

Package: anndata (via r-universe)

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Type Package

Title 'anndata' for R (Superseded)

Version 0.9.0

Description A 'reticulate' wrapper for the Python package 'anndata'.

Provides a scalable way of keeping track of data and learned annotations. Used to read from and write to the h5ad file format. This package is superseded by 'anndataR' <<https://anndataR.scverse.org>>, which provides native R backends for the 'AnnData' data structure, along with conversion to/from 'SingleCellExperiment' and 'Seurat' objects.

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URL <https://anndata.dynverse.org>, <https://github.com/dynverse/anndata>

BugReports <https://github.com/dynverse/anndata/issues>

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anndata-package	<i>anndata - Annotated Data</i>
-----------------	---------------------------------

Description

[Superseded]

Details

This package is superseded by **anndataR.** anndataR provides a pure R implementation of the AnnData data structure with native h5ad file reading/writing and conversion to/from SingleCellExperiment and Seurat objects. Please consider migrating; see `vignette("migration_to_anndataR", package = "anndata")` for guidance.

If you already have Python anndata installed, anndataR's ReticulateAnnData backend lets you keep using your existing Python environment while gaining access to anndataR's unified interface. The native InMemoryAnnData and HDF5AnnData backends (no Python required) are preferred for new workflows.

anndata provides a scalable way of keeping track of data and learned annotations, and can be used to read from and write to the h5ad file format. `AnnData()` stores a data matrix `X` together

with annotations of observations `obs` (`obsm`, `obsp`), variables `var` (`varm`, `varp`), and unstructured annotations `uns`.

This package is an R wrapper for the similarly named Python package `anndata`, with some added functionality to support more R-like syntax.

Check out `?anndata` for a full list of the functions provided by this package.

Creating an AnnData object

- `AnnData()`

Concatenating two or more AnnData objects

- `concat()`

Reading an AnnData object from a file

- `read_csv()`
- `read_excel()`
- `read_h5ad()`
- `read_hdf()`
- `read_loom()`
- `read_mtx()`
- `read_text()`
- `read_umi_tools()`

Writing an AnnData object to a file

- `write_csvs()`
- `write_h5ad()`
- `write_loom()`

Install the anndata Python package

- `install_anndata()`

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See Also

Useful links:

- <https://anndata.dynverse.org>
- <https://github.com/dynverse/anndata>
- Report bugs at <https://github.com/dynverse/anndata/issues>

Examples

```
## Not run:
ad <- AnnData(
  X = matrix(1:6, nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L, 3L), row.names = c("var1", "var2", "var3")),
  layers = list(
    spliced = matrix(4:9, nrow = 2),
    unspliced = matrix(8:13, nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  varm = list(
    ones = matrix(rep(1L, 12), nrow = 3),
    rand = matrix(rnorm(6), nrow = 3),
    zeros = matrix(rep(0L, 12), nrow = 3)
  ),
  uns = list(
    a = 1,
    b = data.frame(i = 1:3, j = 4:6, value = runif(3)),
    c = list(c.a = 3, c.b = 4)
  )
)

ad$X

ad$obs
ad$var

ad$obsm["ones"]
ad$varm["rand"]

ad$layers["unspliced"]
ad$layers["spliced"]

ad$uns["b"]

ad[, c("var1", "var2")]
ad[-1, , drop = FALSE]
ad[, 2] <- 10
```

```
## End(Not run)
```

```
all.equal.AnnDataR6     Test if two objects objects are equal
```

Description

Test if two objects objects are equal

Usage

```
## S3 method for class 'AnnDataR6'
all.equal(target, current, ...)

## S3 method for class 'LayersR6'
all.equal(target, current, ...)

## S3 method for class 'RawR6'
all.equal(target, current, ...)
```

Arguments

target	R object.
current	other R object, to be compared with target.
...	further arguments for different methods, notably the following two, for numerical comparison:

```
AnnData                     Create an Annotated Data Matrix
```

Description

AnnData stores a data matrix X together with annotations of observations `obs` (`obsm`, `obsp`), variables `var` (`varm`, `varp`), and unstructured annotations `uns`.

An AnnData object `adata` can be sliced like a data frame, for instance `adata_subset <- adata[, list_of_variable_names]`. AnnData's basic structure is similar to R's `ExpressionSet`.

If setting an h5ad-formatted HDF5 backing file `filename`, data remains on the disk but is automatically loaded into memory if needed. See this [blog post](#) for more details.

Usage

```
AnnData(
    X = NULL,
    obs = NULL,
    var = NULL,
    uns = NULL,
    obsm = NULL,
    varm = NULL,
    layers = NULL,
    raw = NULL,
    dtype = "float32",
    shape = NULL,
    filename = NULL,
    filemode = NULL,
    obsp = NULL,
    varp = NULL
)
```

Arguments

<code>X</code>	A #observations × #variables data matrix. A view of the data is used if the data type matches, otherwise, a copy is made.
<code>obs</code>	Key-indexed one-dimensional observations annotation of length #observations.
<code>var</code>	Key-indexed one-dimensional variables annotation of length #variables.
<code>uns</code>	Key-indexed unstructured annotation.
<code>obsm</code>	Key-indexed multi-dimensional observations annotation of length #observations. If passing a <code>~numpy.ndarray</code> , it needs to have a structured datatype.
<code>varm</code>	Key-indexed multi-dimensional variables annotation of length #variables. If passing a <code>~numpy.ndarray</code> , it needs to have a structured datatype.
<code>layers</code>	Key-indexed multi-dimensional arrays aligned to dimensions of <code>X</code> .
<code>raw</code>	Store raw version of <code>X</code> and <code>var</code> as <code>\$raw\$X</code> and <code>\$raw\$var</code> .
<code>dtype</code>	Data type used for storage.
<code>shape</code>	Shape list (#observations, #variables). Can only be provided if <code>X</code> is <code>NULL</code> .
<code>filename</code>	Name of backing file. See h5py.File .
<code>filemode</code>	Open mode of backing file. See h5py.File .
<code>obsp</code>	Pairwise annotation of observations, a mutable mapping with array-like values.
<code>varp</code>	Pairwise annotation of observations, a mutable mapping with array-like values.

Details

AnnData stores observations (samples) of variables/features in the rows of a matrix. This is the convention of the modern classics of statistic and machine learning, the convention of dataframes both in R and Python and the established statistics and machine learning packages in Python (statsmodels, scikit-learn).

