

# Package ‘rhdf5client’

October 14, 2021

**Title** Access HDF5 content from h5serv

**Description** Provides functionality for reading data from h5serv server from within R.

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**Suggests** knitr, testthat, BiocStyle, DT, reticulate, rmarkdown

**Imports** S4Vectors, httr, R6, rjson, utils

**Depends** R (>= 3.6), methods, DelayedArray

**License** Artistic-2.0

**LazyLoad** yes

**BiocViews** infrastructure

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**VignetteBuilder** knitr

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as	<i>coercion for remote array to remote matrix</i>
----	---

---

**Description**

coercion for remote array to remote matrix

Coercion method from HSDSMatrix to its superclass HSDSArray

**See Also**

Other HSDSArray: [HSDSArray](#), [HSDSMatrix](#)

---

check_hds	<i>a test request</i>
-----------	-----------------------

---

**Description**

a test request

**Usage**

check\_hds()

---

dataset	<i>Find a dataset on source from its name</i>
---------	---

---

### Description

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

### Usage

```
dataset(h5s, tag)
```

### Arguments

h5s	instance of H5S_source
tag	character string identifying a dataset

### Value

object of type H5S\_dataset

---

dim	<i>Obtain dimensions of an object of type HSDSArraySeed</i>
-----	---

---

### 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

---

 dim,H5S\_ArraySeed-method

*HDF Server content is assumed transposed relative to R matrix layout*

---

### Description

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

### Usage

```
## S4 method for signature 'H5S_ArraySeed'
dim(x)
```

### Arguments

x                    instance of H5S\_ArraySeed

### Value

integer(2) vector of dimensions corresponding to R's layout, assuming 2-d data

---

 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

---

dimnames, H5S\_ArraySeed-method

*dimnames not stored with H5S\_source as of Jan 2018*

---

### Description

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

### Usage

```
## S4 method for signature 'H5S_ArraySeed'
dimnames(x)
```

### Arguments

x                    instance of H5S\_ArraySeed

### Value

currently returns list(NULL, NULL) as we do not store dimnames in HDF5

---

domains

*HSDS server domains accessor*

---

### Description

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

### Usage

```
domains(object, ...)
```

### Arguments

object                H5S\_source instance  
 ...                    not used

### Value

a data frame with domains name

## Examples

```
## Not run:
hsdsCon = H5S_source(URL_hds()) # hsds server connection
setPath(hsdsCon, "/home/stvjc/")-> hsds
domains(hsds)

## End(Not run)
```

---

dsmeta	<i>list information about datasets available in an H5S_source</i>
--------	---

---

## Description

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

## Usage

```
dsmeta(src)
```

## Arguments

src                    H5S\_source instance

## Value

data frame with one row for each group and three columns. The second column has the list of datasets in the group.

## Examples

```
## Not run:
bigec2 = H5S_source(URL_h5serv())
dsm <- dsmeta(bigec2)
dst <- unlist(dsm[1,2])    # all dataset candidates in group 1

## End(Not run)
```

---

extract_array	<i>Access dataset backed by an HSDSArraySeed</i>
---------------	--

---

**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

---

fetchDatasets	<i>fetch datasets of a hdf5 file from the hsdS server</i>
---------------	---

---

**Description**

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

**Usage**

```
fetchDatasets(object)
```

**Arguments**

object	instance of H5S_source
--------	------------------------

**Value**

data.frame with information about the datasets in the file



**Examples**

```
## Not run:
hsdsCon = H5S_source(URL_hds()) # hsds server
hsdsCon@folderPath="/home/stvjc/hdf5_mat.h5"
ds = fetchDatasets(hsdsCon)
ds

## End(Not run)
```

---

 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 (default) 'JSON' or 'binary'

**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_hsd()) {  
  s <- HSDSource('http://hsdshdf1ab.hdfgroup.org')  
  f <- HSDFile(s, '/shared/bioconductor/tenx_full.h5')  
  d <- HSDDataset(f, '/newassay001')  
  x <- getData(d, c('1:4', '1:27998'), transfermode='JSON')  
  # x <- getData(d, c(1:4, 1:27998), transfermode='JSON') # method missing?  
  x <- d[1:4,1:27998]  
}
```

---

getDatasetAttrs

*getDatasetAttrs from hsd server*

---

## Description

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

## Usage

