Package 'HDF5Array'

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Title HDF5 datasets as array-like objects in R

Description The HDF5Array package is an HDF5 backend for DelayedArray objects. It implements the HDF5Array, H5SparseMatrix, H5ADMatrix, and TENxMatrix classes, 4 convenient and memory-efficient array-like containers for representing and manipulating either: (1) a conventional (a.k.a. dense) HDF5 dataset, (2) an HDF5 sparse matrix (stored in CSR/CSC/Yale format), (3) the central matrix of an h5ad file (or any matrix in the /layers group), or (4) a 10x Genomics sparse matrix. All these containers are DelayedArray extensions and thus support all operations (delayed or block-processed) supported by DelayedArray objects.

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BugReports https://github.com/Bioconductor/HDF5Array/issues

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H5SparseMatrix-class.R H5ADMatrixSeed-class.R
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`H5ADMatrix-class` *h5ad central matrices (or matrices in the /layers group) as DelayedMatrix objects*

Description

`h5ad` files are HDF5 files used for on-disk representation of AnnData Python objects. At the very minimum, they contain a central data matrix, named `X`, of shape #observations x #variables, and possibly additional data matrices (stored in the HDF5 group `/layers`) that share the shape and dimnames of `X`. See https://anndata.readthedocs.io/ for more information.

The H5ADMatrix class is a DelayedMatrix subclass for representing and operating on the central matrix of an `h5ad` file, or any matrix in its `/layers` group.

All the operations available for DelayedMatrix objects work on H5ADMatrix objects.

Usage

```
## Constructor function:
H5ADMatrix(filepath, layer=NULL)
```

Arguments

filepath	The path (as a single string) to the h5ad file.
layer	NULL (the default) or the name of a matrix in the /layers group. By default (i.e. when layer is not specified) H5ADMatrix() returns the central matrix (X).

Value

H5ADMatrix() returns an H5ADMatrix object of shape #variables x #observations. Note that in Python and HDF5 the shape of this matrix is considered to be #observations x #variables, but in R it is transposed. This follows the widely adopted convention of transposing HDF5 matrices when they get loaded into R.

References

https://anndata.readthedocs.io/ for AnnData Python objects and the h5ad format.

See Also

- HDF5Array objects for representing conventional (a.k.a. dense) HDF5 datasets as DelayedArray objects.
- H5SparseMatrix objects for representing HDF5 sparse matrices as DelayedMatrix objects.
- DelayedMatrix objects in the **DelayedArray** package.
- The H5ADMatrixSeed helper class.
- readH5AD and writeH5AD in the **zellkonverter** package for importing/exporting an h5ad file as/from a SingleCellExperiment object.
- SparseArray objects in the **SparseArray** package.

Examples

```
library(zellkonverter)
h5ad_file <- system.file("extdata", "krumsiek11.h5ad",
                         package="zellkonverter")
X <- H5ADMatrix(h5ad_file)
X

class(X)  # H5ADMatrix
is(X, "DelayedMatrix")  # TRUE

class(seed(X))  # Dense_H5ADMatrixSeed

dim(X)
path(X)
is_sparse(X)  # FALSE
```

```
## Use coercion to load the full dataset into memory:
as.matrix(X)          # as ordinary array (usually not recommended)

## Not run:
  ## Works only if H5ADMatrix object is sparse!
  as(X, "dgCMatrix")    # as dgCMatrix
  as(X, "SparseArray")  # as SparseArray object (most efficient)
  SparseArray(X)        # equivalent to 'as(X, "SparseArray")'

## End(Not run)
```

`H5ADMatrixSeed-class` *H5ADMatrixSeed objects*

Description

H5ADMatrixSeed is a low-level helper class used to represent a pointer to the central matrix stored of an `h5ad` file, or to one of the matrices in the `/layers` group.

It is a virtual class with three concrete subclasses: Dense_H5ADMatrixSeed, CSC_H5ADMatrixSeed, and CSR_H5ADMatrixSeed:

- The Dense_H5ADMatrixSeed class is used when the matrix is stored as a conventional HDF5 dataset in the `h5ad` file. It is a direct entension of the HDF5ArraySeed class.
- The CSC_H5ADMatrixSeed or CSR_H5ADMatrixSeed classes is used when the matrix is stored in the *Compressed Sparse Column* or *Compressed Sparse Row* format in the `h5ad` file. CSC_H5ADMatrixSeed is a direct entension of CSC_H5SparseMatrixSeed, and CSR_H5ADMatrixSeed a direct entension of CSR_H5SparseMatrixSeed.

Note that an H5ADMatrixSeed derivative is not intended to be used directly. Most end users will typically create and manipulate a higher-level H5ADMatrix object instead. See ?`H5ADMatrix` for more information.

Usage

```
## Constructor function:
H5ADMatrixSeed(filepath, layer=NULL)
```

Arguments

`filepath`, `layer` See ?`H5ADMatrix` for a description of these arguments.

Details

Dense_H5ADMatrixSeed objects support the same limited set of methods as HDF5ArraySeed objects, and CSC_H5ADMatrixSeed and CSR_H5ADMatrixSeed objects support the same limited set of methods as H5SparseMatrixSeed objects. See ?`HDF5ArraySeed` and ?`H5SparseMatrixSeed` for the details.

Value

H5ADMatrixSeed() returns an H5ADMatrixSeed derivative (Dense_H5ADMatrixSeed or CSC_H5ADMatrixSeed or CSR_H5ADMatrixSeed) of shape #variables x #observations.

H5ADMatrixSeed vs H5ADMatrix objects

In order to have access to the full set of operations that are available for DelayedMatrix objects, an H5ADMatrixSeed derivative first needs to be wrapped in a DelayedMatrix object, typically by calling the DelayedArray() constructor on it.

This is what the H5ADMatrix() constructor function does.

Note that the result of this wrapping is an H5ADMatrix object, which is just an H5ADMatrixSeed derivative wrapped in a DelayedMatrix object.

References

https://anndata.readthedocs.io/ for AnnData Python objects and the h5ad format.

See Also

- H5ADMatrix objects.
- HDF5ArraySeed and H5SparseMatrixSeed objects.
- readH5AD and writeH5AD in the **zellkonverter** package for importing/exporting an h5ad file as/from a SingleCellExperiment object.

Examples

```
library(zellkonverter)
h5ad_file <- system.file("extdata", "krumsiek11.h5ad",
                         package="zellkonverter")
seed <- H5ADMatrixSeed(h5ad_file)
seed
path(seed)
dim(seed)
is_sparse(seed)

DelayedArray(seed)
stopifnot(class(DelayedArray(seed)) == "H5ADMatrix")
```

H5SparseMatrix-class *HDF5 sparse matrices as DelayedMatrix objects*

Description

The H5SparseMatrix class is a DelayedMatrix subclass for representing and operating on an HDF5 sparse matrix stored in CSR/CSC/Yale format.

All the operations available for DelayedMatrix objects work on H5SparseMatrix objects.

Usage

```
## Constructor function:
H5SparseMatrix(filepath, group)
```

Arguments

filepath	The path (as a single string) to the HDF5 file (.h5 or .h5ad) where the sparse matrix is located.
group	The name of the group in the HDF5 file where the sparse matrix is stored.

Value

An H5SparseMatrix object.

See Also

- HDF5Array objects for representing conventional (a.k.a. dense) HDF5 datasets as DelayedArray objects.
- H5ADMatrix objects for representing h5ad central matrices (or matrices in the /layers group) as DelayedMatrix objects.
- TENxMatrix objects for representing 10x Genomics datasets as DelayedMatrix objects.
- DelayedMatrix objects in the **DelayedArray** package.
- The H5SparseMatrixSeed helper class.
- h5ls to list the content of an HDF5 file (.h5 or .h5ad).
- SparseArray objects in the **SparseArray** package.

Examples

```
library(zellkonverter)
h5ad_file <- system.file("extdata", "example_anndata.h5ad",
                         package="zellkonverter")
rhdf5::h5ls(h5ad_file)

M <- H5SparseMatrix(h5ad_file, "/obsp/connectivities")
M

class(M)  # H5SparseMatrix
is(M, "DelayedMatrix")  # TRUE

seed(M)
class(seed(M))  # CSC_H5SparseMatrixSeed

dim(M)
path(M)
is_sparse(M)  # TRUE

## Use coercion to load the full dataset into memory:
as.matrix(M)          # as ordinary array (usually not recommended)
```

```
as(M, "dgCMatrix")    # as dgCMatrix
as(M, "SparseArray")  # as SparseArray object (most efficient)
SparseArray(M)        # equivalent to 'as(M, "SparseArray")'
```

H5SparseMatrixSeed-class
H5SparseMatrixSeed objects

Description

H5SparseMatrixSeed is a low-level helper class for representing a pointer to a sparse matrix stored in an HDF5 file and compressed using the CSC or CSR layout.

