

# Package ‘FlowRepositoryR’

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**Type** Package

**Title** FlowRepository R Interface

**Version** 1.2.0

**Author** Josef Spidlen [aut, cre]

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**Description** This package provides an interface to search and download data and annotations from FlowRepository (flowrepository.org). It uses the FlowRepository programming interface to communicate with a FlowRepository server.

**Depends** R (>= 3.2)

**Imports** XML, RCurl, tools, utils

**Suggests** RUnit, BiocGenerics, flowCore, methods

**Collate** AllClasses.R settings.R helper-functions.R parsing-methods.R summary-methods.R accessor-methods.R methods.R exported-functions.R

**License** Artistic-2.0

**biocViews** Infrastructure, FlowCytometry

**NeedsCompilation** no

## R topics documented:

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FlowRepositoryR-package

*Programming interface to access FlowRepository.org*

---

## Description

This package includes functions to locate and review FlowRepository datasets and conveniently download related data to the local file system.

## Author(s)

Author and maintainer: Josef Spidlen <jspidlen@bccrc.ca>

## References

Josef Spidlen. FlowRepository API and Resources for Developers.  
<http://flowrepository.org/developers>

Josef Spidlen, Wayne Moore, David Parks, Michael Goldberg, Chris Bray, Pierre Bierre, Peter Gorombey, Bill Hyun, Mark Hubbard, Simon Lange, Ray Lefebvre, Robert Leif, David Novo, Leo Ostruszka, Adam Treister, James Wood, Robert F. Murphy, Mario Roederer, Damir Sudar, Robert Zigon, and Ryan R. Brinkman.

Data File Standard for Flow Cytometry, Version FCS 3.1

Cytometry A. 2010 Jan; 77(1): 97100. doi: 10.1002/cyto.a.20825

<http://tinyurl.com/fcs3-1-pdf>

---

attachmentProxy-class *'attachmentProxy': a class representing a proxy to an attachment file in FlowRepository*

---

## Description

This class represents basic metadata (i.e., information about) a single attachment file in FlowRepository.

## Details

Objects of class `attachmentProxy` are used to hold information about a `FlowRepository` attachment file. This information includes the file name, URL, size in bytes, MD5 sum, description and a path to the file on the local file system. A `NULL` value in the `localpath` slot indicates that the attachment file has not been downloaded, you can use the [download](#) method to download the file.

## Creating Objects

Objects of the `attachmentProxy` class are created automatically when you create a `flowRepData` object from `FlowRepository` by calling the [flowRep.get](#). A list of `attachmentProxy` objects will be placed in the `attachments` slot of the `flowRepData` object.

Unless you know what you are doing, creating objects using `new` or the constructor (as described below) is discouraged.

Objects can be created using

```
new("attachmentProxy",
  name      = ...., Object of class character
  url       = ...., Object of class character
  size      = ...., Object of class numeric
  md5sum    = ...., Object of class character or NULL
  description = ...., Object of class character or NULL
  localpath = ...., Object of class character or NULL
)
```

or the constructor `attachmentProxy`, with mandatory arguments `name` and `url` and optional arguments `size`, `md5sum`, `description` and `localpath`.

```
attachmentProxy(name, url, size=0, md5sum=NULL,
  description=NULL, localpath=NULL)
```

## Slots

**name:** Object of class character containing the name of the `FlowRepository` attachment file.

**url:** Object of class character containing the url of the `FlowRepository` attachment file.

**size:** Object of class numeric containing the size of the `FlowRepository` attachment file in bytes.

**md5sum:** Object of class character or `NULL` containing the MD5 sum of the `FlowRepository` attachment file.

**description:** Object of class character or `NULL` containing the description of the `FlowRepository` attachment file.

**localpath:** Object of class character or `NULL` containing the path the `FlowRepository` attachment file as saved on the local file system. This slot is used to determine whether the file has been downloaded to the local file system. A value of `NULL` indicates that the attachment file has not been downloaded. The [download](#) method can be used to download the file.

## Extends

Class [fileProxy](#), directly.

## Methods

There are separate documentation pages for some of the methods listed here which may be consulted for more details.

