateAnnData

See Also

[AnnData-usage](#) for details on creating and using AnnData objects

Other AnnData classes: [AbstractAnnData](#), [AnnDataView](#), [HDF5AnnData](#), [InMemoryAnnData](#)

write_h5ad

Write H5AD

Description

Write an H5AD file

Usage

```
write_h5ad(
  object,
  path,
  compression = c("none", "gzip", "lzf"),
  mode = c("w-", "r", "r+", "a", "w", "x"),
  ...
)
```

Arguments

object	The object to write, either a <code>SingleCellExperiment::SingleCellExperiment</code> or a <code>SeuratObject::Seurat</code> object
path	Path of the file to write to
compression	The compression algorithm to use when writing the HDF5 file. Can be one of "none", "gzip" or "lzf". Defaults to "none".
mode	The mode to open the HDF5 file. • a creates a new file or opens an existing one for read/write • r+ opens an existing file for read/write • w creates a file, truncating any existing ones • w-/x are synonyms creating a file and failing if it already exists
...	Additional arguments passed to <code>as_AnnData()</code>

Details

Compression:

Compression is currently not supported for Boolean arrays, they will be written uncompressed.

NULL values:

For compatibility with changes in Python **anndata** 0.12.0, NULL values in uns are written to H5AD files as a NULL dataset (instead of not being written at all). To disable this behaviour, set `option(anndataR.write_null = FALSE)`. This may be required to allow the file to be read by older versions of Python **anndata**.

Value

path invisibly

Examples

```
adata <- AnnData(
  X = matrix(1:5, 3L, 5L),
  layers = list(
    A = matrix(5:1, 3L, 5L),
    B = matrix(letters[1:5], 3L, 5L)
  ),
  obs = data.frame(row.names = LETTERS[1:3], cell = 1:3),
  var = data.frame(row.names = letters[1:5], gene = 1:5)
)
h5ad_file <- tempfile(fileext = ".h5ad")
adata$write_h5ad(h5ad_file)

# Write a SingleCellExperiment as an H5AD
if (requireNamespace("SingleCellExperiment", quietly = TRUE)) {
  ncells <- 100
  counts <- matrix(rpois(20000, 5), ncol = ncells)
  logcounts <- log2(counts + 1)

  pca <- matrix(runif(ncells * 5), ncells)
  tsne <- matrix(rnorm(ncells * 2), ncells)

  sce <- SingleCellExperiment::SingleCellExperiment(
```

```

    assays = list(counts = counts, logcounts = logcounts),
    reducedDims = list(PCA = pca, tSNE = tsne)
  )

  adata <- as_AnnData(sce)
  h5ad_file <- tempfile(fileext = ".h5ad")
  adata$write_h5ad(h5ad_file)
}

# Write a Seurat as a H5AD
if (requireNamespace("Seurat", quietly = TRUE)) {
  library(Seurat)

  counts <- matrix(1:15, 5L, 3L)
  dimnames(counts) <- list(
    LETTERS[1:5],
    letters[1:3]
  )
  cell.metadata <- data.frame(
    row.names = letters[1:3],
    cell = 1:3
  )
  obj <- CreateSeuratObject(counts, meta.data = cell.metadata)
  gene.metadata <- data.frame(
    row.names = LETTERS[1:5],
    gene = 1:5
  )
  obj[["RNA"]] <- AddMetaData(GetAssay(obj), gene.metadata)

  adata <- as_AnnData(obj)
  h5ad_file <- tempfile(fileext = ".h5ad")
  adata$write_h5ad(h5ad_file)
}

```

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