It is a virtual class with two concrete subclasses: CSC_H5SparseMatrixSeed for the *Compressed Sparse Column* layout, and CSR_H5SparseMatrixSeed for the *Compressed Sparse Row* layout. The former is used by 10x Genomics (e.g. "1.3 Million Brain Cell Dataset"). `h5ad` files can use one or the other layout to store a sparse matrix.

Note that an H5SparseMatrixSeed derivative is not intended to be used directly. Most end users will typically create and manipulate a higher-level H5SparseMatrix object instead. See ?`H5SparseMatrix` for more information.

Usage

```
## --- Constructor function ---

H5SparseMatrixSeed(filepath, group, subdata=NULL,
                   dim=NULL, sparse.layout=NULL)

## --- Accessors --------------

## S4 method for signature 'H5SparseMatrixSeed'
path(object)

## S4 method for signature 'H5SparseMatrixSeed'
dim(x)

## S4 method for signature 'H5SparseMatrixSeed'
dimnames(x)

## S4 method for signature 'CSC_H5SparseMatrixSeed'
chunkdim(x)
## S4 method for signature 'CSR_H5SparseMatrixSeed'
chunkdim(x)

## --- Data extraction --------

## S4 method for signature 'H5SparseMatrixSeed'
```

```
extract_array(x, index)

## S4 method for signature 'CSC_H5SparseMatrixSeed'
extract_sparse_array(x, index)
## S4 method for signature 'CSR_H5SparseMatrixSeed'
extract_sparse_array(x, index)

## S4 method for signature 'CSC_H5SparseMatrixSeed'
extractNonzeroDataByCol(x, j)
## S4 method for signature 'CSR_H5SparseMatrixSeed'
extractNonzeroDataByRow(x, i)

## --- Other methods ----------

## S4 method for signature 'H5SparseMatrixSeed'
is_sparse(x)

## S4 method for signature 'H5SparseMatrixSeed'
nzcount(x)
```

Arguments

`filepath`, `group`	See ?`H5SparseMatrix` for a description of these arguments.
`subdata`	Experimental. Don't use!
`dim`, `sparse.layout`	The `H5SparseMatrixSeed()` constructor should be able to automatically detect the dimensions and layout of the sparse matrix stored in the HDF5 file, so the user shouldn't need to specify these arguments. See Details section below for some rare situations where the user might need to specify them.
`object`, `x`	An H5SparseMatrixSeed derivative.
`index`	See ?`extract_array` in the **S4Arrays** package.
`j`	An integer vector containing valid column indices.
`i`	An integer vector containing valid row indices.

Details

*** Layout in R vs physical layout ***

The implementation of CSC_H5SparseMatrixSeed and CSR_H5SparseMatrixSeed objects follows the usual convention of transposing the matrix stored in the HDF5 file when loading it into R. This means that a CSC_H5SparseMatrixSeed object represents a sparse matrix stored physically in the CSR layout (Compressed Sparse Row) at the HDF5 level, and a CSR_H5SparseMatrixSeed object represents a sparse matrix stored physically in the CSC layout (Compressed Sparse Column) at the HDF5 level.

*** Automatic detection of the dimensions and layout ***

The `H5SparseMatrixSeed()` constructor should be able to automatically detect the dimensions and layout of the sparse matrix stored in the HDF5 file. However, in some rare situations, the user might

want to bypass the detection mechanism, or they might be dealing with a sparse matrix stored in an HDF5 group that doesn't provide this information (e.g. the group only contains the `data`, `indices`, and `indptr` components). In which case, they can supply the `dim` and `sparse.layout` arguments:

- `dim` must be an integer vector of length 2.
- `sparse.layout` must be `"CSC"` or `"CSR"`.

Note that both values must describe the dimensions and layout of the R object that will be returned, that is, *after* transposition from the physical layout used at the HDF5 level. Also be aware that the supplied values will take precedence over whatever the HDF5 file says, which means that bad things will happen if they don't reflect the actual dimensions and layout of the sparse matrix. Use these arguments only if you know what you are doing!

*** H5SparseMatrixSeed object vs H5SparseMatrix object ***

Note that H5SparseMatrixSeed derivatives support a very limited set of methods:

- `path()`: Returns the path to the HDF5 file where the sparse matrix is located.
- `dim()`, `dimnames()`.
- `extract_array()`, `is_sparse()`, `extract_sparse_array()`, `chunkdim()`: These generics are defined and documented in other packages e.g. in **S4Arrays** for `extract_array()` and `is_sparse()`, in **SparseArray** for `extract_sparse_array()`, and in **DelayedArray** for `chunkdim()`.
- `nzcount()`: Returns the number of nonzero values in the object.
- `extractNonzeroDataByCol()`: Works on CSC_H5SparseMatrixSeed objects only. Returns a NumericList or IntegerList object *parallel* to `j`, that is, with one list element per column index in `j`. The row indices of the values are not returned. Furthermore, the values within a given list element can be returned in **any order**. In particular, do NOT assume that they are ordered by ascending row index.
- `extractNonzeroDataByRow()`: Works on CSR_H5SparseMatrixSeed objects only. Returns a NumericList or IntegerList object *parallel* to `i`, that is, with one list element per row index in `i`. The column indices of the values are not returned. Furthermore, the values within a given list element can be returned in **any order**. In particular, do NOT assume that they are ordered by ascending column index.

In order to have access to the full set of operations that are available for DelayedMatrix objects, an H5SparseMatrixSeed derivative would first need to be wrapped in a DelayedMatrix object, typically by calling the `DelayedArray()` constructor on it.

Value

`H5SparseMatrixSeed()` returns an H5SparseMatrixSeed derivative (CSC_H5SparseMatrixSeed or CSR_H5SparseMatrixSeed object).

References

https://en.wikipedia.org/wiki/Sparse_matrix for a description of the CSR/CSC/Yale format (section "Compressed sparse row (CSR, CRS or Yale format)").

See Also

- H5SparseMatrix objects.
- h5ls to list the content of an HDF5 file (.h5 or .h5ad).

Examples

```
showClass("H5SparseMatrixSeed")
```

HDF5-dump-management *HDF5 dump management*

Description

A set of utilities to control the location and physical properties of automatically created HDF5 datasets.

Usage

```
setHDF5DumpDir(dir)
setHDF5DumpFile(filepath)
setHDF5DumpName(name)
setHDF5DumpChunkLength(length=1000000L)
setHDF5DumpChunkShape(shape="scale")
setHDF5DumpCompressionLevel(level=6L)

getHDF5DumpDir()
getHDF5DumpFile()
getHDF5DumpName(for.use=FALSE)
getHDF5DumpChunkLength()
getHDF5DumpChunkShape()
getHDF5DumpCompressionLevel()

lsHDF5DumpFile()

showHDF5DumpLog()

## For developers:
getHDF5DumpChunkDim(dim)
appendDatasetCreationToHDF5DumpLog(filepath, name, dim, type,
                                   chunkdim, level)
```

Arguments

dir	The path (as a single string) to the current *HDF5 dump directory*, that is, to the (new or existing) directory where *HDF5 dump files* with automatic names will be created. This is ignored if the user specified an *HDF5 dump file* with setHDF5DumpFile. If dir is missing, then the *HDF5 dump directory* is set back

to its default value i.e. to some directory under `tempdir()` (call `getHDF5DumpDir()` to get the exact path).

`filepath` For `setHDF5DumpFile`: The path (as a single string) to the current *HDF5 dump file*, that is, to the (new or existing) HDF5 file where the *next automatic HDF5 datasets* will be written. If `filepath` is missing, then a new file with an automatic name will be created (in `getHDF5DumpDir()`) and used for each new dataset.

For `appendDatasetCreationToHDF5DumpLog`: See the Note TO DEVELOPERS below.

`name` For `setHDF5DumpName`: The name of the *next automatic HDF5 dataset* to be written to the current *HDF5 dump file*.

For `appendDatasetCreationToHDF5DumpLog`: See the Note TO DEVELOPERS below.

`length` The maximum length of the physical chunks of the *next automatic HDF5 dataset* to be written to the current *HDF5 dump file*.

`shape` A string specifying the shape of the physical chunks of the *next automatic HDF5 dataset* to be written to the current *HDF5 dump file*. See `makeCappedVolumeBox` in the **DelayedArray** package for a description of the supported shapes.

`level` For `setHDF5DumpCompressionLevel`: The compression level to use for writing *automatic HDF5 datasets* to disk. See the `level` argument in `?rhdf5::h5createDataset` (in the **rhdf5** package) for more information about this.