Print a basic summary about an attachmentProxy. See [summary](#) for details. *Usage:* `summary(attachmentProxy)`

**summary.download** Download the referenced attachment file to the local file system, fill out the localpath slot and return an updated copy of the attachmentProxy object. See [download](#) for details. *Usage:* `download(attachmentProxy, dirpath=NULL, filepath=NULL, curlHandle=getCurlHandle(cookiefile=""), show.progress=TRUE, ...)`

**is.downloaded** Return TRUE if the localpath slot is not NULL, which indicates that the file has been downloaded to the local file system. Return FALSE if the localpath is NULL. See [is.downloaded](#) for details. *Usage:* `is.downloaded(attachmentProxy)`

## Author(s)

Josef Spidlen

## See Also

[fileProxy](#), [fcsProxy](#), [flowRepData](#), [download](#)

## Examples

```
myDataset <- flowRep.get("FR-FCM-ZZ3X")
summary(attachments(myDataset)[[1]])
str(attachments(myDataset)[[1]])
```

---

download

*Download dataset files*

---

## Description

This method can download whole datasets (all FCS files and attachments of a [flowRepData](#) object) or individual files based on file proxies ([fileProxy](#) objects).

## Usage

```
download(object, ...)
```

## Arguments

`object` Object of class [fileProxy](#) or [flowRepData](#).  
`...` Additional options, see the details section.

## Details

The full dataset or the file represented by the file proxy will be downloaded to the local file system. If you are downloading the whole dataset (passing a [flowRepData](#) object), then you can specify the following additional options:

`dirpath=NULL` The path to the directory where to download the files. By default, the files will be downloaded to a folder named based on the dataset identifier (FR-FCM-xxxx) that will be created in your working directory.

`use.credentials=TRUE` Whether to use stored credentials to login before downloading the dataset. Credentials will only be used if `use.credentials=TRUE` and they are set (see [setFlowRepositoryCredentials](#)). If your credentials are set, but you are downloading a public dataset that does not need credentials, then you can use `use.credentials=FALSE` to avoid logging in.

`show.progress=TRUE` Whether to show progress as individual files are being downloaded.

If you are downloading a single file by (passing a [fileProxy](#) object), then you can specify the following additional options:

`dirpath=NULL` The path to the directory where to download the file. By default, the file will be downloaded to your working directory. A `filepath` argument as specified below takes precedence over the `dirpath` argument.

`filepath=NULL` The path where to download the file. If provided, this argument takes precedence over `dirpath`.

`curlHandle=getCurlHandle(cookiefile="")` Used to pass cookies to keep track of sessions. This is intended for internal use, not to be used by regular users.

`show.progress=TRUE` Whether to show progress as the file is being downloaded.

## Value

A [fileProxy](#) object if object is a [fileProxy](#) object or a [flowRepData](#) object if object is a [flowRepData](#) object. This is an updated file proxy or a dataset that includes local path to the downloaded files.

## Author(s)

Josef Spidlen

## See Also

[flowRep.get](#)

## Examples

```
## We will get a small dataset
myDataset <- flowRep.get("FR-FCM-ZZJ7")
summary(myDataset)

## And download a single attachment file
## mainly just to demonstrate that one can do one file at a time.
```

```

att1 <- download(attachments(myDataset)[[1]])
localpath(att1)

## We can also find out about individual FCS file proxies
summary(fcs.files(myDataset)[[1]])

## A single FCS file proxy can be downloaded
fcs1 <- download(fcs.files(myDataset)[[1]])
summary(fcs1)

## The file is downloaded to your home directory
localpath(fcs1)

## The code above is just to demonstrate that it is
## possible to get individual files. However, typically,
## we will want to download the whole dataset.
myDataset <- download(myDataset)
summary(myDataset)

## This downloaded all the files to your home directory
## This is where you find your data
unlist(lapply(fcs.files(myDataset), function(x) paste(localpath(x))))

## And this is where you find the attachments of that dataset
unlist(lapply(attachments(myDataset), function(x) paste(localpath(x))))

```

---

fcsProxy-class	<i>'fcsProxy': a class representing a proxy to an FCS file in FlowRepository</i>
----------------	--

---

## Description

This class represents basic metadata (i.e., information about) a single FCS file in FlowRepository.

## Details

Objects of class `fcsProxy` are used to hold information about a FlowRepository FCS file. This information includes the file name, URL, size in bytes, MD5 sum, FCS version and a path to the file on the local file system. A NULL value in the `localpath` slot indicates that the FCS file has not been downloaded, you can use the [download](#) method to download the file.

## Creating Objects

Objects of the `fcsProxy` class are created automatically when you create a `flowRepData` object from FlowRepository by calling the [flowRep.get](#). A list of `fcsProxy` objects will be placed in the `fcs.files` slot of the `flowRepData` object.