Single dimensional annotations of the observation and variables are stored in the `obs` and `var` attributes as data frames. This is intended for metrics calculated over their axes. Multi-dimensional annotations are stored in `obsm` and `varm`, which are aligned to the objects observation and variable dimensions respectively. Square matrices representing graphs are stored in `obsp` and `varp`, with both of their own dimensions aligned to their associated axis. Additional measurements across both observations and variables are stored in `layers`.

Indexing into an `AnnData` object can be performed by relative position with numeric indices, or by labels. To avoid ambiguity with numeric indexing into observations or variables, indexes of the `AnnData` object are converted to strings by the constructor.

Subsetting an `AnnData` object by indexing into it will also subset its elements according to the dimensions they were aligned to. This means an operation like `adata[list_of_obs, ]` will also subset `obs`, `obsm`, and `layers`.

Subsetting an `AnnData` object returns a view into the original object, meaning very little additional memory is used upon subsetting. This is achieved lazily, meaning that the constituent arrays are subset on access. Copying a view causes an equivalent “real” `AnnData` object to be generated. Attempting to modify a view (at any attribute except `X`) is handled in a copy-on-modify manner, meaning the object is initialized in place. Here’s an example

```
batch1 <- adata[adata$obs["batch"] == "batch1", ]
batch1$obs["value"] = 0 # This makes batch1 a “real” AnnData object
```

At the end of this snippet: `adata` was not modified, and `batch1` is its own `AnnData` object with its own data.

Similar to Bioconductor’s `ExpressionSet` and `scipy.sparse` matrices, subsetting an `AnnData` object retains the dimensionality of its constituent arrays. Therefore, unlike with the classes exposed by `pandas`, `numpy`, and `xarray`, there is no concept of a one dimensional `AnnData` object. `AnnData`s always have two inherent dimensions, `obs` and `var`. Additionally, maintaining the dimensionality of the `AnnData` object allows for consistent handling of `scipy.sparse` matrices and `numpy` arrays.

Superseded

[Superseded] This function is superseded by `anndataR::AnnData()` in the `anndataR` package. See `vignette("migration_to_anndataR", package = "anndataR")` for migration guidance.

Active bindings

`X` Data matrix of shape `n_obs × n_vars`.

`filename` Name of the backing file.

Change to backing mode by setting the `filename` of a `.h5ad` file.

- Setting the `filename` writes the stored data to disk.
- Setting the `filename` when the `filename` was previously another name moves the backing file from the previous file to the new file. If you want to copy the previous file, use `copy(filename='new_filename')`.

`layers` A list-like object with values of the same dimensions as `X`. Layers in `AnnData` are inspired by `loompy`’s `layers`.

Overwrite the layers:

```
adata$layers <- list(spliced = spliced, unspliced = unspliced)
```

Return the layer named "unspliced":

```
adata$layers["unspliced"]
```

Create or replace the "spliced" layer:

```
adata$layers["spliced"] = example_matrix
```

Assign the 10th column of layer "spliced" to the variable a:

```
a <- adata$layers["spliced"][, 10]
```

Delete the "spliced":

```
adata$layers["spliced"] <- NULL
```

Return layers' names:

```
names(adata$layers)
```

T Transpose whole object.

Data matrix is transposed, observations and variables are interchanged.

Ignores `.raw`.

is_view TRUE if object is view of another AnnData object, FALSE otherwise.

isbacked TRUE if object is backed on disk, FALSE otherwise.

n_obs Number of observations.

obs One-dimensional annotation of observations (data.frame).

obs_names Names of observations.

obsm Multi-dimensional annotation of observations (matrix).

Stores for each key a two or higher-dimensional matrix with `n_obs` rows.

obsp Pairwise annotation of observations, a mutable mapping with array-like values.

Stores for each key a two or higher-dimensional matrix whose first two dimensions are of length `n_obs`.

n_vars Number of variables.

var One-dimensional annotation of variables (data.frame).

var_names Names of variables.

varm Multi-dimensional annotation of variables (matrix).

Stores for each key a two or higher-dimensional matrix with `n_vars` rows.

varp Pairwise annotation of variables, a mutable mapping with array-like values.

Stores for each key a two or higher-dimensional matrix whose first two dimensions are of length `n_vars`.

shape Shape of data matrix (`n_obs`, `n_vars`).

uns Unstructured annotation (ordered dictionary).

raw Store raw version of X and var as `$raw$X` and `$raw$var`.

The raw attribute is initialized with the current content of an object by setting:

```
adata$raw = adata
```

Its content can be deleted:

```
adata$raw <- NULL
```

Upon slicing an AnnData object along the obs (row) axis, raw is also sliced. Slicing an AnnData object along the vars (columns) axis leaves raw unaffected. Note that you can call:

```
adata$raw[, 'orig_variable_name']$X
```

to retrieve the data associated with a variable that might have been filtered out or "compressed away".

Methods

Public methods:

- [AnnDataR6\\$new\(\)](#)
- [AnnDataR6\\$obs_keys\(\)](#)
- [AnnDataR6\\$obs_names_make_unique\(\)](#)
- [AnnDataR6\\$obs_keys\(\)](#)
- [AnnDataR6\\$var_keys\(\)](#)
- [AnnDataR6\\$var_names_make_unique\(\)](#)
- [AnnDataR6\\$varm_keys\(\)](#)
- [AnnDataR6\\$uns_keys\(\)](#)
- [AnnDataR6\\$chunk_X\(\)](#)
- [AnnDataR6\\$chunked_X\(\)](#)
- [AnnDataR6\\$concatenate\(\)](#)
- [AnnDataR6\\$copy\(\)](#)
- [AnnDataR6\\$rename_categories\(\)](#)
- [AnnDataR6\\$strings_to_categoricals\(\)](#)
- [AnnDataR6\\$to_df\(\)](#)
- [AnnDataR6\\$transpose\(\)](#)
- [AnnDataR6\\$write_csvs\(\)](#)
- [AnnDataR6\\$write_h5ad\(\)](#)
- [AnnDataR6\\$write_loom\(\)](#)
- [AnnDataR6\\$write_zarr\(\)](#)
- [AnnDataR6\\$print\(\)](#)
- [AnnDataR6\\$.set_py_object\(\)](#)
- [AnnDataR6\\$.get_py_object\(\)](#)

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

Usage:

```
AnnDataR6$new(obj)
```

Arguments:

`obj` A Python anndata object

Examples:

```
\dontrun{
# use AnnData() instead of AnnDataR6$new()
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2"))
)
}
```

Method `obs_keys()`: List keys of observation annotation obs.