For `appendDatasetCreationToHDF5DumpLog`: See the Note TO DEVELOPERS below.

`for.use` Whether the returned dataset name is for use by the caller or not. See below for the details.

`dim` The dimensions of the HDF5 dataset to be written to disk, that is, an integer vector of length one or more giving the maximal indices in each dimension. See the `dims` argument in `?rhdf5::h5createDataset` (in the **rhdf5** package) for more information about this.

`type` The type (a.k.a. storage mode) of the data to be written to disk. Can be obtained with `type()` on an array-like object (which is equivalent to `storage.mode()` or `typeof()` on an ordinary array). This is typically what an application writing datasets to the *HDF5 dump* should pass to the `storage.mode` argument of its call to `rhdf5::h5createDataset`. See the Note TO DEVELOPERS below for more information.

`chunkdim` The dimensions of the chunks.

Details

Calling `getHDF5DumpFile()` and `getHDF5DumpName()` with no argument should be *informative* only i.e. it's a mean for the user to know where the *next automatic HDF5 dataset* will be written. Since a given file/name combination can be used only once, the user should be careful to not use that combination to explicitely create an HDF5 dataset because that would get in the way of the creation of the *next automatic HDF5 dataset*. See the Note TO DEVELOPERS below if you actually need to use this file/name combination.

`lsHDF5DumpFile()` is a just convenience wrapper for `h5ls(getHDF5DumpFile())`.

Value

`getHDF5DumpDir` returns the absolute path to the directory where *HDF5 dump files* with automatic names will be created. Only meaningful if the user did NOT specify an *HDF5 dump file* with `setHDF5DumpFile`.

`getHDF5DumpFile` returns the absolute path to the HDF5 file where the *next automatic HDF5 dataset* will be written.

`getHDF5DumpName` returns the name of the *next automatic HDF5 dataset*.

`getHDF5DumpCompressionLevel` returns the compression level currently used for writing *automatic HDF5 datasets* to disk.

`showHDF5DumpLog` returns the dump log in an invisible data frame.

`getHDF5DumpChunkDim` returns the dimensions of the physical chunks that will be used to write the dataset to disk.

Note

TO DEVELOPERS:

If your application needs to write its own dataset to the *HDF5 dump* then it should:

1. Get a file/dataset name combination by calling `getHDF5DumpFile()` and `getHDF5DumpName(for.use=TRUE)`.
2. [OPTIONAL] Call `getHDF5DumpChunkDim(dim)` to get reasonable chunk dimensions to use for writing the dataset to disk. Or choose your own chunk dimensions.
3. Add an entry to the dump log by calling `appendDatasetCreationToHDF5DumpLog`. Typically, this should be done right after creating the dataset (e.g. with `rhdf5::h5createDataset`) and before starting to write the dataset to disk. The values passed to `appendDatasetCreationToHDF5DumpLog` via the `filepath`, `name`, `dim`, `type`, `chunkdim`, and `level` arguments should be those that were passed to `rhdf5::h5createDataset` via the `file`, `dataset`, `dims`, `storage.mode`, `chunk`, and `level` arguments, respectively. Note that `appendDatasetCreationToHDF5DumpLog` uses a lock mechanism so is safe to use in the context of parallel execution.

This is actually what the coercion method to HDF5Array does internally.

See Also

- `writeHDF5Array` for writing an array-like object to an HDF5 file.
- HDF5Array objects.
- The `h5ls` function on which `lsHDF5DumpFile` is based.
- `makeCappedVolumeBox` in the **DelayedArray** package.
- `type` in the **DelayedArray** package.

Examples

```
getHDF5DumpDir()
getHDF5DumpFile()

## Use setHDF5DumpFile() to change the current HDF5 dump file.
## If the specified file exists, then it must be in HDF5 format or
```

```
## an error will be raised. If it doesn't exist, then it will be
## created.
#setHDF5DumpFile("path/to/some/HDF5/file")

lsHDF5DumpFile()

a <- array(1:600, c(150, 4))
A <- as(a, "HDF5Array")
lsHDF5DumpFile()
A

b <- array(runif(6000), c(4, 2, 150))
B <- as(b, "HDF5Array")
lsHDF5DumpFile()
B

C <- (log(2 * A + 0.88) - 5)^3 * t(B[ , 1, ])
as(C, "HDF5Array")  # realize C on disk
lsHDF5DumpFile()

## Matrix multiplication is not delayed: the output matrix is realized
## block by block. The current "realization backend" controls where
## realization happens e.g. in memory if set to NULL or in an HDF5 file
## if set to "HDF5Array". See '?realize' in the DelayedArray package for
## more information about "realization backends".
setAutoRealizationBackend("HDF5Array")
m <- matrix(runif(20), nrow=4)
P <- C %*% m
lsHDF5DumpFile()

## See all the HDF5 datasets created in the current session so far:
showHDF5DumpLog()

## Wrap the call in suppressMessages() if you are only interested in the
## data frame version of the dump log:
dump_log <- suppressMessages(showHDF5DumpLog())
dump_log
```

`HDF5Array-class` *HDF5 datasets as DelayedArray objects*

Description

The HDF5Array class is a DelayedArray subclass for representing and operating on a conventional (a.k.a. dense) HDF5 dataset.

All the operations available for DelayedArray objects work on HDF5Array objects.

Usage

```
## Constructor function:
HDF5Array(filepath, name, as.sparse=FALSE, type=NA)
```

Arguments

`filepath`	The path (as a single string or H5File object) to the HDF5 file (`.h5` or `.h5ad`) where the dataset is located. Note that you must create and use an H5File object if the HDF5 file to access is stored in an Amazon S3 bucket. See `?H5File` for how to do this. Also please note that H5File objects must NOT be used in the context of parallel evaluation at the moment.
`name`	The name of the dataset in the HDF5 file.
`as.sparse`	Whether the HDF5 dataset should be flagged as sparse or not, that is, whether it should be considered sparse (and treated as such) or not. Note that HDF5 doesn't natively support sparse storage at the moment so HDF5 datasets cannot be stored in a sparse format, only in a dense one. However a dataset stored in a dense format can still contain a lot of zeros. Using `as.sparse=TRUE` on such dataset will enable some optimizations that can lead to a lower memory footprint (and possibly better performance) when operating on the HDF5Array. IMPORTANT NOTE: If the dataset is in the 10x Genomics format (i.e. if it uses the HDF5-based sparse matrix representation from 10x Genomics), you should use the `TENxMatrix()` constructor instead of the `HDF5Array()` constructor.
`type`	By default the `type` of the returned object is inferred from the H5 datatype of the HDF5 dataset. This can be overridden by specifying the `type` argument. The specified type must be an *R atomic type* (e.g. `"integer"`) or `"list"`.

Value

An HDF5Array (or HDF5Matrix) object. (Note that HDF5Matrix extends HDF5Array.)

Note

The "1.3 Million Brain Cell Dataset" and other datasets published by 10x Genomics use an HDF5-based sparse matrix representation instead of the conventional (a.k.a. dense) HDF5 representation.

If your dataset uses the conventional (a.k.a. dense) HDF5 representation, use the `HDF5Array()` constructor documented here.

But if your dataset uses the HDF5 sparse matrix representation from 10x Genomics, use the `TENxMatrix()` constructor instead.

See Also

- H5File objects.
- H5SparseMatrix objects for representing HDF5 sparse matrices as DelayedMatrix objects.
- H5ADMatrix objects for representing h5ad central matrices (or matrices in the `/layers` group) as DelayedMatrix objects.
- TENxMatrix objects for representing 10x Genomics datasets as DelayedMatrix objects.
- ReshapedHDF5Array objects for representing HDF5 datasets as DelayedArray objects with a user-supplied upfront virtual reshaping.
- DelayedArray objects in the **DelayedArray** package.

- writeHDF5Array for writing an array-like object to an HDF5 file.
- HDF5-dump-management for controlling the location and physical properties of automatically created HDF5 datasets.
- saveHDF5SummarizedExperiment and loadHDF5SummarizedExperiment in this package (the **HDF5Array** package) for saving/loading an HDF5-based SummarizedExperiment object to/from disk.
- The HDF5ArraySeed helper class.
- h5ls to list the content of an HDF5 file (`.h5` or `.h5ad`).

