Package 'FlowRepositoryR'

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Type Package

Title FlowRepository R Interface

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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, jsonlite

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

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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.

only.files=NULL If not NULL then download only files with names matching a regular expression specified as a single string of characters in this argument. For example, the regular expression "pA.*fcs" will download only files whose name starts with "pA" and ends with "fcs"; the ".*" part of the regular expression means any character (.) repeated 0 or more times (*). This particular example can be used to download FCS files from IMPC panel A as their names are created as pA_specimenId_incrementvalue.fcs. Files will be skipped if the regular expression does not match.

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.

only.files=NULL If not NULL then download the file only if its name is matching a regular expression specified as a single string of characters in this argument. For example, the regular expression "pA.*fcs" will download only files whose name starts with "pA" and ends with "fcs"; the ".*" part of the regular expression means any character (.) repeated 0 or more times (*). This particular example can be used to download FCS files from IMPC panel A as their names are created as pA_specimenId_incrementvalue.fcs. The file will be skipped if the regular expression does not match.

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 individial 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	*'fcsProxy': a class representing a proxy to an FCS file in FlowRepository*

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)

summary download 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) 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,impc.details=FALSE)
```

Arguments

id   An identifier of a FlowRepository dataset. List of available datasets can be ob-
                  tained 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.

impc.details   Whether to include details about IMPC experiments related to that FlowReposi-
                  tory experiment. If set to TRUE and there are related IMPC experiment then de-
                  tails will be placed in the `impc.experiments` slot of the returned `flowRepData`
                  object. Otherwise, the `impc.experiments` slot will be an empty list.

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) via an XML-based API and retrieves
a vector of identifiers of available datasets.

Usage

```
flowRep.ls(
    include.private = FALSE,
    impc.only = FALSE,
    impc.unanalyzed.only = FALSE,
    impc.centre = NULL,
    impc.date.from = NULL, impc.date.to = NULL,
    impc.specimen.geneKO.mgiId=NULL,
    impc.specimen.geneKO.geneSymbol=NULL,
    impc.specimen.baseline=NULL,
    impc.specimen.minCount=NULL
)
```

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.

impc.only   Whether to return only datasets that are related to IMPC experiments and IMPC
specimen.

impc.unanalyzed.only

Whether to return only datasets that are related to an IMPC experiment and that
do not have any automated analysis results associated with.

impc.centre   Whether to return only datasets that are related to an IMPC experiment performed by a specified IMPC centre. If this is not NULL then it shall be an ILAR
code of a known IMPC centre; see also [listKnownIlarCodes](#). The impc.only
will be set to TRUE automatically if impc.centre is provided.

impc.date.from   Whether to return only datasets that are related to an IMPC experiment performed on or after the specified date. If this is not NULL then it shall be
a value of the Date class, e.g., as.Date("2015-11-24","%Y-%m-%d"). The
impc.date.to will be set to TRUE automatically if impc.centre is provided.

impc.date.to   Whether to return only datasets that are related to an IMPC experiment performed on or before the specified date. If this is not NULL then it shall be
a value of the Date class, e.g., as.Date("2015-11-24","%Y-%m-%d"). The
impc.date.to will be set to TRUE automatically if impc.centre is provided.

`impc.specimen.geneKO.mgiId`

> Whether to return only datasets related to an IMPC experiment that involves a specimen with a specified gene knockout (KO). In this argument, the KO gene is referenced by its MGI gene id. The impc.date.to will be set to TRUE automatically if impc.centre is provided.

`impc.specimen.geneKO.geneSymbol`

> Whether to return only datasets related to an IMPC experiment that involves a specimen with a specified gene knockout (KO). In this argument, the KO gene is referenced by its gene symbol. The impc.date.to will be set to TRUE automatically if impc.centre is provided.

`impc.specimen.baseline`

> Whether to return only datasets related to an IMPC experiment that involves a specimen with a specified boolean baseline attribute, the value of which shall match the value of this argument. That means, if impc.specimen.baseline is set to TRUE then only IMPC specimen marked as baseline will be considered. If impc.specimen.baseline is set to FALSE then only IMPC specimen that are not marked as baseline will be considered. If impc.specimen.baseline is left as NULL then both baseline and not baseline specimen will be considered. The impc.date.to will be set to TRUE automatically if impc.centre is provided.

`impc.specimen.minCount`

> Whether to return only datasets related to IMPC experiments that together involve at least the specified minimum number of specimen. The impc.date.to will be set to TRUE automatically if impc.centre is provided.

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 listKnownIlarCodes ilarCodeDescription]()

Examples

