Package ‘rhdf5client’

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Title Access HDF5 content from HDF Scalable Data Service

Description This package provides functionality for reading data from HDF Scalable Data Service from within R. The HSDSArray function bridges from HSDS to the user via the DelayedArray interface. Bioconductor manages an open HSDS instance graciously provided by John Readey of the HDF Group.

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Imports httr, rjson, utils, data.table

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`as` *Coercion method from HSDSMatrix to its superclass HSDSArray*

Description

Coercion method from HSDSMatrix to its superclass HSDSArray

See Also

Other HSDSArray: `HSDSArray`, `HSDSMatrix`

`check_hsds` *a test request*

Description

a test request

Usage

```
check_hsds()
```

Value

logical, TRUE if hsds behaving as expected

Examples

```
check_hsds()
```

`dim` *Obtain dimensions of an object of type HSDSArraySeed*

Description

(required by DelayedArray seed contract) HDF server content is assumed transposed relative to R matrix layout. This anticipates H5 datasets on the server with rows for experimental samples and columns for *-omic features. The Bioconductor SummarizedExperiment requires *-omic features in rows and samples in columns.

Usage

```
## S4 method for signature 'HSDSArraySeed'
dim(x)
```

Arguments

`x`	An object of type HSDSArraySeed

Value

A numeric vector of the dimensions

`dimnames` *Obtain names of dimensions for an object of type HSDSArraySeed*

Description

(required by DelayedArray seed contract, returns NULL list)

Usage

```
## S4 method for signature 'HSDSArraySeed'
dimnames(x)
```

Arguments

`x`	An object of type HSDSArraySeed

Value

A NULL list of length equal to the array dimensionality

`extractCompoundJSON` *compound operation*

Description

compound operation

Usage

```
extractCompoundJSON(type, value)
```

Arguments

`type`	type
`value`	value

`extract_array` *Access dataset backed by an HSDSArraySeed*

Description

Access dataset backed by an HSDSArraySeed

Usage

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

Arguments

`x`	An object of type HSDSArraySeed
`index`	A list of numeric vectors to be accessed, one vector for each dimension of the array object. A NULL vector indicates the entire range of indices in that dimension. A zero-length vector indicates no indices in the relevant dimension. (Accordingly, any zero-length vector of indices will result in an empty array being returned.)

Value

An array containing the data elements corresponding to the indices requested

---

`getData` *extract elements of a one or two-dimensional HSDSDataset*

Description

Fetch data from a remote dataset

Usage

```
getData(dataset, indices, transfermode)

## S4 method for signature 'HSDSDataset,character,character'
getData(dataset, indices, transfermode)

## S4 method for signature 'HSDSDataset,character,missing'
getData(dataset, indices)

## S4 method for signature 'HSDSDataset,list,character'
getData(dataset, indices, transfermode)

## S4 method for signature 'HSDSDataset,list,missing'
getData(dataset, indices)
```

Arguments

`dataset`	An object of type HSDSDataset, the dataset to access.
`indices`	The indices of the data to fetch
`transfermode`	Either 'JSON' or 'binary' (default)

Details

The servers require data to be fetched in slices, i.e., in sets of for which the indices of each dimension are of the form start:stop:step. More complex sets of indices will be split into slices and fetched in multiple requests. This is opaque to the user, but may enter into considerations of data access patterns, e.g., for performance-tuning.

Value

an Array containing the data fetched from the server

Examples

```
if (check_hsds()) {
 s <- HSDSSource(URL_hsds())
 f <- HSDSFile(s, '/shared/bioconductor/patelGBMSC.h5')
 d <- HSDSDataset(f, '/assay001')
 x <- getData(d, c('1:4', '1:27998'), transfermode='JSON')
 xb <- getData(d, c('1:4', '1:27998'), transfermode='binary')
 # x <- getData(d, c(1:4, 1:27998), transfermode='JSON') # method missing?
 x
 xb
}
```

`getHSDSFileList` *List files on a directory on HSDS-server*

Description

This funstions returns a list of all HDF5-files on the server or all files of the collection

Usage

```
getHSDSFileList(url, directory = NULL)
```

Arguments

`url`	containing url of the server and root domain.
`directory`	containing name of the directory

Value

List of all HDF5-files on the server or all files of the collection

Examples

```
if (check_hsds()) {
 url <- 'https://alserglab.wustl.edu/hsds/?domain=/counts'
 getHSDSFileList(url)
}
```

`HSDSArray` *A DelayedArray backend for accessing a remote HDF5 server.*

Description

A DelayedArray backend for accessing a remote HDF5 server.