Examples

```
## ---------------------------------------------------------------------
## A. CONSTRUCTION
## ---------------------------------------------------------------------

## With a local file:
toy_h5 <- system.file("extdata", "toy.h5", package="HDF5Array")
h5ls(toy_h5)

HDF5Array(toy_h5, "M2")
HDF5Array(toy_h5, "M2", type="integer")
HDF5Array(toy_h5, "M2", type="complex")

## With a file stored in an Amazon S3 bucket:
if (Sys.info()[["sysname"]] != "Darwin") {
    public_S3_url <-
     "https://rhdf5-public.s3.eu-central-1.amazonaws.com/rhdf5ex_t_float_3d.h5"
    h5file <- H5File(public_S3_url, s3=TRUE)
    h5ls(h5file)

    HDF5Array(h5file, "a1")
}

## ---------------------------------------------------------------------
## B. BASIC MANIPULATION
## ---------------------------------------------------------------------

library(h5vcData)
tally_file <- system.file("extdata", "example.tally.hfs5",
                          package="h5vcData")
h5ls(tally_file)

## Pick up "Coverages" dataset for Human chromosome 16:
name <- "/ExampleStudy/16/Coverages"
cvg <- HDF5Array(tally_file, name)
cvg

is(cvg, "DelayedArray")  # TRUE
seed(cvg)
path(cvg)
chunkdim(cvg)
```

```
## The data in the dataset looks sparse. In this case it is recommended
## to set 'as.sparse' to TRUE when constructing the HDF5Array object.
## This will make block processing (used in operations like sum()) more
## memory efficient and likely faster:
cvg0 <- HDF5Array(tally_file, name, as.sparse=TRUE)
is_sparse(cvg0)  # TRUE

## Note that we can also flag the HDF5Array object as sparse after
## creation:
is_sparse(cvg) <- TRUE
cvg  # same as 'cvg0'

## dim/dimnames:

dim(cvg0)

dimnames(cvg0)
dimnames(cvg0) <- list(paste0("s", 1:6), c("+", "-"), NULL)
dimnames(cvg0)

## ---------------------------------------------------------------------
## C. SLICING (A.K.A. SUBSETTING)
## ---------------------------------------------------------------------

cvg1 <- cvg0[ , , 29000001:29000007]
cvg1

dim(cvg1)
as.array(cvg1)
stopifnot(identical(dim(as.array(cvg1)), dim(cvg1)))
stopifnot(identical(dimnames(as.array(cvg1)), dimnames(cvg1)))

cvg2 <- cvg0[ , "+", 29000001:29000007]
cvg2
as.matrix(cvg2)

## ---------------------------------------------------------------------
## D. SummarizedExperiment OBJECTS WITH DELAYED ASSAYS
## ---------------------------------------------------------------------

## DelayedArray objects can be used inside a SummarizedExperiment object
## to hold the assay data and to delay operations on them.

library(SummarizedExperiment)

pcvg <- cvg0[ , 1, ]  # coverage on plus strand
mcvg <- cvg0[ , 2, ]  # coverage on minus strand

nrow(pcvg)  # nb of samples
ncol(pcvg)  # length of Human chromosome 16

## The convention for a SummarizedExperiment object is to have 1 column
```

```
## per sample so first we need to transpose 'pcvg' and 'mcvg':
pcvg <- t(pcvg)
mcvg <- t(mcvg)
se <- SummarizedExperiment(list(pcvg=pcvg, mcvg=mcvg))
se
stopifnot(validObject(se, complete=TRUE))

## A GPos object can be used to represent the genomic positions along
## the dataset:
gpos <- GPos(GRanges("16", IRanges(1, nrow(se))))
gpos
rowRanges(se) <- gpos
se
stopifnot(validObject(se))
assays(se)$pcvg
assays(se)$mcvg
```

HDF5Array-internals *HDF5Array internals*

Description

Internal utilities defined in the **HDF5Array** package. These functions are not intended to be used directly.

HDF5ArraySeed-class *HDF5ArraySeed objects*

Description

HDF5ArraySeed is a low-level helper class for representing a pointer to an HDF5 dataset.

Note that an HDF5ArraySeed object is not intended to be used directly. Most end users will typically create and manipulate a higher-level HDF5Array object instead. See ?HDF5Array for more information.

Usage

```
## --- Constructor function ---

HDF5ArraySeed(filepath, name, as.sparse=FALSE, type=NA)

## --- Accessors --------------

## S4 method for signature 'HDF5ArraySeed'
path(object)
```

```
## S4 replacement method for signature 'HDF5ArraySeed'
path(object) <- value

## S4 method for signature 'HDF5ArraySeed'
dim(x)

## S4 method for signature 'HDF5ArraySeed'
dimnames(x)

## S4 method for signature 'HDF5ArraySeed'
type(x)

## S4 method for signature 'HDF5ArraySeed'
is_sparse(x)

## S4 replacement method for signature 'HDF5ArraySeed'
is_sparse(x) <- value

## S4 method for signature 'HDF5ArraySeed'
chunkdim(x)

## --- Data extraction --------

## S4 method for signature 'HDF5ArraySeed'
extract_array(x, index)

## S4 method for signature 'HDF5ArraySeed'
extract_sparse_array(x, index)
```

Arguments

filepath, name, as.sparse, type	See ?HDF5Array for a description of these arguments.
object, x	An HDF5ArraySeed object or derivative.
value	For the path() setter: The new path (as a single string) to the HDF5 file where the dataset is located. For the is_sparse() setter: TRUE or FALSE.
index	See ?extract_array in the **S4Arrays** package.

Details

The HDF5ArraySeed class has one direct subclass: Dense_H5ADMatrixSeed. See ?Dense_H5ADMatrixSeed for more information.

Note that the implementation of HDF5ArraySeed objects follows the widely adopted convention of transposing HDF5 matrices when they get loaded into R.

Finally note that an HDF5ArraySeed object supports a very limited set of methods:

- path(): Returns the path to the HDF5 file where the dataset is located.

- dim(), dimnames().
- type(), extract_array(), is_sparse(), extract_sparse_array(), chunkdim(): These generics are defined and documented in other packages e.g. in **S4Arrays** for extract_array() and is_sparse(), in **SparseArray** for extract_sparse_array(), and in **DelayedArray** for chunkdim().

Value

HDF5ArraySeed() returns an HDF5ArraySeed object.

HDF5ArraySeed vs HDF5Array objects

In order to have access to the full set of operations that are available for DelayedArray objects, an HDF5ArraySeed object first needs to be wrapped in a DelayedArray object, typically by calling the DelayedArray() constructor on it.

This is what the HDF5Array() constructor function does.

Note that the result of this wrapping is an HDF5Array object, which is just an HDF5ArraySeed object wrapped in a DelayedArray object.

See Also

- HDF5Array objects.
- type, extract_array, and is_sparse, in the the **S4Arrays** package.
- extract_sparse_array in the **SparseArray** package.
- chunkdim in the **DelayedArray** package.
- h5ls to list the content of an HDF5 file.

Examples

```
library(h5vcData)
tally_file <- system.file("extdata", "example.tally.hfs5",
                          package="h5vcData")
h5ls(tally_file)

name <- "/ExampleStudy/16/Coverages"  # name of the dataset of interest
seed1 <- HDF5ArraySeed(tally_file, name)
seed1
path(seed1)
dim(seed1)
chunkdim(seed1)

seed2 <- HDF5ArraySeed(tally_file, name, as.sparse=TRUE)
seed2

## Alternatively:
is_sparse(seed1) <- TRUE
seed1  # same as 'seed2'

DelayedArray(seed1)
stopifnot(class(DelayedArray(seed1)) == "HDF5Array")
```

`ReshapedHDF5Array-class` *Virtually reshaped HDF5 datasets as DelayedArray objects*

Description

The ReshapedHDF5Array class is a DelayedArray subclass for representing an HDF5 dataset with a user-supplied upfront virtual reshaping.

All the operations available for DelayedArray objects work on ReshapedHDF5Array objects.

Usage

```
## Constructor function:
ReshapedHDF5Array(filepath, name, dim, type=NA)
```

Arguments

`filepath`, `name`, `type`
: See ?`HDF5Array` for a description of these arguments.

`dim`
: A vector of dimensions that describes the virtual reshaping i.e. the reshaping that is virtually applied upfront to the HDF5 dataset when the ReshapedHDF5Array object gets constructed.

Note that the HDF5 dataset is treated as read-only so is not *effectively* reshaped, that is, the dataset dimensions encoded in the HDF5 file are not mmodified.

Also please note that arbitrary reshapings are not supported. Only reshapings that reduce the number of dimensions by collapsing a group of consecutive dimensions into a single dimension are supported. For example, reshaping a 10 x 3 x 5 x 1000 array as a 10 x 15 x 1000 array or as a 150 x 1000 matrix is supported.

Value

A ReshapedHDF5Array (or ReshapedHDF5Matrix) object. (Note that ReshapedHDF5Matrix extends ReshapedHDF5Array.)