```
getDatasetAttrs(object, duid)
```

## Arguments

object	instance of H5S_source(updated object with path to file set)
duid	character string with dataset uuid

## Value

list of data obtained

## Examples

```
## Not run:  
hsdsCon = H5S_source(URL_hsd()) # hsd server  
hsdsCon@folderPath="/home/stvjc/hdf5_mat.h5"  
ds = fetchDatasets(hsdsCon)# Pick the ID of the dataset you are interested in  
getDatasetAttrs(hsdsCon, "d-a9e4b71c-8ea2-11e8-9306-0242ac120022")  
  
## End(Not run)
```

---

getDatasetSlice      *getDatasetSlice from hsds server*

---

**Description**

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

**Usage**

```
getDatasetSlice(object, dsindex = 1, selectionString, ...)
```

**Arguments**

object	instance of H5S_source(updated object with path to file set)
dsindex	dataset index
selectionString	character with selectionString
...	unused

**Value**

list of data obtained

**Examples**

```
## Not run:
hsdsCon = H5S_source(URL_hsds()) # hsds server
setPath(hsdsCon, "/home/stvjc/hdf5_mat.h5")-> hsds
getDatasetSlice(hsds,dsindex=1,selectionString="[1:2,1:5]")

## End(Not run)
```

---

getDatasetUUIDs      *getDatasetUUIDs from hsds server*

---

**Description**

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

**Usage**

```
getDatasetUUIDs(object)
```

**Arguments**

object	instance of H5S_source(updated object with path to file set)
--------	--

**Value**

character of dataset uuid obtained

**Examples**

```
## Not run:
hsdsCon = H5S_source(URL_hds()) # hds server
setPath(hsdsCon, "/home/stvjc/hdf5_mat.h5")-> hds
getDatasetUUIDs(hsds)

## End(Not run)
```

---

getDims

*getDims from hds server*

---

**Description**

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

**Usage**

```
getDims(object, duid)
```

**Arguments**

object	instance of H5S_source(updated object with path to file set)
duid	character string with dataset uuid

**Value**

numeric content of dimensions

**Examples**

```
## Not run:
hsdsCon = H5S_source(URL_hds()) # hds server
setPath(hsdsCon, "/home/stvjc/hdf5_mat.h5")-> hds
duid <- 'd-a9e4b71c-8ea2-11e8-9306-0242ac120022'
getDims(hsds, duid)

## End(Not run)
```

---

getHRDF	<i>getHRDF from hsds server</i>
---------	---------------------------------

---

**Description**

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

**Usage**

```
getHRDF(object, duid)
```

**Arguments**

object	instance of H5S_source(updated object with path to file set)
duid	character string with dataset uuid

**Value**

DataFrame of data obtained

**Examples**

```
## Not run:
hsdsCon = H5S_source(URL_hsds()) # hsds server
hsdsCon@folderPath="/home/stvjc/hdf5_mat.h5"
ds = fetchDatasets(hsdsCon) #Pick the ID of the dataset you are interested in
getHRDF(hsdsCon, "d-a9e4b71c-8ea2-11e8-9306-0242ac120022")

## End(Not run)
```

---

getReq	<i>list information about server content available in an H5S_source hsds instance</i>
--------	---

---

**Description**

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

**Usage**

```
getReq(src)
```

**Arguments**

src	H5S_source instance
-----	---------------------

**Value**

data frame with 5 columns for one row for each user's data

---

groups	<i>HDF5 server data groups accessor</i>
--------	---

---

**Description**

HDF5 server data groups accessor

**Usage**

```
groups(object, index, ...)