```
flowRep.ls()
```

| flowRep.search | *Search FlowRepository for datasets matching the query and retrieve a vector of identifiers of matching datasets.* |

Description

This function connects to FlowRepository (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")
```

```
flowRep.submitGeneStatus
```
                              *Submit information about an IMPC gene analysis results to
                              FlowRepository.*

Description

This function connects to FlowRepository via a programming interface and submits results of the
analysis of a specified IMPC gene. These results shall contain information about whether the gene
has been found phenodeviant. In addition, a comment may be specified, and information about
whether the analysis of this gene is completed.

Usage

```
        flowRep.submitGeneStatus(mgiGeneId, geneSymbol, isPhenodeviant,
            comment=NULL, isProcessed=TRUE)
```

Arguments

mgiGeneId	MGI gene ID of the gene that the results are for.
geneSymbol	Gene symbol of the gene that the results are for. This shall be consistent with the MGI gene ID.
isPhenodeviant	An object of type logicle (i.e, TRUE or FALSE) indicating whether the gene has been found to couse the specimens to be phenodeviant.
comment	An optional comment about the analysis of this gene.
isProcessed	An object of type logicle (i.e, TRUE or FALSE) indicating whether the gene analysis has been completed for this gene.

Details

An HTTP POST request sends the results to FlowRepository. You need to have your credentials
set (see `setFlowRepositoryCredentials`) and you as the user need to have permissions to subnit
IMPC data analysis results. In addition, the gene needs to be found in FlowRepository, i.e., a
specimen with this gene needs to be known to FlowRepository; both the MGI gene ID and the gene
symbol need to match.

Value

A list of 2 objects named `response` and `status`. The response contains a text of the response from
the server, such as "Results submitted." if the results have been accepted. The status will contain
the HTTP status code of the response, such as "200 OK" if everything was successful. An example
if an unacceptable response is "Bad results (unknown gene)" if you try to specify a gene that is not
known to FlowRepository. The "400 Bad Request" status is to be expected in this case.

Author(s)

Josef Spidlen

References

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

See Also

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

Examples

```
## This will not submit results as the public FlowRepository is not
## accepting those at this point.
tryCatch(
    {
        mgiGeneId <- "geneX1"
        geneSymbol <- "gXr1"
        comment <- "This will not submit anything due to no credentials."
        flowRep.submitGeneStatus(
            mgiGeneId = mgiGeneId,
            geneSymbol = geneSymbol,
            isPhenodeviant = TRUE,
            comment = comment,
            isProcessed = TRUE)
    },
    interrupt = function(ex) { NULL; },
    error = function(ex) { NULL; }
)
```

---

flowRep.submitImpcResults

Submit IMPC data analysis results to FlowRepository.

Description

This function connects to FlowRepository via a programming interface and submits results of the
analysis of a specified IMPC experiment. These results shall contain counts for IMPC defined cell
populations.