Usage:

```
AnnDataR6$obs_keys()
```

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2"))
)
ad$obs_keys()
}
```

Method `obs_names_make_unique()`: Makes the index unique by appending a number string to each duplicate index element: 1, 2, etc.

If a tentative name created by the algorithm already exists in the index, it tries the next integer in the sequence.

The first occurrence of a non-unique value is ignored.

Usage:

```
AnnDataR6$obs_names_make_unique(join = "-")
```

Arguments:

`join` The connecting string between name and integer (default: "-").

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(rep(1, 6), nrow = 3),
  obs = data.frame(field = c(1, 2, 3))
)
ad$obs_names <- c("a", "a", "b")
ad$obs_names_make_unique()
ad$obs_names
}
```

Method `obsm_keys()`: List keys of observation annotation obsm.

Usage:

```
AnnDataR6$obsm_keys()
```

Examples:

```

\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  )
)
ad$obs_keys()
}

```

Method `var_keys()`: List keys of variable annotation var.

Usage:

```
AnnDataR6$var_keys()
```

Examples:

```

\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2"))
)
ad$var_keys()
}

```

Method `var_names_make_unique()`: Makes the index unique by appending a number string to each duplicate index element: 1, 2, etc.

If a tentative name created by the algorithm already exists in the index, it tries the next integer in the sequence.

The first occurrence of a non-unique value is ignored.

Usage:

```
AnnDataR6$var_names_make_unique(join = "-")
```

Arguments:

`join` The connecting string between name and integer (default: "-").

Examples:

```

\dontrun{
ad <- AnnData(
  X = matrix(rep(1, 6), nrow = 2),
  var = data.frame(field = c(1, 2, 3))
)
ad$var_names <- c("a", "a", "b")
ad$var_names_make_unique()
ad$var_names
}

```

Method `varm_keys()`: List keys of variable annotation varm.

Usage:

```
AnnDataR6$varm_keys()
```

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  )
)
ad$varm_keys()
}
```

Method `uns_keys()`: List keys of unstructured annotation `uns`.

Usage:

```
AnnDataR6$uns_keys()
```

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)
}
```

Method `chunk_X()`: Return a chunk of the data matrix `X` with random or specified indices.

Usage:

```
AnnDataR6$chunk_X(select = 1000L, replace = TRUE)
```

Arguments:

`select` Depending on the values:

- 1 integer: A random chunk with `select` rows will be returned.
- multiple integers: A chunk with these indices will be returned.

`replace` if `select` is an integer then `TRUE` means random sampling of indices with replacement, `FALSE` without replacement.

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(runif(10000), nrow = 50)
)

ad$chunk_X(select = 10L) # 10 random samples
ad$chunk_X(select = 1:3) # first 3 samples
}
```

Method `chunked_X()`: Return an iterator over the rows of the data matrix X.

Usage:

```
AnnDataR6$chunked_X(chunk_size = NULL)
```

Arguments:

`chunk_size` Row size of a single chunk.

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(runif(10000), nrow = 50)
)
ad$chunked_X(10)
}
```

Method `concatenate()`: **[Deprecated]**

Use `concat()` instead.

Usage:

```
AnnDataR6$concatenate(...)
```

Arguments:

... Deprecated

Method `copy()`: Full copy, optionally on disk.

Usage:

```
AnnDataR6$copy(filename = NULL)
```

Arguments:

`filename` Path to filename (default: NULL).

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2)
)
ad$copy()
ad$copy("file.h5ad")
}
```

Method `rename_categories()`: Rename categories of annotation key in obs, var, and uns.

Only supports passing a list/array-like `categories` argument. Besides calling `self.obs[key].cat.categories = categories` – similar for var - this also renames categories in unstructured annotation that uses the categorical annotation key.

Usage:

```
AnnDataR6$rename_categories(key, categories)
```

Arguments:

`key` Key for observations or variables annotation.

`categories` New categories, the same number as the old categories.

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2"))
)
ad$rename_categories("group", c(a = "A", b = "B")) # ??
}
```

Method `strings_to_categoricals()`: Transform string annotations to categoricals.

Only affects string annotations that lead to less categories than the total number of observations.

Usage:

```
AnnDataR6$strings_to_categoricals(df = NULL)
```

Arguments:

`df` If `df` is `NULL`, modifies both `obs` and `var`, otherwise modifies `df` inplace.

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
)
ad$strings_to_categoricals() # ??
}
```

Method `to_df()`: Generate shallow data frame.

The data matrix `X` is returned as data frame, where `obs_names` are the rownames, and `var_names` the columns names.

No annotations are maintained in the returned object.

The data matrix is densified in case it is sparse.

Usage:

```
AnnDataR6$to_df(layer = NULL)
```

Arguments:

`layer` Key for layers

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  )
)
```

```
ad$to_df()
ad$to_df("unspliced")
}
```

Method `transpose()`: transpose Transpose whole object.

Data matrix is transposed, observations and variables are interchanged.

Ignores `.raw`.

Usage:

```
AnnDataR6$transpose()
```

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2"))
)

ad$transpose()
}
```

Method `write_csvs()`: Write annotation to `.csv` files.

It is not possible to recover the full AnnData from these files. Use [write_h5ad\(\)](#) for this.

Usage:

```
AnnDataR6$write_csvs(dirname, skip_data = TRUE, sep = ",")
```

Arguments:

`dirname` Name of the directory to which to export.

`skip_data` Skip the data matrix `X`.

`sep` Separator for the data

`anndata` An [AnnData\(\)](#) object

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$to_write_csvs("output")
}
```

```

unlink("output", recursive = TRUE)
}

```

Method `write_h5ad()`: Write .h5ad-formatted hdf5 file.

Generally, if you have sparse data that are stored as a dense matrix, you can dramatically improve performance and reduce disk space by converting to a `csr_matrix`:

Usage:

```

AnnDataR6$write_h5ad(
  filename,
  compression = NULL,
  compression_opts = NULL,
  as_dense = list()
)

```

Arguments:

`filename` Filename of data file. Defaults to backing file.

`compression` See the h5py [filter pipeline](#). Options are "gzip", "lzf" or NULL.

`compression_opts` See the h5py [filter pipeline](#).

`as_dense` Sparse in AnnData object to write as dense. Currently only supports "X" and "raw/X".

Examples:

```

\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$write_h5ad("output.h5ad")

file.remove("output.h5ad")
}

```

Method `write_loom()`: Write .loom-formatted hdf5 file.