See Also

- HDF5Array objects for representing HDF5 datasets as DelayedArray objects without upfront virtual reshaping.
- DelayedArray objects in the **DelayedArray** package.
- `writeHDF5Array` for writing an array-like object to an HDF5 file.
- `saveHDF5SummarizedExperiment` and `loadHDF5SummarizedExperiment` in this package (the **HDF5Array** package) for saving/loading an HDF5-based SummarizedExperiment object to/from disk.
- The ReshapedHDF5ArraySeed helper class.
- `h5ls` to list the content of an HDF5 file.

Examples

```
library(h5vcData)
tally_file <- system.file("extdata", "example.tally.hfs5",
                          package="h5vcData")
h5ls(tally_file)

## Pick up "Coverages" dataset for Human chromosome 16 and collapse its
## first 2 dimensions:
cvg <- ReshapedHDF5Array(tally_file, "/ExampleStudy/16/Coverages",
                         dim=c(12, 90354753))
cvg

is(cvg, "DelayedArray")  # TRUE
seed(cvg)
path(cvg)
dim(cvg)
chunkdim(cvg)
```

ReshapedHDF5ArraySeed-class

ReshapedHDF5ArraySeed objects

Description

ReshapedHDF5ArraySeed is a low-level helper class for representing a pointer to a virtually reshaped HDF5 dataset.

ReshapedHDF5ArraySeed objects are not intended to be used directly. Most end users should create and manipulate ReshapedHDF5Array objects instead. See ?ReshapedHDF5Array for more information.

Usage

```
## Constructor function:
ReshapedHDF5ArraySeed(filepath, name, dim, type=NA)
```

Arguments

`filepath`, `name`, `dim`, `type`

See ?ReshapedHDF5Array for a description of these arguments.

Details

No operation can be performed directly on a ReshapedHDF5ArraySeed object. It first needs to be wrapped in a DelayedArray object. The result of this wrapping is a ReshapedHDF5Array object (a ReshapedHDF5Array object is just a ReshapedHDF5ArraySeed object wrapped in a DelayedArray object).

Value

A ReshapedHDF5ArraySeed object.

See Also

- ReshapedHDF5Array objects.
- `h5ls` to list the content of an HDF5 file.

Examples

```
library(h5vcData)
tally_file <- system.file("extdata", "example.tally.hfs5",
                          package="h5vcData")
h5ls(tally_file)

## Collapse the first 2 dimensions:
seed <- ReshapedHDF5ArraySeed(tally_file, "/ExampleStudy/16/Coverages",
                              dim=c(12, 90354753))
seed
path(seed)
dim(seed)
chunkdim(seed)
```

---

saveHDF5SummarizedExperiment

Save/load an HDF5-based SummarizedExperiment object

Description

`saveHDF5SummarizedExperiment` and `loadHDF5SummarizedExperiment` can be used to save/load an HDF5-based SummarizedExperiment object to/from disk.

NOTE: These functions use functionalities from the **SummarizedExperiment** package internally and so require this package to be installed.

Usage

```
saveHDF5SummarizedExperiment(x, dir="my_h5_se", prefix="", replace=FALSE,
                                chunkdim=NULL, level=NULL, as.sparse=NA,
                                verbose=NA)

loadHDF5SummarizedExperiment(dir="my_h5_se", prefix="")

quickResaveHDF5SummarizedExperiment(x, verbose=FALSE)
```

Arguments

x	A SummarizedExperiment object or derivative. For quickResaveHDF5SummarizedExperiment the object must have been previously saved with saveHDF5SummarizedExperiment (and has been possibly modified since then).
dir	The path (as a single string) to the directory where to save the HDF5-based SummarizedExperiment object or to load it from. When saving, the directory will be created if it doesn't already exist. If the directory already exists and no prefix is specified and replace is set to TRUE, then it's replaced with an empty directory.
prefix	An optional prefix to add to the names of the files created inside dir. Allows saving more than one object in the same directory.
replace	When no prefix is specified, should a pre-existing directory be replaced with a new empty one? The content of the pre-existing directory will be lost!
chunkdim, level	The dimensions of the chunks and the compression level to use for writing the assay data to disk. Passed to the internal calls to writeHDF5Array. See ?writeHDF5Array for more information.
as.sparse	Whether the assay data should be flagged as sparse or not. If set to NA (the default), then the specific as.sparse value to use for each assay is determined by calling is_sparse() on them. Passed to the internal calls to writeHDF5Array. See ?writeHDF5Array for more information and an IMPORTANT NOTE.
verbose	Set to TRUE to make the function display progress. In the case of saveHDF5SummarizedExperiment(), verbose is set to NA by default, in which case verbosity is controlled by DelayedArray:::get_verbose_block_processing(). Setting verbose to TRUE or FALSE overrides this.

Details

saveHDF5SummarizedExperiment(): Creates the directory specified thru the dir argument and populates it with the HDF5 datasets (one per assay in x) plus a serialized version of x that contains pointers to these datasets. This directory provides a self-contained HDF5-based representation of x that can then be loaded back in R with loadHDF5SummarizedExperiment.

Note that this directory is *relocatable* i.e. it can be moved (or copied) to a different place, on the same or a different computer, before calling loadHDF5SummarizedExperiment on it. For convenient sharing with collaborators, it is suggested to turn it into a tarball (with Unix command tar), or zip file, before the transfer.

Please keep in mind that saveHDF5SummarizedExperiment and loadHDF5SummarizedExperiment don't know how to produce/read tarballs or zip files at the moment, so the process of packaging/extracting the tarball or zip file is entirely the user responsibility. This is typically done from outside R.

Finally please note that, depending on the size of the data to write to disk and the performance of the disk, saveHDF5SummarizedExperiment can take a long time to complete. Use verbose=TRUE to see its progress.

`loadHDF5SummarizedExperiment()`: Typically very fast, even if the assay data is big, because all the assays in the returned object are HDF5Array objects pointing to the on-disk HDF5 datasets located in `dir`. HDF5Array objects are typically light-weight in memory.

`quickResaveHDF5SummarizedExperiment()`: Preserves the HDF5 file and datasets that the assays in `x` are already pointing to (and which were created by an earlier call to `saveHDF5SummarizedExperiment`). All it does is re-serialize `x` on top of the `.rds` file that is associated with this HDF5 file (and which was created by an earlier call to `saveHDF5SummarizedExperiment` or `quickResaveHDF5SummarizedExperimen` Because the delayed operations possibly carried by the assays in `x` are not realized, this is very fast.

Value

`saveHDF5SummarizedExperiment` returns an invisible SummarizedExperiment object that is the same as what `loadHDF5SummarizedExperiment` will return when loading back the object. All the assays in the object are HDF5Array objects pointing to datasets in the HDF5 file saved in `dir`.

Difference between saveHDF5SummarizedExperiment() and saveRDS()

Roughly speaking, `saveRDS()` only serializes the part of an object that resides in memory (the reality is a little bit more nuanced, but discussing the full details is not important here, and would only distract us). For most objects in R, that's the whole object, so `saveRDS()` does the job.

However some objects are pointing to on-disk data. For example: a TxDb object (the TxDb class is implemented and documented in the **GenomicFeatures** package) points to an SQLite db; an HDF5Array object points to a dataset in an HDF5 file; a SummarizedExperiment derivative can have one or more of its assays that point to datasets (one per assay) in an HDF5 file. These objects have 2 parts: one part is in memory, and one part is on disk. The 1st part is sometimes called the *object shell* and is generally thin (i.e. it has a small memory footprint). The 2nd part is the data and is typically big. The object shell and data are linked together via some kind of pointer stored in the shell (e.g. an SQLite connection, or a path to a file, etc...). Note that this is a *one way link* in the sense that the object shell "knows" where to find the on-disk data but the on-disk data knows nothing about the object shell (and is completely agnostic about what kind of object shell could be pointing to it). Furthermore, at any given time on a given system, there could be more than one object shell pointing to the same on-disk data. These object shells could exist in the same R session or in sessions in other languages (e.g. Python). These various sessions could be run by the same or by different users.

Using `saveRDS()` on such object will only serialize the shell part so will produce a small `.rds` file that contains the serialized object shell but not the object data.

This is problematic because:

1. If you later unserialize the object (with `readRDS()`) on the same system where you originally serialized it, it is possible that you will get back an object that is fully functional and semantically equivalent to the original object. But here is the catch: this will be the case ONLY if the data is still at the original location and has not been modified (i.e. nobody wrote or altered the data in the SQLite db or HDF5 file in the mean time), and if the serialization/unserialization cycle didn't break the link between the object shell and the data (this serialization/unserialization cycle is known to break open SQLite connections).
2. After serialization the object shell and data are stored in separate files (in the new `.rds` file for the shell, still in the original SQLite or HDF5 file for the data), typically in very different

places on the file system. But these 2 files are not relocatable, that is, moving or copying them to another system or sending them to collaborators will typically break the link between them. Concretely this means that the object obtained by using `readRDS()` on the destination system will be broken.