Usage

```
flowRep.submitImpcResults(gatedByIlar, impcExpId, results, final=TRUE)
```

Arguments

gatedByIlar	The ILAR code of the laboratory that performed the data analysis. See http://dels.nas.edu/global for more info about ILAR codes. The laboratory needs to be listed among those allowed to submit IMPC data analysis results to FlowRepository
impcExpId	The IMPC experiment id of the experiment that the results are being submitted for.
results	The results that are being submitted. This shall be a list of objects with names corresponding to IMPC parameter codes as defined in https://www.mousephenotype.org/impress (e.g., IMPC_IMM_011_001 to state the number of CD4 NKT cells in IMPC panel A). See also [impcResultsCopy]().

final   Whether the results being submitted shall be considered to be the final results.
                 This should be set to TRUE only if a final (complete) set of results is being
                 submitted (i.e., results for both panels are there). If you are submitting inter-
                 mediate results, such as results for one of the panel only, you should set this to
                 FALSE and then you can use FlowRepository to store your intermediate results
                 now with the intention to add to those later.

Details

An HTTP POST request sends the results to FlowRepository. You need to have your credentials
set (see [setFlowRepositoryCredentials](#)) and you as the user need to have permissions to subnit
IMPC data analysis results. In addition, the laboratory needs to be listed among those allowed to
submit IMPC data analysis results to FlowRepository. You may need to contact your FlowReposi-
tory administrators if you are not allowed to submit IMPC results. In addition, note that at this point,
the public FlowRepository (available at FlowRepository.org) does not contain IMPC data and is not
accepting these sorts of results. There are private FlowRepository instances only for IMPC data
at this point. Also, note that some basic consistency checks are in place and FlowRepository may
refuse results that appear to be wrong.

Value

A list of 2 objects named `response` and `status`. The response contains a text of the response from
the server, such as "Results submitted." if the results have been accepted. The status will contain the
HTTP status code of the response, such as "200 OK" if everything was successful. An example if an
unacceptable response is "Bad results (impc_imm_049_001 out of range, value should be between
0 and 100)" if you try to specify the percentage of live gated events in Panel B outside of the 0-100
range. The "400 Bad Request" status is to be expected in this case.

Author(s)

Josef Spidlen

References

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

See Also

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

Examples

```
## This will not submit results as the public FlowRepository is not
## accepting those at this point, "H" is probably not allowed to submit
## IMPC results, "impcEx0001" is a made up IMPC experiment ID,
## and finally, the user did not set her credentials...
tryCatch(
    {
        centreILAR <- "H"
        expId <- "impcEx0001"
        results <- list(
            impc_imm_001_001 = 0.12,
            impc_imm_026_001 = 1000000,
            impc_imm_002_001 = 87.345,
```

```
                impc_imm_027_001 = 1000000,
                impc_imm_049_001 = 91.567,
                impc_imm_002_001 = 543213)
            flowRep.submitImpcResults(centreILAR, expId, results)
        },
        interrupt = function(ex) { NULL; },
        error = function(ex) { NULL; }
    )
```

flowRepData-class   *'flowRepData': a class for storing metadata about a FlowRepository*
                             dataset

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 up-
loader, 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
impc.experiments = ....,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`, `attachments` and `impc.experiments`.

```
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(),impc.experiments=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 ara available here: http://flowrepository.org/quick_start_guide#MIFlowCytSc

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 "PM-CID: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.

impc.experiments: Object of class list enumerating IMPC experiments associated with this FlowRepository experiment.

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.

impc.experiments Return an object of class list of objects enumerating IMPC experiments associated with this dataset.

impcResultsCopy Return an object of class list with a copy of IMPC analysis results. See [impcResultsCopy](#) for details. *Usage:* impcResultsCopy(flowRepData,experimentIndex,resultIndex) The result is a copy of what can typically be found in flowRepData@impc.experiments[[experimentIndex]]$ impc_parameter_sets[[resultIndex]] but without the updated_at, created_at, id, gated_by, gated_by_id, and impc_experiment_id.

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 organiza-*
> *tion 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 evaluting 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 addresss.*

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   *Retrieve the identifier of flowRepData objects*

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)
```

---

ilarCodeDescription   *Get the name of a lab from it's ILAR code*

Description

This function returns the name of a lab based on its ILAR code, see `http://dels.nas.edu/global/ilar/Lab-Codes`.
This function works only with a very limited set of ILAR codes defined for IMPC centers. A NULL
value will be returned for all unknown centers.