Unless you know what you are doing, creating objects using `new` or the constructor (as described below) is discouraged.

Objects can be created using

```
new("fcsProxy",
  name      = ...., Object of class character
  url       = ...., Object of class character
  size      = ...., Object of class numeric
  md5sum    = ...., Object of class character or NULL
  fcs.version = ...., Object of class character or NULL
  localpath = ...., Object of class character or NULL
)
```

or the constructor `fcsProxy`, with mandatory arguments `name` and `url` and optional arguments `size`, `md5sum`, `fcs.version` and `localpath`.

```
fcsProxy(name, url, size=0, md5sum=NULL,
  fcs.version=NULL, localpath=NULL)
```

### Slots

**name:** Object of class character containing the name of the FlowRepository FCS file.

**url:** Object of class character containing the url of the FlowRepository FCS file.

**size:** Object of class numeric containing the size of the FlowRepository FCS file in bytes.

**md5sum:** Object of class character or NULL containing the MD5 sum of the FlowRepository FCS file.

**fcs.version:** Object of class character or NULL containing the FCS version identifier of the FlowRepository FCS file. This version identifier corresponds to the first 6 bytes of the FCS file and typically contains one of the following strings: `FCS1.0`, `FCS2.0`, `FCS3.0`, or `FCS3.1`.

**localpath:** Object of class character or NULL containing the path the FlowRepository FCS file as saved on the local file system. This slot is used to determine whether the file has been downloaded to the local file system. A value of NULL indicates that the FCS file has not been downloaded. The [download](#) method can be used to download the file.

### Extends

Class [fileProxy](#), directly.

### Methods

There are separate documentation pages for some of the methods listed here which may be consulted for more details.

Print a basic summary about an `fcsProxy`. See [summary](#) for details. *Usage:* `summary(fcsProxy)`

**summarydownload** Download the referenced FCS file to the local file system, fill out the `localpath` slot and return an updated copy of the `fcsProxy` object. See [download](#) for details. *Usage:* `download(fcsProxy, dirpath=NULL, filepath=NULL, curlHandle=getCurlHandle(cookiefile=""), show.progress=TRUE, ...)`

**is.downloaded** Return TRUE if the localpath slot is not NULL, which indicates that the file has been downloaded to the local file system. Return FALSE if the localpath is NULL. See [is.downloaded](#) for details. *Usage:* `is.downloaded(fcsProxy)`

### Author(s)

Josef Spidlen

### References

Josef Spidlen, Wayne Moore, David Parks, Michael Goldberg, Chris Bray, Pierre Bierre, Peter Gorombey, Bill Hyun, Mark Hubbard, Simon Lange, Ray Lefebvre, Robert Leif, David Novo, Leo Ostruszka, Adam Treister, James Wood, Robert F. Murphy, Mario Roederer, Damir Sudar, Robert Zigon, and Ryan R. Brinkman.

Data File Standard for Flow Cytometry, Version FCS 3.1

Cytometry A. 2010 Jan; 77(1): 97100. doi: 10.1002/cyto.a.20825

<http://tinyurl.com/fcs3-1-pdf>

### See Also

[fileProxy](#), [attachmentProxy](#), [flowRepData](#), [download](#)

### Examples

```
myDataset <- flowRep.get("FR-FCM-ZZZG")
summary(fcs.files(myDataset)[[1]])
str(fcs.files(myDataset)[[1]])
```

---

fileProxy-class

*'fileProxy': a class representing a proxy to a file in FlowRepository*

---

### Description

This class represents basic metadata (i.e., information about) a single file in FlowRepository.

### Details

Objects of class `fileProxy` are used to hold information about a FlowRepository file. This is a common parent class for `fcsProxy` and `attachmentProxy` classes, which hold information about an FCS file and about an attachment, respectively. Direct instances of the `fileProxy` are not expected.

### Creating Objects

The `fileProxy` class is used as a common parent for `fcsProxy` and `attachmentProxy` classes. Objects of the `fileProxy` class shall not be created directly, unless you know exactly what you are doing.

There is no constructor defined, but objects can be created using `new("fileProxy",`



```

name      = ...., Object of class character
url       = ...., Object of class character
size      = ...., Object of class numeric
md5sum    = ...., Object of class character or NULL
localpath = ...., Object of class character or NULL
)

```

### Slots

**name:** Object of class character containing the name of the FlowRepository file.

**url:** Object of class character containing the url of the FlowRepository file.

**size:** Object of class numeric containing the size of the FlowRepository file in bytes.

**md5sum:** Object of class character or NULL containing the MD5 sum of the FlowRepository file.

**localpath:** Object of class character or NULL containing the path the FlowRepository file as saved on the local file system. This slot is used to determine whether the file has been downloaded to the local file system. A value of NULL indicates that the file has not been downloaded.