`saveHDF5SummarizedExperiment()` addresses these issues by saving the object shell and assay data in a folder that is relocatable.

Note that it only works on SummarizedExperiment derivatives. What it does exactly is (1) write all the assay data to an HDF5 file, and (2) serialize the object shell, which in this case is everything in the object that is not the assay data. The 2 files (HDF5 and `.rds`) are written to the directory specified by the user. The resulting directory contains a full representation of the object and is relocatable, that is, it can be moved or copied to another place on the system, or to another system (possibly after making a tarball of it), where `loadHDF5SummarizedExperiment()` can then be used to load the object back in R.

Note

The files created by `saveHDF5SummarizedExperiment` in the user-specified directory `dir` should not be renamed.

The user-specified *directory* created by `saveHDF5SummarizedExperiment` is relocatable i.e. it can be renamed and/or moved around, but not the individual files in it.

Author(s)

Hervé Pagès

See Also

- SummarizedExperiment and RangedSummarizedExperiment objects in the **SummarizedExperiment** package.
- The `writeHDF5Array` function which `saveHDF5SummarizedExperiment` uses internally to write the assay data to disk.
- `base::saveRDS`

Examples

```
## ---------------------------------------------------------------------
## saveHDF5SummarizedExperiment() / loadHDF5SummarizedExperiment()
## ---------------------------------------------------------------------
library(SummarizedExperiment)

nrow <- 200
ncol <- 6
counts <- matrix(as.integer(runif(nrow * ncol, 1, 1e4)), nrow)
colData <- DataFrame(Treatment=rep(c("ChIP", "Input"), 3),
                     row.names=LETTERS[1:6])
se0 <- SummarizedExperiment(assays=list(counts=counts), colData=colData)
se0

## Save 'se0' as an HDF5-based SummarizedExperiment object:
```

```
dir <- tempfile("h5_se0_")
h5_se0 <- saveHDF5SummarizedExperiment(se0, dir)
list.files(dir)

h5_se0
assay(h5_se0, withDimnames=FALSE)   # HDF5Matrix object

h5_se0b <- loadHDF5SummarizedExperiment(dir)
h5_se0b
assay(h5_se0b, withDimnames=FALSE)  # HDF5Matrix object

## Sanity checks:
stopifnot(is(assay(h5_se0, withDimnames=FALSE), "HDF5Matrix"))
stopifnot(identical(assay(se0), as.matrix(assay(h5_se0))))
stopifnot(is(assay(h5_se0b, withDimnames=FALSE), "HDF5Matrix"))
stopifnot(identical(assay(se0), as.matrix(assay(h5_se0b))))

## ---------------------------------------------------------------------
## More sanity checks
## ---------------------------------------------------------------------

## Make a copy of directory 'dir':
somedir <- tempfile("somedir")
dir.create(somedir)
file.copy(dir, somedir, recursive=TRUE)
dir2 <- list.files(somedir, full.names=TRUE)

## 'dir2' contains a copy of 'dir'. Call loadHDF5SummarizedExperiment()
## on it.
h5_se0c <- loadHDF5SummarizedExperiment(dir2)

stopifnot(is(assay(h5_se0c, withDimnames=FALSE), "HDF5Matrix"))
stopifnot(identical(assay(se0), as.matrix(assay(h5_se0c))))

## ---------------------------------------------------------------------
## Using a prefix
## ---------------------------------------------------------------------

se1 <- se0[51:100, ]
saveHDF5SummarizedExperiment(se1, dir, prefix="xx_")
list.files(dir)
loadHDF5SummarizedExperiment(dir, prefix="xx_")

## ---------------------------------------------------------------------
## quickResaveHDF5SummarizedExperiment()
## ---------------------------------------------------------------------

se2 <- loadHDF5SummarizedExperiment(dir, prefix="xx_")
se2 <- se2[1:14, ]
assay1 <- assay(se2, withDimnames=FALSE)
assays(se2, withDimnames=FALSE) <- c(assays(se2), list(score=assay1/100))
rowRanges(se2) <- GRanges("chr1", IRanges(1:14, width=5))
rownames(se2) <- letters[1:14]
```

```
se2

## This will replace saved 'se1'!
quickResaveHDF5SummarizedExperiment(se2, verbose=TRUE)
list.files(dir)
loadHDF5SummarizedExperiment(dir, prefix="xx_")
```

TENxMatrix-class *10x Genomics datasets as DelayedMatrix objects*

Description

A 10x Genomics dataset like the "1.3 Million Brain Cell Dataset" is an HDF5 sparse matrix stored in CSR/CSC/Yale format ("Compressed Sparse Row").

The TENxMatrix class is a DelayedMatrix subclass for representing and operating on this kind of dataset.

All the operations available for DelayedMatrix objects work on TENxMatrix objects.

Usage

```
## Constructor function:
TENxMatrix(filepath, group="matrix")
```

Arguments

`filepath`	The path (as a single string) to the HDF5 file where the 10x Genomics dataset is located.
`group`	The name of the group in the HDF5 file containing the 10x Genomics data.

Details

In addition to all the methods defined for DelayedMatrix objects, TENxMatrix objects support the following specialized methods: `nzcount()` and `extractNonzeroDataByCol()`. See `?H5SparseMatrixSeed` for more information about what these methods do.

Value

`TENxMatrix()` returns a TENxMatrix object.

Note

If your dataset uses the HDF5 sparse matrix representation from 10x Genomics, use the `TENxMatrix()` constructor documented here.

But if your dataset uses the conventional (a.k.a. dense) HDF5 representation, use the `HDF5Array()` constructor instead.

See Also

- HDF5Array objects for representing conventional (a.k.a. dense) HDF5 datasets as DelayedArray objects.
- DelayedMatrix objects in the **DelayedArray** package.
- `writeTENxMatrix` for writing a matrix-like object as an HDF5-based sparse matrix.
- The `TENxBrainData` dataset (in the **TENxBrainData** package).
- `detectCores` from the **parallel** package.
- `setAutoBPPARAM` and `setAutoBlockSize` in the **DelayedArray** package.
- `colAutoGrid` and `blockApply` in the **DelayedArray** package.
- The TENxMatrixSeed helper class.
- `h5ls` to list the content of an HDF5 file.
- NumericList and IntegerList objects in the **IRanges** package.
- SparseArray objects in the **SparseArray** package.