Usage:

```

AnnDataR6$write_loom(filename, write_obs_m_varm = FALSE)

```

Arguments:

`filename` The filename.

`write_obs_m_varm` Whether or not to also write the varm and obsm.

Examples:

```

\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$write_loom("output.loom")

file.remove("output.loom")
}

```

Method `write_zarr()`: Write a hierarchical Zarr array store.

Usage:

```
AnnDataR6$write_zarr(store, chunks = NULL)
```

Arguments:

`store` The filename, a `MutableMapping`, or a Zarr storage class.

`chunks` Chunk size.

Method `print()`: Print `AnnData` object

Usage:

```
AnnDataR6$print(...)
```

Arguments:

`...` optional arguments to print method.

Examples:

```

\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  varm = list(

```

```

        ones = matrix(rep(1L, 10), nrow = 2),
        rand = matrix(rnorm(6), nrow = 2),
        zeros = matrix(rep(0L, 10), nrow = 2)
    ),
    uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$print()
print(ad)
}

```

Method `.set_py_object()`: Set internal Python object

Usage:

```
AnnDataR6$.set_py_object(obj)
```

Arguments:

`obj` A python anndata object

Method `.get_py_object()`: Get internal Python object

Usage:

```
AnnDataR6$.get_py_object()
```

See Also

[read_h5ad\(\)](#) [read_csv\(\)](#) [read_excel\(\)](#) [read_hdf\(\)](#) [read_loom\(\)](#) [read_mtx\(\)](#) [read_text\(\)](#)
[read_umi_tools\(\)](#) [write_h5ad\(\)](#) [write_csvs\(\)](#) [write_loom\(\)](#)

Examples

```

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

```

```

value <- matrix(c(1, 2, 3, 4), nrow = 2)
ad$X <- value
ad$X

ad$layers
ad$layers["spliced"]
ad$layers["test"] <- value
ad$layers

ad$to_df()
ad$uns

as.matrix(ad)
as.matrix(ad, layer = "unspliced")
dim(ad)
rownames(ad)
colnames(ad)

## End(Not run)

## -----
## Method `AnnDataR6$new`
## -----

## Not run:
# use AnnData() instead of AnnDataR6$new()
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2"))
)

## End(Not run)

## -----
## Method `AnnDataR6$obs_keys`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2"))
)
ad$obs_keys()

## End(Not run)

## -----
## Method `AnnDataR6$obs_names_make_unique`
## -----

## Not run:
ad <- AnnData(

```

```

    X = matrix(rep(1, 6), nrow = 3),
    obs = data.frame(field = c(1, 2, 3))
)
ad$obs_names <- c("a", "a", "b")
ad$obs_names_make_unique()
ad$obs_names

## End(Not run)

## -----
## Method `AnnDataR6$obs_keys`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  )
)
ad$obs_keys()

## End(Not run)

## -----
## Method `AnnDataR6$var_keys`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2"))
)
ad$var_keys()

## End(Not run)

## -----
## Method `AnnDataR6$var_names_make_unique`
## -----

## Not run:
ad <- AnnData(
  X = matrix(rep(1, 6), nrow = 2),
  var = data.frame(field = c(1, 2, 3))
)
ad$var_names <- c("a", "a", "b")
ad$var_names_make_unique()
ad$var_names

```

```

## End(Not run)

## -----
## Method `AnnDataR6$varm_keys`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  )
)
ad$varm_keys()

## End(Not run)

## -----
## Method `AnnDataR6$uns_keys`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

## End(Not run)

## -----
## Method `AnnDataR6$chunk_X`
## -----

## Not run:
ad <- AnnData(
  X = matrix(runif(10000), nrow = 50)
)

ad$chunk_X(select = 10L) # 10 random samples
ad$chunk_X(select = 1:3) # first 3 samples

## End(Not run)

## -----
## Method `AnnDataR6$chunked_X`
## -----

## Not run:

```

```

ad <- AnnData(
  X = matrix(runif(10000), nrow = 50)
)
ad$chunked_X(10)

## End(Not run)

## -----
## Method `AnnDataR6$copy`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2)
)
ad$copy()
ad$copy("file.h5ad")

## End(Not run)

## -----
## Method `AnnDataR6$rename_categories`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2"))
)
ad$rename_categories("group", c(a = "A", b = "B")) # ??

## End(Not run)

## -----
## Method `AnnDataR6$strings_to_categoricals`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
)
ad$strings_to_categoricals() # ??

## End(Not run)

## -----
## Method `AnnDataR6$to_df`
## -----

## Not run:
ad <- AnnData(

```

```

X = matrix(c(0, 1, 2, 3), nrow = 2),
obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
layers = list(
  spliced = matrix(c(4, 5, 6, 7), nrow = 2),
  unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
)
)

ad$to_df()
ad$to_df("unspliced")

## End(Not run)

## -----
## Method `AnnDataR6$transpose`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2"))
)

ad$transpose()

## End(Not run)

## -----
## Method `AnnDataR6$write_csvs`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$to_write_csvs("output")

unlink("output", recursive = TRUE)

## End(Not run)

## -----

```

```

## Method `AnnDataR6$write_h5ad`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$write_h5ad("output.h5ad")

file.remove("output.h5ad")

## End(Not run)

## -----
## Method `AnnDataR6$write_loom`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$write_loom("output.loom")

file.remove("output.loom")

## End(Not run)

## -----
## Method `AnnDataR6$print`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),

```

```

var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
layers = list(
  spliced = matrix(c(4, 5, 6, 7), nrow = 2),
  unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
),
obsm = list(
  ones = matrix(rep(1L, 10), nrow = 2),
  rand = matrix(rnorm(6), nrow = 2),
  zeros = matrix(rep(0L, 10), nrow = 2)
),
varm = list(
  ones = matrix(rep(1L, 10), nrow = 2),
  rand = matrix(rnorm(6), nrow = 2),
  zeros = matrix(rep(0L, 10), nrow = 2)
),
uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$print()
print(ad)

## End(Not run)

```

concat

*concat***Description**

[Superseded] Concatenates AnnData objects along an axis.

Usage

```

concat(
  adata,
  axis = 0L,
  join = "inner",
  merge = NULL,
  uns_merge = NULL,
  label = NULL,
  keys = NULL,
  index_unique = NULL,
  fill_value = NULL,
  pairwise = FALSE
)

```

Arguments

adata The objects to be concatenated. If a Mapping is passed, keys are used for the keys argument and values are concatenated.