Usage

```
ilarCodeDescription(ilarCode)
```

Arguments

ilarCode   ILAR code of an IMPC centre, or a list of ILAR codes, or a vector of ILAR
                    codes. The code (or codes) will be looked in an internal database of ILAR codes,
                    which contains labs from IMPC centers only. The codes are case sensitive.

Details

ILAR codes of IMPC centers are stored in an internal database (environment serving as a hash
table), which is used to lookup the results of this function. The ILAR codes are case sensiteve. The
function can handle a single code as well as a list (or vector) of codes.

Value

An object of class `character` containing a human readable name of the lab corresponding to this
ILAR code. If a list (or vector) of multiple codes is submitted, then a vector of multiple descriptions
will be returned. The length of the output will match the length of the input.

Author(s)

Josef Spidlen

See Also

[listKnownIlarCodes](#)

Examples

```
## Checking internal dictionary
## Codes are case sensitive
ilarCodeDescription("H")
ilarCodeDescription(listKnownIlarCodes())
```

---

impcCodeDescription   *Get a human readable description of an IMPC code.*

Description

This function returns a human readable description of an IMPC code based on `https://www.mousephenotype.org/impr` as of November 6, 2015. This includes IMPC parameters as well as IMPC metadata.

Usage

```
impcCodeDescription(code)
```

Arguments

code   Either a single IMPC code, or a list of IMPC codes, or a vector of IMPC codes. The code (or codes) will be looked in an internal database of IMPC codes. The codes are not case sensitive.

Details

IMPC parameter and metadata codes are stored in an internal database (environment serving as a hash table), which is used to lookup the results of this function. The codes are not case sensitive. The function can handle a single code as well as a list (or vector) of codes.

Value

An object of class `character` containing a human readable description of the IMPC code. If a list (or vector) of multiple codes is submitted, then a vector of multiple human readable descriptions will be returned. The length of the output will match the length of the input.

Author(s)

Josef Spidlen

References

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

See Also

[impcResultsCopy](#)

Examples

```
## Checking IMPC dictionary
## codes are not case sensitive
impcCodeDescription("impc_imm_010_001")
impcCodeDescription("IMPC_IMM_013_001")
impcCodeDescription("ImpC_iMm_019_001")
impcCodeDescription(c("impc_imm_022_001", "IMPC_IMM_028_001"))
```

---

impcResultsCopy   *Retrieve a copy of IMPC results associated with a flowRepData object*

Description

This method retrieves a copy of the results associated with a parameter set of an IMPC experiment
related to a [flowRepData](#) object (i.e., to a FlowRepository dataset).

Usage

```
impcResultsCopy(object, ...)
```

Arguments

object   Object of class [flowRepData](#).

...   Additional options, see the details section.

Details

This method will return an object of class `list` with a copy of IMPC analysis results. This is what
can typically be found in `object@impc.experiments[[experimentIndex]]$ impc_parameter_sets[[resultIndex]`
but without the `updated_at`, `created_at`, `id`, `gated_by`, `gated_by_id`, and `impc_experiment_id`
items. You can specify the following additional options:

experimentIndex Index of the IMPC experiment that shall be used. Usually, there is no more than
   1 IMPC experiment related to a [flowRepData](#) object, but this argument is available for the
   odd case where there would be multiple IMPC experiments related to a single FlowRepository
   dataset.

resultIndex Index of which IMPC parameter set of the IMPC experiment shall be used. When
   new IMPC results are submitted to FlowRepository, those will create a new paramater set
   associated with the particular IMPC experiment (i.e., previous results will not be overwritten).
   This argument can be used to specify which results are supposed to be coppied.