Examples

```
## ---------------------------------------------------------------------
## SIMPLE TENxMatrix EXAMPLE
## ---------------------------------------------------------------------

sm <- Matrix::rsparsematrix(10, 7, density=0.3)
M <- writeTENxMatrix(sm)
M

class(M)  # TENxMatrix
is(M, "DelayedMatrix")  # TRUE

seed(M)
class(seed(M))  # TENxMatrixSeed

rhdf5::h5ls(path(M))

is_sparse(M)  # TRUE

## Use coercion to load the full dataset into memory:
as.matrix(M)          # as ordinary array (usually not recommended)
as(M, "dgCMatrix")    # as dgCMatrix (brings back 'sm')
as(M, "SparseArray")  # as SparseArray object (most efficient)
SparseArray(M)        # equivalent to 'as(M, "SparseArray")'

## ---------------------------------------------------------------------
## THE "1.3 Million Brain Cell Dataset" AS A DelayedMatrix OBJECT
## ---------------------------------------------------------------------

## The 1.3 Million Brain Cell Dataset from 10x Genomics is available
## via ExperimentHub:

library(ExperimentHub)
```

```
hub <- ExperimentHub()
query(hub, "TENxBrainData")
fname <- hub[["EH1039"]]

## 'fname' is an HDF5 file. Use h5ls() to list its content:
h5ls(fname)

## The 1.3 Million Brain Cell Dataset is represented by the "mm10"
## group. We point the TENxMatrix() constructor to this group to
## create a TENxMatrix object representing the dataset:
oneM <- TENxMatrix(fname, group="mm10")
oneM

is(oneM, "DelayedMatrix")  # TRUE
seed(oneM)
path(oneM)
nzcount(oneM)  # nb of nonzero values in the dataset

## Some examples of delayed operations:
oneM != 0
oneM^2

## ---------------------------------------------------------------------
## SOME EXAMPLES OF ROW/COL SUMMARIZATION
## ---------------------------------------------------------------------

## In order to reduce computation times, we'll use only the first
## 25000 columns of the 1.3 Million Brain Cell Dataset:
oneM25k <- oneM[ , 1:25000]

## Row/col summarization methods like rowSums() use a block-processing
## mechanism behind the scene that can be controlled via global
## settings. 2 important settings that can have a strong impact on
## performance are the automatic number of workers and automatic block
## size, controlled by setAutoBPPARAM() and setAutoBlockSize()
## respectively.
library(BiocParallel)
if (.Platform$OS.type != "windows") {
    ## On a modern Linux laptop with 8 cores (as reported by
    ## parallel::detectCores()) and 16 Gb of RAM, reasonably good
    ## performance is achieved by setting the automatic number of workers
    ## to 5 or 6 and the automatic block size between 300 Mb and 400 Mb:
    workers <- 5
    block_size <- 3e8  # 300 Mb
    setAutoBPPARAM(MulticoreParam(workers))
} else {
    ## MulticoreParam() is not supported on Windows so we use SnowParam()
    ## on this platform. Also we reduce the block size to 200 Mb on
    ## 32-bit Windows to avoid memory allocation problems (they tend to
    ## be common there because a process cannot use more than 3 Gb of
    ## memory).
    workers <- 4
    setAutoBPPARAM(SnowParam(workers))
```

```
    block_size <- if (.Platform$r_arch == "i386") 2e8 else 3e8
}
setAutoBlockSize(block_size)

## We're ready to compute the library sizes, number of genes expressed
## per cell, and average expression across cells:
system.time(lib_sizes <- colSums(oneM25k))
system.time(n_exprs <- colSums(oneM25k != 0))
system.time(ave_exprs <- rowMeans(oneM25k))

## Note that the 3 computations above load the data in oneM25k 3 times
## in memory. This can be avoided by computing the 3 summarizations in
## a single pass with blockApply(). First we define the function that
## we're going to apply to each block of data:
FUN <- function(block)
  list(colSums(block), colSums(block != 0), rowSums(block))

## Then we call blockApply() to apply FUN() to each block. The blocks
## are defined by the grid passed to the 'grid' argument. In this case
## we supply a grid made with colAutoGrid() to generate blocks of full
## columns (see ?colAutoGrid for more information):
system.time({
  block_results <- blockApply(oneM25k, FUN, grid=colAutoGrid(oneM25k),
                              verbose=TRUE)
})

## 'block_results' is a list with 1 list element per block in
## colAutoGrid(oneM25k). Each list element is the result that was
## obtained by applying FUN() on the block so is itself a list of
## length 3.
## Let's combine the results:
lib_sizes2 <- unlist(lapply(block_results, `[[`, 1L))
n_exprs2 <- unlist(lapply(block_results, `[[`, 2L))
block_rowsums <- unlist(lapply(block_results, `[[`, 3L), use.names=FALSE)
tot_exprs <- rowSums(matrix(block_rowsums, nrow=nrow(oneM25k)))
ave_exprs2 <- setNames(tot_exprs / ncol(oneM25k), rownames(oneM25k))

## Sanity checks:
stopifnot(all.equal(lib_sizes, lib_sizes2))
stopifnot(all.equal(n_exprs, n_exprs2))
stopifnot(all.equal(ave_exprs, ave_exprs2))

## Turn off parallel evaluation and reset automatic block size to factory
## settings:
setAutoBPPARAM()
setAutoBlockSize()

## ---------------------------------------------------------------------
## extractNonzeroDataByCol()
## ---------------------------------------------------------------------

## extractNonzeroDataByCol() provides a convenient and very efficient
## way to extract the nonzero data in a compact form:
```

```
nonzeros <- extractNonzeroDataByCol(oneM, 1:25000)  # takes < 5 sec.

## The data is returned as an IntegerList object with one list element
## per column and no row indices associated to the values in the object.
## Furthermore, the values within a given list element can be returned
## in any order:
nonzeros

names(nonzeros) <- colnames(oneM25k)

## This can be used to compute some simple summaries like the library
## sizes and the number of genes expressed per cell. For these use
## cases, it is a lot more efficient than using colSums(oneM25k) and
## colSums(oneM25k != 0):
lib_sizes3 <- sum(nonzeros)
n_exprs3 <- lengths(nonzeros)

## Sanity checks:
stopifnot(all.equal(lib_sizes, lib_sizes3))
stopifnot(all.equal(n_exprs, n_exprs3))
```

`TENxMatrixSeed-class` *TENxMatrixSeed objects*

Description

TENxMatrixSeed is a low-level helper class that is a direct extension of the H5SparseMatrixSeed class. It is used to represent a pointer to an HDF5 sparse matrix that is stored in the CSR/CSC/Yale format ("Compressed Sparse Row") and follows the 10x Genomics convention for storing the dimensions of the matrix.

Note that a TENxMatrixSeed object is not intended to be used directly. Most end users will typically create and manipulate a higher-level TENxMatrix object instead. See ?`TENxMatrix` for more information.

Usage

```
## Constructor function:
TENxMatrixSeed(filepath, group="matrix")
```

Arguments

`filepath`, `group` See ?`TENxMatrix` for a description of these arguments.

Details

A TENxMatrixSeed object supports the same limited set of methods as an H5SparseMatrixSeed object. See ?`H5SparseMatrixSeed` for the details.

Value

`TENxMatrixSeed()` returns a TENxMatrixSeed object.

TENxMatrixSeed vs TENxMatrix objects

In order to have access to the full set of operations that are available for DelayedMatrix objects, a TENxMatrixSeed object first needs to be wrapped in a DelayedMatrix object, typically by calling the `DelayedArray()` constructor on it.

This is what the `TENxMatrix()` constructor function does.

Note that the result of this wrapping is a TENxMatrix object, which is just a TENxMatrixSeed object wrapped in a DelayedMatrix object.

See Also

- TENxMatrix objects.
- H5SparseMatrixSeed objects.
- The `TENxBrainData` dataset (in the **TENxBrainData** package).
- `h5ls` to list the content of an HDF5 file.

Examples

```
## The 1.3 Million Brain Cell Dataset from 10x Genomics is available
## via ExperimentHub:
library(ExperimentHub)
hub <- ExperimentHub()
query(hub, "TENxBrainData")
fname <- hub[["EH1039"]]

## 'fname' is an HDF5 file. Use h5ls() to list its content:
h5ls(fname)

## The 1.3 Million Brain Cell Dataset is represented by the "mm10"
## group. We point the TENxMatrixSeed() constructor to this group
## to create a TENxMatrixSeed object representing the dataset:
seed <- TENxMatrixSeed(fname, group="mm10")
seed
path(seed)
dim(seed)
is_sparse(seed)
sparsity(seed)

DelayedArray(seed)
stopifnot(class(DelayedArray(seed)) == "TENxMatrix")
```

writeHDF5Array *Write an array-like object to an HDF5 file*

Description

A function for writing an array-like object to an HDF5 file.

Usage

```
writeHDF5Array(x, filepath=NULL, name=NULL,
               H5type=NULL, chunkdim=NULL, level=NULL, as.sparse=NA,
               with.dimnames=TRUE, verbose=NA)
```

Arguments

x	The array-like object to write to an HDF5 file. If x is a DelayedArray object, writeHDF5Array *realizes* it on disk, that is, all the delayed operations carried by the object are executed while the object is written to disk. See "On-disk realization of a DelayedArray object as an HDF5 dataset" section below for more information.
filepath	NULL or the path (as a single string) to the (new or existing) HDF5 file where to write the dataset. If NULL, then the dataset will be written to the current *HDF5 dump file* i.e. to the file whose path is getHDF5DumpFile.
name	NULL or the name of the HDF5 dataset to write. If NULL, then the name returned by getHDF5DumpName will be used.
H5type	The H5 datatype to use for the HDF5 dataset to be written to the HDF5 file is automatically inferred from the type of x (type(x)). Advanced users can override this by specifying the H5 datatype they want via the H5type argument. See rhdf5::h5const("H5T") for a list of available H5 datatypes. See References section below for the link to the HDF Group's Support Portal where H5 predefined datatypes are documented. A typical use case is to use a datatype that is smaller than the automatic one in order to reduce the size of the dataset on disk. For example you could use "H5T_IEEE_F32LE" when type(x) is "double" and you don't care about preserving the precision of 64-bit floating-point numbers (the automatic H5 datatype used for "double" is "H5T_IEEE_F64LE"). Another example is to use "H5T_STD_U16LE" when x contains small non-negative integer values like counts (the automatic H5 datatype used for "integer" is "H5T_STD_I32LE").
chunkdim	The dimensions of the chunks to use for writing the data to disk. By default (i.e. when chunkdim is set to NULL), getHDF5DumpChunkDim(dim(x)) will be used. See ?getHDF5DumpChunkDim for more information. Set chunkdim to 0 to write *unchunked data* (a.k.a. *contiguous data*).
level	The compression level to use for writing the data to disk. By default, getHDF5DumpCompressionLevel() will be used. See ?getHDF5DumpCompressionLevel for more information.