Construct an object of type HSDSArray directly from the data members of its seed

Usage

```
HSDSArray(endpoint, svrtype, domain, dsetname)
```

Arguments

`endpoint`	URL of remote server
`svrtype`	type of server, must be either 'hsds' or 'h5serv'
`domain`	HDF5 domain of H5 file on server
`dsetname`	complete internal path to dataset in H5 file

Value

An initialized object of type HSDSArray

See Also

Other HSDSArray: `HSDSMatrix`, `as`()

Examples

```
if (check_hsds()) {
 HSDSArray(URL_hsds(),
    "hsds", "/shared/bioconductor/patelGBMSC.h5", "/assay001")
}
```

`HSDSArraySeed` *HSDSArraySeed for HSDSArray backend to DelayedArray*

Description

HSDSArraySeed for HSDSArray backend to DelayedArray

Construct an object of type HSDSArraySeed

Usage

```
HSDSArraySeed(endpoint, svrtype, domain, dsetname)
```

Arguments

`endpoint`	URL of remote server
`svrtype`	type of server, must be either 'hsds' or 'h5serv'
`domain`	HDF5 domain of H5 file on server
`dsetname`	complete internal path to dataset in H5 file

Value

An initialized object of type HSDSArraySeed

Slots

`endpoint` URL of remote server

`svrtype` type of server, must be either 'hsds' or 'h5serv'

`domain` HDF5 domain of H5 file on server

`dsetname` complete internal path to dataset in H5 file

`dataset` object of type HSDSDataset for access to the H5 dataset

`HSDSDataset` *Construct an object of type HSDSDataset A HSDSDataset is a representation of a dataset in a HDF5 file.*

Description

Construct an object of type HSDSDataset A HSDSDataset is a representation of a dataset in a HDF5 file.

Usage

```
HSDSDataset(file, path)
```

Arguments

`file`	An object of type HSDSFile which hosts the dataset
`path`	The complete intrafile path to the dataset

Value

An initialized object of type HSDSDataset

Examples

```
if (check_hsds()) {
 src <- HSDSSource(URL_hsds())
 f <- HSDSFile(src, '/shared/bioconductor/patelGBMSC.h5')
 d <- HSDSDataset(f, '/assay001')
}
```

`HSDSDataset-class` *An S4 class to represent a dataset in a HDF5 file.*

Description

An S4 class to represent a dataset in a HDF5 file.

Slots

`file` An object of type HSDSFile; the file in which the dataset is resident.

`path` The dataset's path in the internal HDF5 hiearchy.

`uuid` The unique unit ID by which the dataset is accessed in the server database system.

`shape` The dimensions of the dataset

`type` The dataset's HDF5 datatype

`HSDSFile` *Construct an object of type HSDSFile*

Description

A HSDSFile is a representation of an HDF5 file the contents of which are accessible exposed by a HDF5 server.

Usage

```
HSDSFile(src, domain)
```

Arguments

`src`	an object of type HSDSSource, the server which exposes the file
`domain`	the domain string; the file's location on the server's file system.

Details

This function is deprecated and will be defunct in the next release.

Value

an initialized object of type HSDSFile

Examples

```
if (check_hsds()) {
 src <- HSDSSource(URL_hsds())
 f10x <- HSDSFile(src, '/shared/bioconductor/patelGBMSC.h5')
}
```

`HSDSFile-class` *An S4 class to represent an HDF5 file accessible from a server.*

Description

An S4 class to represent an HDF5 file accessible from a server.

Slots

- `HSDSSource` an object of type HSDSSource
- `domain` the file's domain on the server; more or less, an alias for its location in the external server file system
- `dsetdf` a data.frame that caches often-used information about the file
- `type` string representing type of the file: "domain" for file and "folder" for directory

---

`HSDSMatrix` *DelayedMatrix subclass for a two-dimensional HSDSArray*

Description

DelayedMatrix subclass for a two-dimensional HSDSArray

See Also

Other HSDSArray: `HSDSArray`, `as()`

`HSDSSource` *Construct an object of type HSDSSource.*

Description

A HSDSSource is a representation of a URL which provides access to a HDF5 server (either h5serv or hsds.)

Usage

```
HSDSSource(endpoint, type = "hsds")
```

Arguments

`endpoint`	URL for server
`type`	Type of server software at the source; must be

Details

This function is deprecated and will be defunct in the next release.

Value

An object of type HSDSSource

Examples

```
if (check_hsds()) {
 src.hsds <- HSDSSource(URL_hsds())
}
```

`HSDSSource-class` *An S4 class to represent a HDF5 server listening on a port.*

Description

This class is deprecated and will be defunct in the next release.