Value

A list representing the results of IMPC gating. This list will usually include: `impc_imm_001_001`,
`impc_imm_002_001`, `impc_imm_003_001`, `impc_imm_004_001`, `impc_imm_005_001`, `impc_imm_006_001`,
`impc_imm_007_001`, `impc_imm_008_001`, `impc_imm_009_001`, `impc_imm_010_001`, `impc_imm_011_001`,
`impc_imm_012_001`, `impc_imm_013_001`, `impc_imm_014_001`, `impc_imm_015_001`, `impc_imm_016_001`,
`impc_imm_017_001`, `impc_imm_018_001`, `impc_imm_019_001`, `impc_imm_020_001`, `impc_imm_021_001`,
`impc_imm_022_001`, `impc_imm_023_001`, `impc_imm_024_001`, `impc_imm_025_001`, `impc_imm_026_001`,
`impc_imm_027_001`, `impc_imm_028_001`, `impc_imm_029_001`, `impc_imm_030_001`, `impc_imm_031_001`,
`impc_imm_032_001`, `impc_imm_033_001`, `impc_imm_034_001`, `impc_imm_035_001`, `impc_imm_036_001`,
`impc_imm_037_001`, `impc_imm_038_001`, `impc_imm_039_001`, `impc_imm_040_001`, `impc_imm_041_001`,
`impc_imm_042_001`, `impc_imm_043_001`, `impc_imm_044_001`, `impc_imm_045_001`, `impc_imm_046_001`,
`impc_imm_047_001`, `impc_imm_048_001`, `impc_imm_049_001`, `impc_imm_050_001`, `impc_imm_051_001`,
`impc_imm_052_001`, `impc_imm_053_001`, `impc_imm_054_001`, `impc_imm_055_001`, `impc_imm_056_001`,
`impc_imm_057_001`, `impc_imm_058_001`, `impc_imm_059_001`, `impc_imm_060_001`, `impc_imm_061_001`,
`impc_imm_062_001`, `impc_imm_063_001`, `impc_imm_064_001`, `impc_imm_065_001`, `impc_imm_066_001`,
`impc_imm_067_001`, `impc_imm_068_001`, `impc_imm_069_001`, `impc_imm_070_001`, `impc_imm_071_001`,
`impc_imm_072_001`, `impc_imm_073_001`, `impc_imm_074_001`, `impc_imm_075_001`, `impc_imm_076_001`.
Those are IMPC codes defined at `https://www.mousephenotype.org/impress/protocol/174/7`

Author(s)

Josef Spidlen

Examples

```
## Get dataset from FlowRepository
mySmallDataset <- flowRep.get("FR-FCM-ZZ3X", impc.details = TRUE)
impcResultsCopy(mySmallDataset, experimentIndex = 1, resultIndex = 1)
## The result will be NULL since the "FR-FCM-ZZ3X" does not include
## any IMPC details. Right now, IMPC details are only in private instances
## of FlowRepository. This example will be updated to a better once once
## IMPC data is also included and public in the main public FlowRepository
## (flowrepository.org).
```

---

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]])
```

---

listKnownIlarCodes   *List all known ILAR codes.*

Description

This function returns a vector of ILAR codes of all IMPC centers stored in an internal database.

Usage

```
listKnownIlarCodes()
```

Details

ILAR codes of IMPC centers are stored in an internal database (environment serving as a hash table), which is used to provide the results of this function.

Value

An vector of class character containing a ILAR codes of IMPC centers known to this library.

Author(s)

Josef Spidlen

See Also

[ilarCodeDescription](#)

Examples

```
## Checking internal dictionary
## Codes are case sensitive
listKnownIlarCodes()
ilarCodeDescription(listKnownIlarCodes())
```

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 than 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 credetials 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 addresss.*

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 evaluting 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)
```

Index