<code>axis</code>	Which axis to concatenate along.
<code>join</code>	How to align values when concatenating. If "outer", the union of the other axis is taken. If "inner", the intersection. See concatenation for more.
<code>merge</code>	How elements not aligned to the axis being concatenated along are selected. Currently implemented strategies include: * NULL: No elements are kept. * "same": Elements that are the same in each of the objects. * "unique": Elements for which there is only one possible value. * "first": The first element seen at each from each position. * "only": Elements that show up in only one of the objects.
<code>uns_merge</code>	How the elements of <code>.uns</code> are selected. Uses the same set of strategies as the <code>merge</code> argument, except applied recursively.
<code>label</code>	Column in axis annotation (i.e. <code>.obs</code> or <code>.var</code>) to place batch information in. If it's NULL, no column is added.
<code>keys</code>	Names for each object being added. These values are used for column values for <code>label</code> or appended to the index if <code>index_unique</code> is not NULL. Defaults to incrementing integer labels.
<code>index_unique</code>	Whether to make the index unique by using the keys. If provided, this is the delimiter between <code>orig_idx + index_unique + key</code> . When NULL, the original indices are kept.
<code>fill_value</code>	When <code>join="outer"</code> , this is the value that will be used to fill the introduced indices. By default, sparse arrays are padded with zeros, while dense arrays and DataFrames are padded with missing values.
<code>pairwise</code>	Whether pairwise elements along the concatenated dimension should be included. This is FALSE by default, since the resulting arrays are often not meaningful.

Details

See the concatenation section in the docs for a more in-depth description.

warning: This function is marked as experimental for the 0.7 release series, and will supercede the `AnnData$concatenate()` method in future releases.

warning: If you use `join='outer'` this fills 0s for sparse data when variables are absent in a batch. Use this with care. Dense data is filled with NaN.

Superseded

This function is superseded. The **anndataR** package supports working with `AnnData` objects natively in R without Python. See `vignette("migration_to_anndataR", package = "anndataR")` for migration guidance.

Examples

```
## Not run:
# Preparing example objects
a <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2, byrow = TRUE),
```

```

obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
varm = list(
  ones = matrix(rep(1L, 10), nrow = 2),
  rand = matrix(rnorm(6), nrow = 2),
  zeros = matrix(rep(0L, 10), nrow = 2)
),
uns = list(
  a = 1,
  b = 2,
  c = list(
    c.a = 3,
    c.b = 4
  )
)
)

b <- AnnData(
  X = matrix(c(4, 5, 6, 7, 8, 9), nrow = 2, byrow = TRUE),
  obs = data.frame(group = c("b", "c"), row.names = c("s3", "s4")),
  var = data.frame(type = c(1L, 2L, 3L), row.names = c("var1", "var2", "var3")),
  varm = list(
    ones = matrix(rep(1L, 15), nrow = 3),
    rand = matrix(rnorm(15), nrow = 3)
  ),
  uns = list(
    a = 1,
    b = 3,
    c = list(
      c.a = 3
    )
  )
)

c <- AnnData(
  X = matrix(c(10, 11, 12, 13), nrow = 2, byrow = TRUE),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(3L, 4L), row.names = c("var3", "var4")),
  uns = list(
    a = 1,
    b = 4,
    c = list(
      c.a = 3,
      c.b = 4,
      c.c = 5
    )
  )
)

# Concatenating along different axes
concat(list(a, b))$to_df()
concat(list(a, c), axis = 1L)$to_df()

```

```

# Inner and outer joins
inner <- concat(list(a, b))
inner
inner$obs_names
inner$var_names

outer <- concat(list(a, b), join = "outer")
outer
outer$var_names
outer$to_df()

# Keeping track of source objects
concat(list(a = a, b = b), label = "batch")$obs
concat(list(a, b), label = "batch", keys = c("a", "b"))$obs
concat(list(a = a, b = b), index_unique = "-")$obs

# Combining values not aligned to axis of concatenation
concat(list(a, b), merge = "same")
concat(list(a, b), merge = "unique")
concat(list(a, b), merge = "first")
concat(list(a, b), merge = "only")

# The same merge strategies can be used for elements in .uns
concat(list(a, b, c), uns_merge = "same")$uns
concat(list(a, b, c), uns_merge = "unique")$uns
concat(list(a, b, c), uns_merge = "first")$uns
concat(list(a, b, c), uns_merge = "only")$uns

## End(Not run)

```

dimnames.AnnDataR6 *AnnData Helpers*

Description

AnnData Helpers

Usage

```

## S3 method for class 'AnnDataR6'
dimnames(x)

## S3 replacement method for class 'AnnDataR6'
dimnames(x) <- value

## S3 method for class 'AnnDataR6'
dim(x)

## S3 method for class 'AnnDataR6'

```

```

as.data.frame(x, row.names = NULL, optional = FALSE, layer = NULL, ...)

## S3 method for class 'AnnDataR6'
as.matrix(x, layer = NULL, ...)

## S3 method for class 'AnnDataR6'
r_to_py(x, convert = FALSE)

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

## S3 method for class 'AnnDataR6'
x[oidx, vidx]

## S3 method for class 'AnnDataR6'
t(x)

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

## S3 method for class 'h5py._hl.dataset.Dataset'
py_to_r(x)

```

Arguments

<code>x</code>	An AnnData object.
<code>value</code>	a possible value for <code>dimnames(ad)</code> . The <code>dimnames</code> of an <code>AnnData</code> can be <code>NULL</code> (which is not stored) or a list of the same length as <code>dim(ad)</code> . If a list, its components are either <code>NULL</code> or a character vector with positive length of the appropriate dimension of <code>ad</code> .
<code>row.names</code>	Not used.
<code>optional</code>	Not used.
<code>layer</code>	An AnnData layer. If <code>NULL</code> , will use <code>ad\$X</code> , otherwise <code>ad\$layers[layer]</code> .
<code>...</code>	Parameters passed to the underlying function.
<code>convert</code>	Not used.
<code>oidx</code>	Observation indices
<code>vidx</code>	Variable indices

Examples

```

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3, 4, 5), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c("1L", "2L", "3L"), row.names = c("var1", "var2", "var3")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7, 8, 9), nrow = 2),

```

```

    unspliced = matrix(c(8, 9, 10, 11, 12, 13), nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  varm = list(
    ones = matrix(rep(1L, 12), nrow = 3),
    rand = matrix(rnorm(6), nrow = 3),
    zeros = matrix(rep(0L, 12), nrow = 3)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

dimnames(ad)
dim(ad)
as.data.frame(ad)
as.data.frame(ad, layer = "unspliced")
as.matrix(ad)
as.matrix(ad, layer = "unspliced")
ad[2, , drop = FALSE]
ad[, -1]
ad[, c("var1", "var2")]

## End(Not run)

```

dimnames.RawR6

Raw Helpers

Description

Raw Helpers

Usage

```

## S3 method for class 'RawR6'
dimnames(x)

## S3 method for class 'RawR6'
dim(x)

## S3 method for class 'RawR6'
as.matrix(x, ...)

## S3 method for class 'RawR6'
r_to_py(x, convert = FALSE)

## S3 method for class 'anndata._core.raw.Raw'

```

```

py_to_r(x)

## S3 method for class 'RawR6'
x[...]
```

Arguments

x	An AnnData object.
...	Parameters passed to the underlying function.
convert	Not used.