Slots

`endpoint` URL for server

`type` Type of server software at the source; must be either 'h5serv' or (default) 'hsds'

`isplit` *This function is deprecated and will be defunct in the next release.*

Description

isplit converts a numeric vector into a list of sequences for compact reexpression

Usage

```
isplit(x)

sproc(spl)
```

Arguments

`x`	a numeric vector (should be integers)
`spl`	output of isplit

Value

list of vectors of integers which can be expressed as initial/final/stride triplets

list of colon-delimited strings each with initial/final/stride triplet

Examples

```
inds = c(1:10, seq(25,50,2), seq(200,150,-2))
sproc(isplit(inds))
```

`listDatasets` *Search inner file hierarchy for datasets*

Description

The datasets in an HDF5 file are organized internally by groups. This routine traverses the internal group hiearchy, locates all datasets and prints a list of them. Note that if the file's group hiearchy is complex, this could be time-consuming.

Usage

```
listDatasets(file)
```

Arguments

`file`	an object of type HSDSFile to be searched

Details

This function is deprecated and will be defunct in the next release.

Value

a list of inner-paths

Examples

```
if (check_hsds()) {
 src <- HSDSSource(URL_hsds())
 f <- HSDSFile(src, '/shared/bioconductor/patelGBMSC.h5')
 listDatasets(f)
}
```

`listDomains` *List files and subdirectories of a domain*

Description

The user needs to give the domain to start in. The search will be non-recursive. I.e., output for domain '/home/jreadey/' will not return the files in '/home/jreadey/HDFLabTutorial/'

Usage

```
listDomains(object, rootdir)

## S4 method for signature 'HSDSSource,character'
listDomains(object, rootdir)

## S4 method for signature 'HSDSSource,missing'
listDomains(object)
```

Arguments

`object`	An object of type HSDSSource
`rootdir`	A slash-separated directory in the HSDSSource file system.

Details

This function is deprecated and will be defunct in the next release.

Value

a vector of domains in the rootdir

Examples

```
src.hsds <- HSDSSource(URL_hsds())
listDomains(src.hsds, '/shared')
```

`rhdf5client` *rhdf5client: A package for accessing HDFGroup HDF5 servers from R.*

Description

The rhdf5client package provides read-only access to HDF5 files maintained on a server. The HDFGroup provides two servers, an obsolescent one called ‘h5serv‘ and the newer prototype called ‘hsds‘.

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`rhdf5client-deprecated` *Deprecated functions in package ‘rhdf5client’*

Description

These functions are provided for compatibility with older versions of ‘rhdf5client’ only, and will be defunct at the next release.

Details

The following functions are deprecated and will be made defunct in the next release:

- URL_h5serv
- URL_hsds
- dsmeta
- getReq
- groups
- setPath
- links
- transfermode
- dataset
- internalDim
- hsdsInfo
- domains

- getDatasetUUIDs
- getDatasetAttrs
- getDims
- getHRDF
- H5S_dataset2
- getDatasetSlice
- fetchDatasets
- isplit
- sproc
- listDomains
- listDatasets
- getData

The following classes are deprecated and will be made defunct in the next release:

- H5S_source
- H5S_dataset
- H5S_Array
- H5S_Matrix
- HSDSSource
- HSDSFile
- HSDSDataset

`URL_hsds` *manage hsds URL*

Description

manage hsds URL

Usage

```
URL_hsds()
```

Value

URL of hsds server

Examples

```
URL_hsds()
```

`[,HSDSDataset,numeric,ANY,ANY-method` *bracket method for 1d request from HSDSDataset*

Description

bracket method for 1d request from HSDSDataset

Usage

```
## S4 method for signature 'HSDSDataset,numeric,ANY,ANY'
x[i, j, ..., drop = TRUE]
```

Arguments

`x`	object of type HSDSDataset
`i`	vector of indices (first dimension)
`j`	not used
`...`	not used
`drop`	logical(1) if TRUE return has no array character

Value

an array with the elements requested from the HSDSDataset

`[,HSDSDataset,numeric,numeric,ANY-method` *bracket method for 2d request from HSDSDataset*

Description

bracket method for 2d request from HSDSDataset

Usage

```
## S4 method for signature 'HSDSDataset,numeric,numeric,ANY'
x[i, j, ..., drop = TRUE]
```

Arguments

`x`	object of type HSDSDataset
`i`	vector of indices (first dimension)
`j`	vector of indices (second dimension)
`...`	not used
`drop`	logical(1) if TRUE return has no array character

Value

an array with the elements requested from the HSDSDataset

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