## S4 method for signature 'H5S_source,missing'
groups(object, index, ...)

## S4 method for signature 'H5S_source,numeric'
groups(object, index, ...)
```

**Arguments**

object	H5S_source instance This function is deprecated and will be defunct in the next release.
index	numeric, if present, extracts metadata about selected group (sequential ordering of groups as returned by server) access for group information for HDF5 server
...	not used

**Value**

a data frame with group name and number of links for each group

**Examples**

```
## Not run:
bigec2 = H5S_source(URL_h5serv())
groups(bigec2)

## End(Not run)
```

---

H5S_Array	<i>create H5S_Array instance given url (filepath) and entity (host) name</i>
-----------	--

---

**Description**

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

**Usage**

```
H5S_Array(endpoint, filepath, host)
```

**Arguments**

```
endpoint      a character(1) URL to port for HDF Server
filepath      path and name of the H5 file
host          a character(1) name of 'host' in server
```

**Value**

an instance of [DelayedArray-class](#)

**Examples**

```
# The true values from yriMulti data element 'banovichSE':
# > assay(banovichSE[c(1:5,329465:329469),c(1:3,63:64)])
#
# NA18498 NA18499 NA18501 | NA18489 NA18909
# cg00000029 0.47339629 1.2943041 -0.8084735 | 0.6708168 -0.86093022
# cg00000165 1.23640861 0.2099817 -0.2683763 | 0.4446088 0.99868231
# cg00000236 -0.22258183 1.6236857 -0.8654838 | 0.1958195 -0.06090929
# cg00000289 0.65720581 0.5527470 -1.8458295 | -0.4618782 0.34934164
# cg00000363 -0.15063083 0.7498020 0.3254333 | 0.7342878 0.12940774
# #-----
# ch.9.98936572R -0.07954958 0.2139431 -0.4719621 | 0.6835012 0.57758798
# ch.9.98937537R 0.04254705 1.0702770 1.7356387 | -0.1531732 -1.52889773
# ch.9.98959675F -1.59253143 0.2982456 -1.1954030 | -1.3703135 0.28974909
# ch.9.98989607R -1.80646652 0.4760022 1.4771808 | 0.9479602 0.49921375
# ch.9.991104F 0.08180195 -0.2434306 1.0281002 | -0.1653721 0.55612215
#
```

---

H5S\_Array-class      *extension of DelayedArray for HDF Server content*

---

**Description**

extension of DelayedArray for HDF Server content

---

H5S\_ArraySeed-class      *H5S\_Array for HDF Server content*

---

**Description**

H5S\_Array for HDF Server content

---

H5S_dataset	<i>construct H5S_dataset object</i>
-------------	-------------------------------------

---

**Description**

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

**Slots**

source instance of H5S\_source instance  
 simpleName character string naming dataset  
 shapes list including dimension information  
 hrefs DataFrame of hrefs as defined in the API  
 allatts list of all attributes  
 preselect string prepared for select operation in GET  
 transfermode default "JSON" or "binary" for binary transfer

---

H5S_dataset2	<i>H5S_dataset2 for datasets in hds server</i>
--------------	--

---

**Description**

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

**Usage**

```
H5S_dataset2(object, duid)
```

**Arguments**

object	instance of H5S_source(updated object with path to file set)
duid	character vector with dataset uuid of interest

**Value**

H5S\_dataset object

**Examples**

```
## Not run:
hdsCon = H5S_source(URL_hds()) # hds server
hdsCon@folderPath="/home/stvjc/hdf5_mat.h5"
ds = fetchDatasets(hdsCon) #Pick the dataset id of interest
H5S_dataset2(hdsCon, "d-a9e4b71c-8ea2-11e8-9306-0242ac120022")

## End(Not run)
```



---

H5S_Matrix-class	<i>extension of DelayedMatrix for HDF Server content</i>
------------------	--

---

**Description**

extension of DelayedMatrix for HDF Server content

---

H5S_source	<i>H5S_source identifies an HDF5/HSDS server and manages some metadata about contents</i>
------------	---

---

**Description**

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

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

**Usage**

```
H5S_source(serverURL, domain, ...)
```

**Arguments**

serverURL	a URL for a port for HDF5Server
domain	character string with path to file for HSDS
...	not used

**Value**

an initialized object of type H5S\_source

**Slots**

serverURL	character string with a URL
dsmeta	DataFrame instance with metadata about content of h5serv server
dmains	DataFrame instance with metadata about the content of hsdS server
getReq	DataFrame instance with metadata about hsdS server
folderPath	character string with path to user's folder/file on hsdS server

**Note**

The dsmeta slot holds a DataFrame with a column dsnames that is a list with ith element a character vector of all dsnames available for the ith group. There is no effort at present to search all groups for candidate datasets.

If the domain for the HSDS server is known, pass the domain path as a character string along with the serverURL

**Examples**