`as.sparse` Whether the data in the returned HDF5Array object should be flagged as sparse or not. If set to `NA` (the default), then `is_sparse(x)` is used.

IMPORTANT NOTE: This only controls the `as.sparse` flag of the returned HDF5Array object. See man page of the `HDF5Array()` constructor for more information. In particular this does NOT affect how the data will be laid out in the HDF5 file in any way (HDF5 doesn't natively support sparse storage at the moment). In other words, the data will always be stored in a dense format, even when `as.sparse` is set to `TRUE`.

`with.dimnames` Whether the dimnames on `x` should also be written to the HDF5 file or not. `TRUE` by default.

Note that `h5writeDimnames` is used internally to write the dimnames to disk. Setting `with.dimnames` to `FALSE` and calling `h5writeDimnames` is another way to write the dimnames on `x` to disk that gives more control. See `?h5writeDimnames` for more information.

`verbose` Whether block processing progress should be displayed or not. If set to `NA` (the default), verbosity is controlled by `DelayedArray:::get_verbose_block_processing()`. Setting `verbose` to `TRUE` or `FALSE` overrides this.

Details

Please note that, depending on the size of the data to write to disk and the performance of the disk, `writeHDF5Array()` can take a long time to complete. Use `verbose=TRUE` to see its progress.

Use `setHDF5DumpFile` and `setHDF5DumpName` to control the location of automatically created HDF5 datasets.

Use `setHDF5DumpChunkLength`, `setHDF5DumpChunkShape`, and `setHDF5DumpCompressionLevel`, to control the physical properties of automatically created HDF5 datasets.

Value

An HDF5Array object pointing to the newly written HDF5 dataset on disk.

On-disk realization of a DelayedArray object as an HDF5 dataset

When passed a DelayedArray object, `writeHDF5Array` *realizes* it on disk, that is, all the delayed operations carried by the object are executed on-the-fly while the object is written to disk. This uses a block-processing strategy so that the full object is not realized at once in memory. Instead the object is processed block by block i.e. the blocks are realized in memory and written to disk one at a time.

In other words, `writeHDF5Array(x, ...)` is semantically equivalent to `writeHDF5Array(as.array(x), ...)`, except that `as.array(x)` is not called because this would realize the full object at once in memory.

See `?DelayedArray` for general information about DelayedArray objects.

References

Documentation of the H5 predefined datatypes on the HDF Group's Support Portal: https://portal.hdfgroup.org/display/HDF5/Predefined+Datatypes

See Also

- HDF5Array objects.
- h5writeDimnames for writing the dimnames of an HDF5 dataset to disk.
- saveHDF5SummarizedExperiment and loadHDF5SummarizedExperiment in this package (the **HDF5Array** package) for saving/loading an HDF5-based SummarizedExperiment object to/from disk.
- HDF5-dump-management to control the location and physical properties of automatically created HDF5 datasets.
- h5ls to list the content of an HDF5 file.

Examples

```
## ---------------------------------------------------------------------
## WRITE AN ORDINARY ARRAY TO AN HDF5 FILE
## ---------------------------------------------------------------------
m0 <- matrix(runif(364, min=-1), nrow=26,
             dimnames=list(letters, LETTERS[1:14]))

h5file <- tempfile(fileext=".h5")
M1 <- writeHDF5Array(m0, h5file, name="M1", chunkdim=c(5, 5))
M1
chunkdim(M1)

## By default, writeHDF5Array() writes the dimnames to the HDF5 file:
dimnames(M1)   # same as 'dimnames(m0)'

## Use 'with.dimnames=FALSE' to not write the dimnames to the file:
M1b <- writeHDF5Array(m0, h5file, name="M1b", with.dimnames=FALSE)
dimnames(M1b)  # no dimnames

## With sparse data:
sm <- rsparsematrix(20, 8, density=0.1)
M2 <- writeHDF5Array(sm, h5file, name="M2", chunkdim=c(5, 5))
M2
is_sparse(M2)  # TRUE

## ---------------------------------------------------------------------
## WRITE A DelayedArray OBJECT TO AN HDF5 FILE
## ---------------------------------------------------------------------
M3 <- log(t(DelayedArray(m0)) + 1)
M3 <- writeHDF5Array(M3, h5file, name="M3", chunkdim=c(5, 5))
M3
chunkdim(M3)

library(h5vcData)
tally_file <- system.file("extdata", "example.tally.hfs5",
                          package="h5vcData")
h5ls(tally_file)

cvg0 <- HDF5Array(tally_file, "/ExampleStudy/16/Coverages")
```

```
cvg1 <- cvg0[ , , 29000001:29000007]

writeHDF5Array(cvg1, h5file, "cvg1")
h5ls(h5file)
```

---

writeTENxMatrix *Write a matrix-like object as an HDF5-based sparse matrix*

Description

The 1.3 Million Brain Cell Dataset and other datasets published by 10x Genomics use an HDF5-based sparse matrix representation instead of the conventional (a.k.a. dense) HDF5 representation.

writeTENxMatrix writes a matrix-like object to this format.

IMPORTANT NOTE: Only use writeTENxMatrix if the matrix-like object to write is sparse, that is, if most of its elements are zero. Using writeTENxMatrix on dense data is very inefficient! In this case, you should use writeHDF5Array instead.

Usage

```
writeTENxMatrix(x, filepath=NULL, group=NULL, level=NULL, verbose=NA)
```

Arguments

x	The matrix-like object to write to an HDF5 file. The object to write should typically be sparse, that is, most of its elements should be zero. If x is a DelayedMatrix object, writeTENxMatrix *realizes* it on disk, that is, all the delayed operations carried by the object are executed while the object is written to disk.
filepath	NULL or the path (as a single string) to the (new or existing) HDF5 file where to write the data. If NULL, then the data will be written to the current *HDF5 dump file* i.e. to the file whose path is getHDF5DumpFile.
group	NULL or the name of the HDF5 group where to write the data. If NULL, then the name returned by getHDF5DumpName will be used.
level	The compression level to use for writing the data to disk. By default, getHDF5DumpCompressionLevel() will be used. See ?getHDF5DumpCompressionLevel for more information.
verbose	Whether block processing progress should be displayed or not. If set to NA (the default), verbosity is controlled by DelayedArray:::get_verbose_block_processing(). Setting verbose to TRUE or FALSE overrides this.

Details

Please note that, depending on the size of the data to write to disk and the performance of the disk, writeTENxMatrix can take a long time to complete. Use verbose=TRUE to see its progress.

Use setHDF5DumpFile and setHDF5DumpName to control the location of automatically created HDF5 datasets.

Value

A TENxMatrix object pointing to the newly written HDF5 data on disk.

See Also

- TENxMatrix objects.
- The TENxBrainData dataset (in the **TENxBrainData** package).
- HDF5-dump-management to control the location and physical properties of automatically created HDF5 datasets.
- h5ls to list the content of an HDF5 file.

Examples

```
## ---------------------------------------------------------------------
## A SIMPLE EXAMPLE
## ---------------------------------------------------------------------
m0 <- matrix(0L, nrow=25, ncol=12,
             dimnames=list(letters[1:25], LETTERS[1:12]))
m0[cbind(2:24, c(12:1, 2:12))] <- 100L + sample(55L, 23, replace=TRUE)
out_file <- tempfile()
M0 <- writeTENxMatrix(m0, out_file, group="m0")
M0
sparsity(M0)

path(M0)  # same as 'out_file'

## Use h5ls() to list the content of this HDF5 file:
h5ls(path(M0))

## ---------------------------------------------------------------------
## USING THE "1.3 Million Brain Cell Dataset"
## ---------------------------------------------------------------------

## The 1.3 Million Brain Cell Dataset from 10x Genomics is available via
## ExperimentHub:
library(ExperimentHub)
hub <- ExperimentHub()
query(hub, "TENxBrainData")
fname <- hub[["EH1039"]]
oneM <- TENxMatrix(fname, group="mm10")  # see ?TENxMatrix for the details
oneM

## Note that the following transformation preserves sparsity:
M2 <- log(oneM + 1)  # delayed
M2                   # a DelayedMatrix instance

## In order to reduce computation times, we'll write only the first
## 5000 columns of M2 to disk:
out_file <- tempfile()
M3 <- writeTENxMatrix(M2[ , 1:5000], out_file, group="mm10", verbose=TRUE)
M3                   # a TENxMatrix instance
```

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