### Methods

There are separate documentation pages for some of the methods listed here which may be consulted for more details.

Print a basic summary about a fileProxy. See [summary](#) for details. *Usage:* `summary(fileProxy)`

**summary.download** Download the referenced file to the local file system, fill out the localpath slot and return an updated copy of the fileProxy object. See [download](#) for details. *Usage:*  
`download(fileProxy, dirpath=NULL, filepath=NULL,  
curlHandle=getCurlHandle(cookiefile=""), )  
show.progress=TRUE, ...)`

**is.downloaded** Return TRUE if the localpath slot is not NULL, which indicates that the file has been downloaded to the local file system. Return FALSE if the localpath is NULL. See [is.downloaded](#) for details. *Usage:* `is.downloaded(fileProxy)`

**localpath** Return and object of class character or NULL containing the path the FlowRepository file as saved on the local file system. This slot is used to determine whether the file has been downloaded to the local file system. A value of NULL indicates that the file has not been downloaded.

### Author(s)

Josef Spidlen

### See Also

[fcsProxy](#), [attachmentProxy](#)

## Examples

```
## Obtain dataset information from FlowRepository
myDataset <- flowRep.get("FR-FCM-ZZZG")
is(fcs.files(myDataset)[[1]], "fileProxy")
## It should be as fcsProxy is a fileProxy
is(attachments(myDataset)[[1]], "fileProxy")
## It should be as attachmentProxy is a fileProxy
```

---

flowRep.get

*Retrieve information about a specified FlowRepository dataset.*

---

## Description

This function connects to FlowRepository ([flowrepository.org](http://flowrepository.org)) via an XML-based API and retrieves metadata about a specified dataset in the form of a [flowRepData](#) object.

## Usage

```
flowRep.get(id, use.credentials=TRUE)
```

## Arguments

- id** An identifier of a FlowRepository dataset. List of available datasets can be obtained by calling the [flowRep.ls](#) function.
- use.credentials** Whether to use your credentials (email and password) to access FlowRepository. Your credentials can only be used if previously set by calling the [setFlowRepositoryCredentials](#), function. Otherwise, this parameter will be ignored. Using credentials will allow you to access private datasets that are either yours or that have been shared with you. Without credentials, you will have access to public datasets only. If you are accessing a public dataset and you have stored your credentials, then setting `use.credentials=FALSE` will skip authentication (login/logout) and therefore perform a little bit faster.

## Details

An HTTP GET request retrieves an XML from FlowRepository, and this XML is parsed to extract metadata about the specified experiment (i.e., dataset).

## Value

A [flowRepData](#) object as long as referenced dataset is found in FlowRepository and the user has access to it. An error is thrown otherwise.

## Author(s)

Josef Spidlen

## References

Spidlen Josef. FlowRepository Resources for Developers.  
<http://flowrepository.org/developers>

## See Also

[flowRep.ls](#), [setFlowRepositoryCredentials](#), [download](#)

## Examples

```
myDataset <- flowRep.get("FR-FCM-ZZ46")
```

---

flowRep.ls

*List identifiers of datasets available in FlowRepository*

---

## Description

This function connects to FlowRepository ([flowrepository.org](http://flowrepository.org)) via an XML-based API and retrieves a vector of identifiers of available datasets.

## Usage

```
flowRep.ls(include.private=FALSE)
```

## Arguments

`include.private`

Whether to include private experiments in the list. This only works if credentials to access FlowRepository have been provided. By default, only public experiments will be listed.

## Details

An HTTP GET request retrieves an XML from FlowRepository, and this XML is parsed to extract the list of identifiers of public experiments.

## Value

A vector of objects of class `character` containing strings with FlowRepository dataset identifiers available.

## Author(s)

Josef Spidlen

## References

Spidlen Josef. FlowRepository Resources for Developers.  
<http://flowrepository.org/developers>

**See Also**

[flowRep.get](#), [setFlowRepositoryCredentials](#)

**Examples**

```
flowRep.ls()
```

---

flowRep.search	<i>Search FlowRepository for datasets matching the query and retrieve a vector of identifiers of matching datasets.</i>
----------------	---

---

**Description**

This function connects to FlowRepository ([flowrepository.org](http://flowrepository.org)) via an XML-based API and searches for datasets matching the query term. The search covers experiment names, repository identifiers, keywords, researcher first and last names, reagents and reagent manufactures, instruments and instrument manufactures, sample annotations and manuscript identifiers. A vector of identifiers of matching datasets is retrieved. NULL is returned if no matching datasets are found.