Examples

```

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3, 4, 5), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L, 3L), row.names = c("var1", "var2", "var3")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7, 8, 9), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11, 12, 13), nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  varm = list(
    ones = matrix(rep(1L, 12), nrow = 3),
    rand = matrix(rnorm(6), nrow = 3),
    zeros = matrix(rep(0L, 12), nrow = 3)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)
ad$raw <- ad

dimnames(ad$raw)
dim(ad$raw)
as.matrix(ad$raw)
ad$raw[2, , drop = FALSE]
ad$raw[, -1]
ad$raw[, c("var1", "var2")]

## End(Not run)
```

Description**[Deprecated]**

Needs to be run after installing the anndata R package.

Usage

```
install_anndata(method = "auto", conda = "auto")
```

Arguments

method	Installation method. By default, "auto" automatically finds a method that will work in the local environment. Change the default to force a specific installation method. Note that the "virtualenv" method is not available on Windows.
conda	The path to a conda executable. Use "auto" to allow reticulate to automatically find an appropriate conda binary. See Finding Conda and conda_binary() for more details.

Examples

```
## Not run:
reticulate::conda_install()
install_anndata()

## End(Not run)
```

Layers

Create a Layers object

Description

Create a Layers object

Usage

```
Layers(parent, vals = NULL)
```

Arguments

parent	An AnnData object.
vals	A named list of matrices with the same dimensions as parent.

Active bindings

parent Reference to parent AnnData view

Methods**Public methods:**

- `LayersR6$new()`
- `LayersR6$print()`
- `LayersR6$get()`
- `LayersR6$set()`
- `LayersR6$del()`
- `LayersR6$keys()`
- `LayersR6$length()`
- `LayersR6$.set_py_object()`
- `LayersR6$.get_py_object()`

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

Usage:

`LayersR6$new(obj)`

Arguments:

`obj` A Python Layers object

Method `print()`: Print Layers object

Usage:

`LayersR6$print(...)`

Arguments:

`...` optional arguments to print method.

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  )
)

print(ad$layers)
}
```

Method `get()`: Get a layer

Usage:

`LayersR6$get(name)`

Arguments:

`name` Name of the layer

Method `set()`: Set a layer

Usage:

`LayersR6$set(name, value)`

Arguments:

name Name of the layer

value A matrix

Method `del()`: Delete a layer

Usage:

`LayersR6$del(name)`

Arguments:

name Name of the layer

Method `keys()`: Get the names of the layers

Usage:

`LayersR6$keys()`

Method `length()`: Get the number of layers

Usage:

`LayersR6$length()`

Method `.set_py_object()`: Set internal Python object

Usage:

`LayersR6$.set_py_object(obj)`

Arguments:

obj A Python layers object

Method `.get_py_object()`: Get internal Python object

Usage:

`LayersR6$.get_py_object()`

Examples

```
## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  )
)
ad$layers["spliced"]
ad$layers["test"] <- matrix(c(1, 3, 5, 7), nrow = 2)
```

```

length(ad$layers)
names(ad$layers)

## End(Not run)

## -----
## Method `LayersR6$print`
## -----

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  )
)

print(ad$layers)

## End(Not run)

```

names.LayersR6

Layers Helpers

Description

Layers Helpers

Usage

```

## S3 method for class 'LayersR6'
names(x)

## S3 method for class 'LayersR6'
length(x)

## S3 method for class 'LayersR6'
r_to_py(x, convert = FALSE)

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

## S3 method for class 'LayersR6'
x[name]

## S3 replacement method for class 'LayersR6'

```

```

x[name] <- value

## S3 method for class 'LayersR6'
x[[name]]

## S3 replacement method for class 'LayersR6'
x[[name]] <- value

```

Arguments

x	An AnnData object.
convert	Not used.
name	Name of the layer.
value	Replacement value.

Examples

```

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3, 4, 5), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L, 3L), row.names = c("var1", "var2", "var3")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7, 8, 9), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11, 12, 13), nrow = 2)
  )
)

ad$layers["spliced"]
ad$layers["test"] <- matrix(c(1, 3, 5, 7), nrow = 2)

length(ad$layers)
names(ad$layers)

## End(Not run)

```

Description

Convert between Python and R objects

Usage

```
## S3 replacement method for class 'collections.abc.MutableMapping'
x[[name]] <- value

## S3 method for class 'collections.abc.Mapping'
x[[name]]

## S3 replacement method for class 'collections.abc.MutableMapping'
x[name] <- value

## S3 method for class 'collections.abc.Mapping'
x[name]

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

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

## S3 method for class 'pandas.core.indexes.base.Index'
py_to_r(x)

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

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

## S3 method for class 'anndata.abc._AbstractCSDataset'
py_to_r(x)
```

Arguments

x	A Python object.
name	A name
value	A value

Value

An R object, as converted from the Python object.

Raw

Create a Raw object

Description

Create a Raw object

Usage

```
Raw(adata, X = NULL, var = NULL, varm = NULL)
```

Arguments

adata	An AnnData object.
X	A #observations × #variables data matrix.
var	Key-indexed one-dimensional variables annotation of length #variables.
varm	Key-indexed multi-dimensional variables annotation of length #variables.

Active bindings

X Data matrix of shape $n_{\text{obs}} \times n_{\text{vars}}$.

n_{obs} Number of observations.

obs_names Names of observations.

n_{vars} Number of variables.

var One-dimensional annotation of variables (data.frame).

var_names Names of variables.

varm Multi-dimensional annotation of variables (matrix).

Stores for each key a two or higher-dimensional matrix with n_{var} rows.

shape Shape of data matrix (n_{obs} , n_{vars}).

Methods**Public methods:**

- `RawR6$new()`
- `RawR6$copy()`
- `RawR6$to_adata()`
- `RawR6$print()`
- `RawR6$.set_py_object()`
- `RawR6$.get_py_object()`

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

Usage:

```
RawR6$new(obj)
```

Arguments:

obj A Python Raw object

Method `copy()`: Full copy, optionally on disk.

Usage:

```
RawR6$copy()
```

Arguments:

filename Path to filename (default: NULL).

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2)
)
ad$copy()
ad$copy("file.h5ad")
}
```

Method `to_adata()`: Create a full AnnData object

Usage:

```
RawR6$to_adata()
```

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  )
)
ad$raw <- ad

ad$raw$to_adata()
}
```

Method `print()`: Print Raw object

Usage:

```
RawR6$print(...)
```

Arguments:

... optional arguments to print method.

Examples:

```
\dontrun{
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
  )
)
```

```

      zeros = matrix(rep(0L, 10), nrow = 2)
    ),
    varm = list(
      ones = matrix(rep(1L, 10), nrow = 2),
      rand = matrix(rnorm(6), nrow = 2),
      zeros = matrix(rep(0L, 10), nrow = 2)
    ),
    uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
  )
  ad$raw <- ad

  library(reticulate)
  sc <- import("scanpy")
  sc$pp$normalize_per_cell(ad)

  ad[]
  ad$raw[]

  ad$print()
  print(ad)
}

```

Method `.set_py_object()`: Set internal Python object

Usage:

```
RawR6$.set_py_object(obj)
```

Arguments:

`obj` A Python Raw object

Method `.get_py_object()`: Get internal Python object

Usage:

```
RawR6$.get_py_object()
```

Examples

```

## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  varm = list(

```

```

      ones = matrix(rep(1L, 10), nrow = 2),
      rand = matrix(rnorm(6), nrow = 2),
      zeros = matrix(rep(0L, 10), nrow = 2)
    ),
    uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
  )
  ad$raw <- ad

  library(reticulate)
  sc <- import("scanpy")
  sc$pp$normalize_per_cell(ad)

  ad[]
  ad$raw[]

  ## End(Not run)

  ## -----
  ## Method `RawR6$copy`
  ## -----

  ## Not run:
  ad <- AnnData(
    X = matrix(c(0, 1, 2, 3), nrow = 2)
  )
  ad$copy()
  ad$copy("file.h5ad")

  ## End(Not run)

  ## -----
  ## Method `RawR6$to_adata`
  ## -----

  ## Not run:
  ad <- AnnData(
    X = matrix(c(0, 1, 2, 3), nrow = 2),
    obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
    var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
    layers = list(
      spliced = matrix(c(4, 5, 6, 7), nrow = 2),
      unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
    )
  )
  ad$raw <- ad

  ad$raw$to_adata()

  ## End(Not run)

  ## -----
  ## Method `RawR6$print`
  ## -----

```

```
## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  layers = list(
    spliced = matrix(c(4, 5, 6, 7), nrow = 2),
    unspliced = matrix(c(8, 9, 10, 11), nrow = 2)
  ),
  obsm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)
ad$raw <- ad

library(reticulate)
sc <- import("scanpy")
sc$pp$normalize_per_cell(ad)

ad[]
ad$raw[]

ad$print()
print(ad)

## End(Not run)
```

read_csv

read_csv

Description

[Superseded] Read .csv file.

Usage

```
read_csv(
  filename,
  delimiter = ",",
  first_column_names = NULL,
  dtype = "float32"
)
```

Arguments

filename	Data file.
delimiter	Delimiter that separates data within text file. If NULL, will split at arbitrary number of white spaces, which is different from enforcing splitting at single white space ' '.
first_column_names	Assume the first column stores row names.
dtype	Numpy data type.

Details

Same as `read_text()` but with default delimiter ' , '.

Superseded

This function is superseded. Please use `anndataR` for reading and working with AnnData objects in R. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- read_csv("matrix.csv")

## End(Not run)
```

read_excel

read_excel

Description

[Superseded] Read .xlsx (Excel) file.

Usage

```
read_excel(filename, sheet, dtype = "float32")
```

Arguments

filename	File name to read from.
sheet	Name of sheet in Excel file.
dtype	Numpy data type.

Details

Assumes that the first columns stores the row names and the first row the column names.

Superseded

This function is superseded. Please use **anndataR** for reading and working with AnnData objects in R. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- read_excel("spreadsheet.xls")

## End(Not run)
```

read_h5ad

read_h5ad

Description

[Superseded] Read .h5ad-formatted hdf5 file.

Usage

```
read_h5ad(filename, backed = NULL)
```

Arguments

filename	File name of data file.
backed	If 'r', load <code>~anndata.AnnData</code> in backed mode instead of fully loading it into memory (memory mode). If you want to modify backed attributes of the AnnData object, you need to choose 'r+'.

Superseded

This function is superseded by **anndataR::read_h5ad()** in the **anndataR** package, which reads .h5ad files natively without requiring Python. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- read_h5ad("example_formats/pbmc_1k_protein_v3_processed.h5ad")

## End(Not run)
```

read_hdf	<i>read_hdf</i>
----------	-----------------

Description

[Superseded] Read .h5 (hdf5) file.

Usage

```
read_hdf(filename, key)
```

Arguments

filename	Filename of data file.
key	Name of dataset in the file.

Details

Note: Also looks for fields row_names and col_names.

Superseded

This function is superseded. Please use **anndataR** for reading and working with AnnData objects in R. See vignette("migration_to_anndataR", package = "anndata") for migration guidance.

Examples

```
## Not run:  
ad <- read_hdf("file.h5")  
  
## End(Not run)
```

read_loom	<i>read_loom</i>
-----------	------------------

Description

[Superseded] Read .loom-formatted hdf5 file.

Usage

```
read_loom(
  filename,
  sparse = TRUE,
  cleanup = FALSE,
  X_name = "spliced",
  obs_names = "CellID",
  obsm_names = NULL,
  var_names = "Gene",
  varm_names = NULL,
  dtype = "float32",
  ...
)
```

Arguments

filename	The filename.
sparse	Whether to read the data matrix as sparse.
cleanup	Whether to collapse all obs/var fields that only store one unique value into .uns['loom-.'].
X_name	Loompy key with which the data matrix AnnData.X is initialized.
obs_names	Loompy key where the observation/cell names are stored.
obsm_names	Loompy keys which will be constructed into observation matrices
var_names	Loompy key where the variable/gene names are stored.
varm_names	Loompy keys which will be constructed into variable matrices
dtype	Numpy data type.
...	Arguments to loompy.connect

Details

This reads the whole file into memory. Beware that you have to explicitly state when you want to read the file as sparse data.