```
## Not run:
bigec2 = H5S_source(URL_h5serv()) # h5serv
bigec2
dsmeta(bigec2)[1:2,]          # two groups
dsmeta(bigec2)[1,2][[1]]     # all dataset candidates in group 1
hsdsCon = H5S_source(URL_h5serv()) # hsds server connection
hsdsCon
getReq(hsdsCon)
setPath(hsdsCon, "/home/stvjc/hdf5_mat.h5") -> hsds
fetchDatasets(hsds)         # grab the dataset id of interest
H5S_dataset2(hsds, "d-a9e4b71c-8ea2-11e8-9306-0242ac120022")

## End(Not run)
```

---

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_h5serv()) {
  HSDSArray(URL_h5serv(),
            "hsds", "/shared/bioconductor/darmgcls.h5", "/assay001")
}
```

---

HSDSArraySeed	<i>HSDSArraySeed for HSDSArray backend to DelayedArray</i>
---------------	--

---

**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	<i>Construct an object of type HSDSDataset A HSDSDataset is a representation of a dataset in a HDF5 file.</i>
-------------	---

---

**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_hsd()) {
  src <- HSDSource('http://hsdshdfiab.hdfgroup.org')
  f <- HSDSFile(src, '/shared/bioconductor/tenx_full.h5')
  d <- HSDSDataset(f, '/newassay001')
}
```

---

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 hierarchy.  
 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_hds()) {
  src <- HSDSSource('http://hdsdshdflab.hdfgroup.org')
  f10x <- HSDSFile(src, '/shared/bioconductor/tenx_full.h5')
}
```

---

HSDSFile-class	<i>An S4 class to represent an HDF5 file accessible from a server.</i>
----------------	--

---

**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

---

hdsInfo	<i>HSDS server get request accessor</i>
---------	---

---

**Description**

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

**Usage**

```
hdsInfo(object)
```

**Arguments**

object            H5S\_source instance

**Value**

a data frame with response

**Examples**

```
## Not run:
hsdsCon = H5S_source(URL_hds()) # hds server connection
hsdsInfo(hsdsCon)

## End(Not run)
```

---

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 hds.)

**Usage**

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

**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_hsd()) {
  src.hsd <- HSDSSource('http://hsdshdf1lab.hdfgroup.org')
}
```

---

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) 'hds'

---

HSDS\_Matrix      *simplify construction of DelayedMatrix from url and path in HSDS*

---

**Description**

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

**Usage**

```
HSDS_Matrix(url, path, title)
```

**Arguments**

url                    character(1) URL for HSDS object store with port  
 path                   character(1) path from root defining HDF Cloud resource  
 title                   character(1) name of dataset to use

**Value**

instance of DelayedArray

**Examples**

```
## Not run:
HSDS_Matrix(URL_hsd(), "/shared/bioconductor/darmgcls.h5")

## End(Not run)
```

---

HSDS_Matrix_OLD	<i>simplify construction of DelayedMatrix from url and path in HS</i>
-----------------	---

---

**Description**

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

**Usage**

```
HSDS_Matrix_OLD(url, path)
```

**Arguments**

url	character(1) URL for HS object store with port
path	character(1) path from root defining HDF Cloud resource

**Value**

instance of DelayedArray

**Examples**

```
## Not run:
HSDS_Matrix
## End(Not run)
```

---

internalDim	<i>acquire internal HDF5 dimension information for matrix</i>
-------------	---

---

**Description**

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

**Usage**

```
internalDim(h5d)
```

**Arguments**

h5d	instance of H5S_dataset
-----	-------------------------

**Value**

vector with dimensions of dataset



**Examples**

```
## Not run:
bigec2 = H5S_source(URL_h5serv())
tex <- bigec2[["tenx_100k_sorted"]]
internalDim(tex)

## End(Not run)
```

---

**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))
```

---

links	<i>access for link metadata for HDF5 server groups</i>
-------	--

---

**Description**

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

**Usage**

```
links(object, index, ...)
```

**Arguments**

object	H5S_source instance
index	numeric group index
...	not used

**Value**

an object of type H5S\_linkset with the linkset of the group

**Examples**

```
## Not run:
bigec2 = H5S_source(URL_h5serv())
lks <- links(bigec2, 1) # linkset for root group
urls <- targets(lks)   # URLs of datasets in linkset

## End(Not run)
```