**Usage**

```
flowRep.search(query.string)
```

**Arguments**

query.string    The query term used to search FlowRepository datasets for.

**Details**

An HTTP GET request is sent to FlowRepository to perform the search, this retrieves an XML from FlowRepository, and this XML is parsed to extract the list of identifiers of matching experiments.

**Value**

A vector of objects of class `character` containing strings with FlowRepository dataset identifiers available. NULL if no matching datasets were found.

**Author(s)**

Josef Spidlen

**References**

Spidlen Josef. FlowRepository Resources for Developers.  
<http://flowrepository.org/developers>

**See Also**

[flowRep.ls](#), [flowRep.get](#)

**Examples**

```
flowRep.search("K562 BCR")
```

---

flowRepData-class	<i>'flowRepData': a class for storing metadata about a FlowRepository dataset</i>
-------------------	---

---

**Description**

This class represents the metadata (i.e., information about) a dataset stored in FlowRepository.

**Details**

Objects of class `flowRepData` can be used to hold information about a FlowRepository dataset. This includes the FlowRepository dataset identifier, name, primary researcher, investigator and uploader, information about the purpose, conclusions, comments and funding, experiment dates, QC measures, MIFlowCyt score, keywords, organizations, publications, list of FCS file names and attachment names, and whether or not it is a public dataset. Using this objects, FCS files and attachments can be easily downloaded to your local file system. See the [download](#) method.

**Creating Objects**

To create a `flowRepData` directly from an FlowRepository, use function [flowRep.get](#). This is the recommended and safest way of object creation, since `flowRep.get` will perform basic quality checks and populate all the slots accordingly. Unless you know exactly what you are doing, creating objects using `new` or the constructor (as described below) is discouraged.

Objects can be created using

```
new("flowRepData",
  id           = ..., Object of class character
  public.url   = ..., Object of class character or NULL
  name        = ..., Object of class character or NULL
  public      = ..., Object of class logical or NULL
  primary.researcher = ..., Object of class character or NULL
  primary.investigator = ..., Object of class character or NULL
  uploader    = ..., Object of class character or NULL
  experiment.dates = ..., Object of class character or NULL
  purpose     = ..., Object of class character or NULL
  conclusion  = ..., Object of class character or NULL
  comments    = ..., Object of class character or NULL
  funding     = ..., Object of class character or NULL
  qc.measures = ..., Object of class character or NULL
  miflowcyt.score = ..., Object of class numeric or NULL
  keywords    = ..., Object of class list
```

```

publications      = ..., Object of class list
organizations     = ..., Object of class list
fcs.files         = ..., Object of class list
attachments       = ..., Object of class list
)

```

or the constructor `flowRepData`, with mandatory argument `id` and optional arguments `public.url`, `name`, `public`, `primary.researcher`, `primary.investigator`, `uploader`, `experiment.dates`, `purpose`, `conclusion`, `comments`, `funding`, `qc.measures`, `miflowcyt.score`, `keywords`, `publications`, `organizations`, `fcs.files`, and `attachments`.

```

flowRepData(id, public.url=NULL, name=NULL, public=NULL,
primary.researcher=NULL, primary.investigator=NULL,
uploader=NULL, experiment.dates=NULL,
purpose=NULL, conclusion=NULL, comments=NULL,
funding=NULL, qc.measures=NULL, miflowcyt.score=NULL,
keywords=list(), publications=list(), organizations=list(),
fcs.files=list(), attachments=list())

