

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

**Imports** httr, rjson, utils, data.table

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**License** Artistic-2.0

**LazyLoad** yes

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'Dataset.R' 'RHDF5Array.R'

**VignetteBuilder** knitr

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check_hsd	<i>a test request</i>
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**Description**

a test request

**Usage**

```
check_hsd()
```

**Value**

logical, TRUE if hsd behaving as expected

**Examples**

```
check_hsd()
```

---

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

---

dimnames	<i>Obtain names of dimensions for an object of type HSDSArraySeed</i>
----------	---

---

**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	<i>compound operation</i>
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---

**Description**

compound operation

**Usage**

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

**Arguments**

type	type
value	value

---

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

---

getData	<i>extract elements of a one or two-dimensional HSDSDataset</i>
---------	---

---

**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_hsd()) {
  s <- HSDSource(URL_hsd())
  f <- HSDFile(s, '/shared/bioconductor/patelGBMSC.h5')
  d <- HSDDataset(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
}
```

---

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 'hds' 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_hsd()) {
  HSDSArray(URL_hsd(),
            "hsds", "/shared/bioconductor/darmgcls.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	<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(URL_hsd())
  f <- HSDSFile(src, '/shared/bioconductor/patelGBMSC.h5')
  d <- HSDSDataset(f, '/assay001')
}
```

---

HSDSDataset-class	<i>An S4 class to represent a dataset in a HDF5 file.</i>
-------------------	---

---

**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	<i>Construct an object of type HSDSFile</i>
----------	---

---

**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_hsd()) {
  src <- HSDSSource(URL_hsd())
  f10x <- HSDSFile(src, '/shared/bioconductor/patelGBMSC.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

---

HSDSMatrix	<i>DelayedMatrix subclass for a two-dimensional HSDSArray</i>
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---

**Description**

DelayedMatrix subclass for a two-dimensional HSDSArray

**See Also**

Other HSDSArray: [HSDSArray](#), [as\(\)](#)

---

HSDSSource	<i>Construct an object of type HSDSSource.</i>
------------	--

---

**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_hds()) {
  src.hds <- HSDSSource(URL_hds())
}
```

---

HSDSSource-class	<i>An S4 class to represent a HDF5 server listening on a port.</i>
------------------	--

---

**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'

---

isplit	<i>This function is deprecated and will be defunct in the next release.</i>
--------	---

---

**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	<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_hds()) {  
  src <- HSDSource(URL_hds())  
  f <- HSDSFile(src, '/shared/bioconductor/patelGBMSC.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(URL_hsds())
listDomains(src.hsds, '/shared')
```

---

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

*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\_hsd
- dsmeta
- getReq
- groups
- setPath
- links
- transfermode
- dataset
- internalDim
- hsdInfo
- 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\_hsd

*manage hsd URL*


---

### Description

manage hsd URL

### Usage

URL\_hsd()

### Value

URL of hsd server

### Examples

URL\_hsd()

---

 [,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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