---

listDatasets	<i>Search inner file hierarchy for datasets</i>
--------------	---

---

**Description**

The datasets in an HDF5 file are organized internally by groups. This routine traverses the internal group hierarchy, locates all datasets and prints a list of them. Note that if the file's group hierarchy 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_hsd()) {  
  src <- HSDSSource('http://hsdshdfiab.hdfgroup.org')  
  f <- HSDSFile(src, '/shared/bioconductor/tenx_full.h5')  
  listDatasets(f)  
}
```

---

listDomains	<i>List files and subdirectories of a domain</i>
-------------	--

---

**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('http://hsdshdf1ab.hdfgroup.org')
src.chan <- HSDSSource('http://h5s.channingremotedata.org:5000', 'h5serv')
listDomains(src.chan)
listDomains(src.hsds, '/home/jreadey')
```

---

rhdf5client	<i>rhdf5client: A package for accessing HDFGroup HDF5 servers from R.</i>
-------------	---

---

## 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’.

---

rhdf5client-deprecated	<i>Deprecated functions in package ‘rhdf5client’</i>
------------------------	--

---

## 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

---

setPath

*set path for hds server resource*

---

### Description

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

### Usage

```
setPath(object, folderPath, ...)
```

### Arguments

object	H5S_source instance
folderPath	character string with path to user's folder on hds server
...	not used

### Value

an updated object with folderPath set

## Examples

```
## Not run:
hsdsCon = H5S_source(URL_hds()) # hsds server connection
setPath(hsdsCon, "/home/stvjc/hdf5_mat.h5")-> hsds

## End(Not run)
```

---

targets	<i>provide the full URLs for link members</i>
---------	---

---

## Description

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

## Usage

```
targets(h5linkset, index)
```

## Arguments

h5linkset	instance of H5S_linkset
index	numeric index into link vector - ignored

## Value

a vector of dataset tags

## Examples

```
## Not run:
bigec2 = H5S_source(URL_h5serv())
lks <- links(bigec2, 1) # linkset for root group
urls <- targets(lks) # URLs of datasets in linkset

## End(Not run)
```

---

transfermode<-            *replace transfer mode*

---

**Description**

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

**Usage**

```
transfermode(object) <- value
```

**Arguments**

object	instance of H5S_linkset
value	either "JSON" (default) or "binary"

**Value**

updated object of type H5S\_dataset

---

URL\_h5serv            *manage h5serv URL*

---

**Description**

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

**Usage**

```
URL_h5serv()
```

**Value**

URL of h5serv server

**Examples**

```
URL_h5serv()
```

---

URL_hds	<i>manage hds URL</i>
---------	-----------------------

---

**Description**

manage hds URL

**Usage**

URL\_hds()

**Value**

URL of hds server

**Examples**

URL\_hds()

---

[,H5S_dataset,character,character,ANY-method	<i>extract elements from H5S_dataset</i>
--	--

---

**Description**

extract elements from H5S\_dataset

**Usage**

```
## S4 method for signature 'H5S_dataset,character,character,ANY'
x[i, j, ..., drop = FALSE]
```

**Arguments**

x	instance of H5S_dataset
i	character vector of row selections
j	character vector of column selections
...	not used
drop	logical(1) set TRUE to drop array character



---

```
[,H5S_dataset,numeric,numeric,ANY-method
      extract elements from H5S_dataset
```

---

**Description**

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

**Usage**

```
## S4 method for signature 'H5S_dataset,numeric,numeric,ANY'
x[i, j, ..., drop = FALSE]
```

**Arguments**

x	instance of H5S_dataset
i	select option for first matrix index in HDF5 server value API
j	select option for second matrix index in HDF5 server value API
...	unused
drop	logical defaults to FALSE

**Value**

matrix of data obtained

---

```
[,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

---

```
[[      Subscript operator
```

---

**Description**

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

**Usage**

```
## S4 method for signature 'H5S_source,character'
x[[i, j]]
```

**Arguments**

x	instance of H5S_source
i	character string intended to identify dataset on server
j	not used

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