```

## Slots

- id:** Object of class character containing the FlowRepository identified of the dataset. These identifiers are typically in the form of FR-FCM-xxxx where xxxx represents 4 alphanumeric characters.
- public.url:** Object of class character or NULL containing the public URL of this dataset. This will commonly be in the form of `https://flowrepository.org/id/identifier`, where identifier is the FlowRepository identified of the dataset.
- name:** Object of class character or NULL containing the name of this dataset.
- public:** Object of class logical or NULL containing the information whether this dataset is public.
- primary.researcher:** Object of class character or NULL containing the name of the primary researcher associated with this dataset.
- primary.investigator:** Object of class character or NULL containing the name of the primary investigator associated with this dataset.
- uploader:** Object of class character or NULL containing the name of the uploader of this dataset.
- experiment.dates:** Object of class character or NULL containing the dates associated with this dataset. Typically, there will be two dates associated with the dataset, the first one for the start of the experiment, the second one for the end of the experiment. A single date indicates the start of an experiment that may still be ongoing. The dates shall be encoded as "YYYY-MM-DD".
- purpose:** Object of class character or NULL stating the purpose of this dataset (experiment).
- conclusion:** Object of class character or NULL stating the conclusion associated with this dataset (typically conclusions reached by analyzing the data).
- comments:** Object of class character or NULL stating additional comments associated with this dataset.

- funding:** Object of class character or NULL stating the funding used to collect the data in this dataset.
- qc.measures:** Object of class character or NULL stating the quality control measures taken in order to ensure the quality of data in this dataset.
- miflowcyt.score:** Object of class numeric or NULL stating the MIFlowCyt compliance score of this experiment. MIFlowCyt is the Minimum Information about a Flow Cytometry Experiment - an ISAC Recommendation listing the minimum information that shall be provided as annotation of flow cytometry datasets. The MIFlowCyt compliance score is a value between 0 and 100 percent indicating the level of compliance with MIFlowCyt. Details about how FlowRepository calculates this score are available here: [http://flowrepository.org/quick\\_start\\_guide#MIFlowCytScoreR](http://flowrepository.org/quick_start_guide#MIFlowCytScoreR)
- keywords:** Object of class list (of objects of class character) enumerating keywords associated with this dataset.
- publications:** Object of class list (of objects of class character) enumerating publications associated with this dataset. Publications are typically listed as "PMID:12345678" or "PMCID:PMC1234567".
- organizations:** Object of class list of objects of class [flowRepOrganization](#) enumerating organizations associated with this dataset.
- fcs.files:** Object of class list of objects of class [fcsProxy](#) enumerating FCS files associated with this dataset.
- attachments:** Object of class list of objects of class [attachmentProxy](#) enumerating attachments associated with this dataset.

## Methods

There are separate documentation pages for some of the methods listed here which may be consulted for more details.

Print a basic summary about a `flowRepData`. See [summary](#) for details. *Usage:* `summary(flowRepData)`

**summary.download** Download all the referenced FCS files and attachments, fill out their `localpath` slots and return an updated copy of the `flowRepData` object. See [download](#) for details. *Usage:* `download(flowRepData)`

**is.downloaded** Return TRUE if all FCS files and attachments referenced from this `flowRepData` object are downloaded to your local file system. This is determined by the `localpath` slot of the [fileProxy](#) objects in the `fcs.files` list and `attachments` list. No other checks are performed. See [is.downloaded](#) for details. *Usage:* `is.downloaded(flowRepData)`

**id** Return the character vector representing the identifier to the FlowRepository dataset. See [id](#) for details. *Usage:* `id(flowRepData)`

**fcs.files** Return an object of class list of objects of class [fcsProxy](#) enumerating FCS files associated with this dataset.

**attachments** Return an object of class list of objects of class [attachmentProxy](#) enumerating attachments associated with this dataset.

**organizations** Return an object of class list of objects of class [flowRepOrganization](#) enumerating organizations associated with this dataset.

## Author(s)

Josef Spidlen

**See Also**

[flowRep.get](#), [download](#)

**Examples**

```
## Obtain dataset information from FlowRepository
myDataset <- flowRep.get("FR-FCM-ZZZG")
id(myDataset)
is.downloaded(myDataset)
summary(myDataset)
```

---

flowRepOrganization-class

*'flowRepOrganization': a class for storing details about an organization associated with a FlowRepository dataset*

---

**Description**

This class represents the name and address of an organization associated with a dataset stored in FlowRepository.

**Details**

Objects of class `flowRepOrganization` can be used to hold information about an organization that is associated with a FlowRepository dataset. A list of these objects will typically be placed in the `organizations` slot of a `flowRepData` object when this is obtained using the `flowRep.get` function (assuming there are any organizations associated with that dataset).