Superseded

This function is superseded. Please use **anndataR** for reading and working with AnnData objects in R. See vignette("migration_to_anndataR", package = "anndata") for migration guidance.

Examples

```
## Not run:
ad <- read_loom("dataset.loom")

## End(Not run)
```

read_mtx	<i>read_mtx</i>
----------	-----------------

Description

[Superseded] Read .mtx file.

Usage

```
read_mtx(filename, dtype = "float32")
```

Arguments

filename	The filename.
dtype	Numpy data type.

Superseded

This function is superseded. Please use **anndataR** for reading and working with AnnData objects in R. See vignette("migration_to_anndataR", package = "anndata") for migration guidance.

Examples

```
## Not run:  
ad <- read_mtx("matrix.mtx")  
  
## End(Not run)
```

read_text	<i>read_text</i>
-----------	------------------

Description

[Superseded] Read .txt, .tab, .data (text) file.

Usage

```
read_text(  
  filename,  
  delimiter = NULL,  
  first_column_names = NULL,  
  dtype = "float32"  
)
```

Arguments

filename	Data file, filename or stream.
delimiter	Delimiter that separates data within text file. If NULL, will split at arbitrary number of white spaces, which is different from enforcing splitting at single white space ' '.
first_column_names	Assume the first column stores row names.
dtype	Numpy data type.

Details

Same as `read_csv()` but with default delimiter NULL.

Superseded

This function is superseded. Please use `anndataR` for reading and working with AnnData objects in R. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- read_text("matrix.tab")

## End(Not run)
```

read_umi_tools	<i>read_umi_tools</i>
----------------	-----------------------

Description

[Superseded] Read a gzipped condensed count matrix from umi_tools.

Usage

```
read_umi_tools(filename, dtype = "float32")
```

Arguments

filename	File name to read from.
dtype	Numpy data type.

Superseded

This function is superseded. Please use `anndataR` for reading and working with AnnData objects in R. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- read_umi_tools(...)

## End(Not run)
```

read_zarr	<i>Read from a hierarchical Zarr array store.</i>
-----------	---

Description

[Superseded]

Usage

```
read_zarr(store)
```

Arguments

store The filename, a MutableMapping, or a Zarr storage class.

Superseded

This function is superseded. Please use **anndataR** for reading and working with AnnData objects in R. See vignette("migration_to_anndataR", package = "anndata") for migration guidance.

Examples

```
## Not run:
ad <- read_zarr(...)

## End(Not run)
```

write_csvs	<i>Write annotation to .csv files.</i>
------------	--

Description

[Superseded]

Usage

```
write_csvs(anndata, dirname, skip_data = TRUE, sep = ",")
```

Arguments

anndata	An <code>AnnData()</code> object
dirname	Name of the directory to which to export.
skip_data	Skip the data matrix X .
sep	Separator for the data

Details

It is not possible to recover the full `AnnData` from these files. Use `write_h5ad()` for this.

Superseded

This function is superseded. Please use `anndataR` for reading and working with `AnnData` objects in R. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2, byrow = TRUE),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

write_csvs(ad, "output")

unlink("output", recursive = TRUE)

## End(Not run)
```

write_h5ad

Write .h5ad-formatted hdf5 file.

Description

[Superseded]

Usage

```
write_h5ad(
  anndata,
  filename,
  compression = NULL,
  compression_opts = NULL,
  as_dense = list()
)
```

Arguments

anndata	An <code>AnnData()</code> object
filename	Filename of data file. Defaults to backing file.
compression	See the <code>h5py</code> filter pipeline . Options are "gzip", "lzf" or NULL.
compression_opts	See the <code>h5py</code> filter pipeline .
as_dense	Sparse in <code>AnnData</code> object to write as dense. Currently only supports "X" and "raw/X".

Details

Generally, if you have sparse data that are stored as a dense matrix, you can dramatically improve performance and reduce disk space by converting to a `csr_matrix`:

Superseded

This function is superseded by `anndataR::write_h5ad()` in the `anndataR` package, which writes .h5ad files natively without requiring Python. See `vignette("migration_to_anndataR", package = "anndataR")` for migration guidance.

Examples

```
## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2, byrow = TRUE),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

write_h5ad(ad, "output.h5ad")

file.remove("output.h5ad")

## End(Not run)
```

write_loom	<i>Write .loom-formatted hdf5 file.</i>
------------	---

Description**[Superseded]****Usage**

```
write_loom(anndata, filename, write_obs_m_varm = FALSE)
```

Arguments

anndata	An <code>AnnData()</code> object
filename	The filename.
write_obs_m_varm	Whether or not to also write the varm and obsm.

Superseded

This function is superseded. Please use `anndataR` for reading and working with `AnnData` objects in R. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2, byrow = TRUE),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

write_loom(ad, "output.loom")

file.remove("output.loom")

## End(Not run)
```

write_zarr

Write a hierarchical Zarr array store.

Description

[Superseded]

Usage

```
write_zarr(anndata, store, chunks = NULL)
```

Arguments

anndata	An <code>AnnData()</code> object
store	The filename, a <code>MutableMapping</code> , or a Zarr storage class.
chunks	Chunk shape.

Superseded

This function is superseded. Please use `anndataR` for reading and working with `AnnData` objects in R. See `vignette("migration_to_anndataR", package = "anndata")` for migration guidance.

Examples

```
## Not run:
ad <- AnnData(
  X = matrix(c(0, 1, 2, 3), nrow = 2, byrow = TRUE),
  obs = data.frame(group = c("a", "b"), row.names = c("s1", "s2")),
  var = data.frame(type = c(1L, 2L), row.names = c("var1", "var2")),
  varm = list(
    ones = matrix(rep(1L, 10), nrow = 2),
    rand = matrix(rnorm(6), nrow = 2),
    zeros = matrix(rep(0L, 10), nrow = 2)
  ),
  uns = list(a = 1, b = 2, c = list(c.a = 3, c.b = 4))
)

ad$write_zarr("output.zarr")
write_zarr(ad, "output.zarr")

unlink("output.zarr", recursive = TRUE)

## End(Not run)
```

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