**Creating Objects**

Objects can be created using

```
new("flowRepOrganization",
  name = ..., Object of class character
  street = ..., Object of class character or NULL
  city = ..., Object of class character or NULL
  zip = ..., Object of class character or NULL
  state = ..., Object of class character or NULL
  country = ..., Object of class character or NULL
)
```

or the constructor `flowRepOrganization`, with mandatory argument `name` and optional arguments `street`, `city`, `zip`, `state` and `country`.

```
flowRepOrganization(name, street=NULL, city=NULL,
  zip=NULL, state=NULL, country=NULL)
```



**Slots**

- name:** Object of class character containing the name of the organization.
- street:** Object of class character or NULL containing the street of the address of the organization.
- city:** Object of class character or NULL containing the city of the address of the organization.
- zip:** Object of class character or NULL containing the zip (or postal code) of the address of the organization.
- state:** Object of class character or NULL containing the state (or province) of the address of the organization.
- country:** Object of class character or NULL containing the country of the address of the organization.

**Methods**

There are separate documentation pages for some of the methods listed here which may be consulted for more details.

Print the name and address of the organization. See [summary](#) for details. *Usage:* `summary(flowRepOrganization)`

**Author(s)**

**summary** Josef Spidlen

**See Also**

[flowRep.get](#)

**Examples**

```
myDataset <- flowRep.get("FR-FCM-ZZ47")
summary(organizations(myDataset)[[1]])
```

---

forgetFlowRepositoryCredentials

*Forgets credentials (email and password) to login to FlowRepository.*

---

**Description**

This function removes (forgets) your credentials (email and password) to access FlowRepository if they were set using the [setFlowRepositoryCredentials](#) function. If you set your credentials based on an external credentials file, this file will not be affected, only credentials stored internally in your R session will be removed.

**Usage**

```
forgetFlowRepositoryCredentials()
```

**Details**

The credentials are stored locally in an environment within the namespace in the FlowRepositoryR library. Your credentials will be forgotten when you quit your R session.

**Value**

The return value is not expected to be useful. It is just the the value of evaluating the credentials assignment expression, which is typically an object of class character containing a copy of the password that was just set.

**Author(s)**

Josef Spidlen

**References**

Spidlen Josef. FlowRepository Resources for Developers.  
<http://flowrepository.org/developers>

**See Also**

[setFlowRepositoryCredentials](#)

**Examples**

```
## Let's set credentials
setFlowRepositoryCredentials(
  email="boo@gmail.com", password="foo123456")
## Now do some work with FlowRepository...
## ...
## And now let's forget those credentials
forgetFlowRepositoryCredentials()
```

---

getFlowRepositoryURL *Get FlowRepository URL address.*

---

**Description**

This function returns the FlowRepository URL. Unless the URL has been changed by the [setFlowRepositoryURL](#), this function will return "https://flowrepository.org/".

**Usage**

```
getFlowRepositoryURL()
```

**Details**

FlowRepository URL is being stored with other settings in a global environment in the library namespace. The `getFlowRepositoryURL` and `setFlowRepositoryURL` are being used to get and set the URL, respectively.

**Value**

An object of class character containing the FlowRepository URL.

**Author(s)**

Josef Spidlen

**References**

Spidlen Josef. FlowRepository Resources for Developers.  
<http://flowrepository.org/developers>

**See Also**

[setFlowRepositoryURL](#)

**Examples**

```
getFlowRepositoryURL()
```

---

id	<i>Retrieve the identifier of flowRepData objects</i>
----	---

---

**Description**

This method retrieves the identifier of a `flowRepData` object. These identifiers are typically in the form of FR-FCM-xxxx where xxxx represents 4 alphanumeric characters.

**Usage**

```
id(object)
```

**Arguments**

object            Object of class `flowRepData`.

**Details**

FlowRepository dataset (experiment) identifiers 12 character strings in the form of FR-FCM-xxxx where xxxx represents 4 alphanumeric characters. Bases on this identifier, a corresponding dataset can be obtained from <http://flowrepository.org/id/FR-FCM-xxxx>.

**Value**

Character vector representing the identifier to the FlowRepository dataset.

**Methods**

**object="flowRepData"** Return identifier of a `flowRepData` object.

**Author(s)**

Josef Spidlen

**Examples**

```
## Get dataset from FlowRepository
mySmallDataset <- flowRep.get("FR-FCM-ZZ3X")
id(mySmallDataset)
```

---

is.downloaded

*Check if a dataset or a file proxy is downloaded*

---

**Description**

Return TRUE if the argument is (fully) downloaded to the local file system, FALSE otherwise.

**Usage**

```
is.downloaded(object, ...)
```

**Arguments**

**object** Object of class `fileProxy` or `flowRepData`.  
**...** Just a placeholder for now, no additional attributes are used at this point.

**Details**

This method checks whether the argument (either a `flowRepData` object or a `fileProxy` object) is downloaded. If a dataset (`flowRepData` object) is passed as an argument, then all the files in that dataset need to be downloaded in order for this method to return TRUE. The method is based on the `localpath` attribute of the `fileProxy` of the argument, or of all the file proxies associated with a dataset (if `flowRepData` object is used).

**Value**

TRUE if object is (fully) downloaded to a local file system, FALSE otherwise. 'Fully' is only applicable to `flowRepData` objects and it means that all FCS data files and all attachments of the `flowRepData` object are downloaded.

**Author(s)**

Josef Spidlen

**See Also**[download](#)**Examples**

```
myDataset <- flowRep.get("FR-FCM-ZZ3X")
is.downloaded(myDataset)
is.downloaded(fcs.files(myDataset)[[1]])
```

---

`setFlowRepositoryCredentials`*Set credentials (email and password) to login to FlowRepository.*

---

**Description**

This function sets your credentials (email and password) to access FlowRepository. These credentials will then be used to access private datasets that you have access to (i.e., that are either yours or that have been shared with you). The email must correspond to the email that you are using to login to FlowRepository, and the password must correspond to the password that is set for FlowRepository API access in your FlowRepository profile. Click on your name when logged-in to FlowRepository in your web browser in order to setup your API password.

This function can set your credentials based on credentials stored in a file (2 lines, email address in the first line, password in the second line), or you can provide email and/or password as arguments of this function, or the function will ask for credentials if called without arguments in an interactive mode.

**Usage**

```
setFlowRepositoryCredentials(filename=NULL, email=NULL, password=NULL)
```

**Arguments**

filename	The file with credentials. If specified, this argument will take precedence over the email and password arguments (so do not use it together with the email and password arguments). The file is expected to be a text file with 2 lines. The first line is expected to contain the email, the second line the password.
email	An email address as registered with FlowRepository. Use only if you are not providing a filename. If neither filename, nor email are provided, then the function will ask for email as long as it is executed in an interactive mode.
password	A password as registered for API access with FlowRepository. Use only if you are not providing a filename. If neither filename, nor password are provided, then the function will ask for a password as long as it is executed in an interactive mode.

### Details

The credentials are stored locally in an environment within the namespace in the FlowRepositoryR library. Your credentials will be forgotten when you quit your R session, or when you call the [forgetFlowRepositoryCredentials](#) function.

### Value

The return value is not expected to be useful. An empty string (an object of class character with 0 characters).

### Author(s)

Josef Spidlen

### References

Spidlen Josef. FlowRepository Resources for Developers.  
<http://flowrepository.org/developers>

### See Also

[forgetFlowRepositoryCredentials](#)

### Examples

```
## Let's set credentials
setFlowRepositoryCredentials(email="boo@gmail.com", password="foo123456")
## Now do some work with FlowRepository...
## ...
## And now let's forget those credentials
forgetFlowRepositoryCredentials()
```

---

setFlowRepositoryURL *Set FlowRepository URL address.*

---

### Description

This function sets the FlowRepository URL. Normally, the URL should be <https://flowrepository.org/>. This function can be used if we want this library to communicate with a different instance of FlowRepository (e.g., some third party FlowRepository installation, or a testing installation used by developers).

### Usage

```
setFlowRepositoryURL(url)
```

**Arguments**

url                      URL of the FlowRepository instance that the library should be communicating with.

**Details**

FlowRepository URL is being stored with other settings in a global environment in the library namespace. The [getFlowRepositoryURL](#) and `setFlowRepositoryURL` are being used to get and set the URL, respectively.

**Value**

The return value is not expected to be useful. It is just the the value of evaluating the URL assignment expression, which is typically an object of class character containing a copy of the URL that was set.

**Author(s)**

Josef Spidlen

**References**

Spidlen Josef. FlowRepository Resources for Developers.  
<http://flowrepository.org/developers>

**See Also**

[getFlowRepositoryURL](#)

**Examples**

```
## Save current URL
tmpURL <- getFlowRepositoryURL()

## Temporarily set the URL to localhost
setFlowRepositoryURL("http://localhost")

## Check that it is set
getFlowRepositoryURL()

## You would need to run your own local
## FlowRepository instance on that URL for this to make sense

## Communicate with your local FlowRepository instance

## Now set it back to the original URL
setFlowRepositoryURL(tmpURL)
```

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