Package 'rbiouml'

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Type Package

Title Interact with BioUML Server

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Description Functions for connecting to BioUML server, querying BioUML repository and launching BioUML analyses.

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R topics documented:

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biouml.analysis   *Run BioUML analysis*

Description

Run BioUML analysis optionaly tracking progress

Usage

```
biouml.analysis(analysisName, parameters=list(), wait=T, verbose=T)
```

Arguments

analysisName	name of BioUML analysis to run, use `biouml.analysis.list` to get the list of possible values
parameters	list of parameters to BioUML analysis, use `biouml.analysis.parameters` to get the list of parameters
wait	whether to wait for analysis completion or return immediately
verbose	print messages and progress from BioUML analysis, only meaningful if `wait` is TRUE

Value

Job id that can be passed to `biouml.job.info` and `biouml.job.wait`

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biouml.analysis.list   *List available BioUML analyses*

Description

`biouml.analysis.list` fetches list of available analyses from current BioUML server

Usage

```
biouml.analysis.list()
```

Value

A data frame (`data.frame`) with two column 'Group' and 'Name'.

biouml.analysis.parameters
Get BioUML analysis parameters

Description

Get BioUML analysis parameters names and description

Usage

```
biouml.analysis.parameters(analysisName)
```

Arguments

analysisName   name of BioUML analysis, , use `biouml.analysis.list` to get the list of possible values

Value

A data frame ([`data.frame`](data.frame)) with row.names corresponding to parameter names and one column 'description' with parameter description

biouml.export
Export data from BioUML

Description

`biouml.export` exports data from BioUML server to local file in given format

Usage

```
biouml.export(path, exporter="Tab-separated text (*.txt)",
                exporter.params=list(), target.file="biouml.out")
```

Arguments

path   path in BioUML repository

exporter   character string specifying format, `biouml.exporters` provides possible values

exporter.params

        list of parameters to exporter

target.file   a character string naming a file to export to

Value

None (invisible NULL).

biouml.export.parameters

Get BioUML export parameters

Description

Get BioUML export parameters

Usage

```
biouml.export.parameters(path, exporter)
```

Arguments

path	path to data element in BioUML repository to export
exporter	name of BioUML exporter, use `biouml.exporters` to get the list of possible values

Value

A data frame (`data.frame`) with row.names corresponding to parameter names and one column 'description' with parameter description

biouml.exporters   *List BioUML exporters*

Description

`biouml.exporters` fetches the list of exporters from BioUML server, these exporters can be used in `biouml.export` function

Usage

```
biouml.exporters()
```

Value

Character vector of BioUML exporters.

---

biouml.get *Fetch BioUML table*

Description

`biouml.get` fetches table data from BioUML server

Usage

```
biouml.get(path)
```

Arguments

path   Path to table in BioUML repository

Value

A data frame ([data.frame](#)) representation of BioUML table from `path`.

Examples

```
## Not run:
## fetch table from public BioUML server
biouml.login("https://ict.biouml.org")
x <- biouml.get("data/Examples/Optimization/Data/Experiments/exp_data_1")
head(x)
biouml.logout()

## End(Not run)
```

---

biouml.import *Import file to BioUML*

Description

`biouml.import` imports file to BioUML repository

Usage

```
biouml.import(file, parentPath, importer, importer.params=list())
```

Arguments

file	The name of file to import
parentPath	Path to folder in BioUML repository
importer	character string specifying format, [biouml.importers](#) provides list of posible values
importer.params	
	list of parameters to exporter

Value

Resulting path in BioUML repository

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biouml.import.parameters

Get BioUML import parameters

Description

Get BioUML import parameters

Usage

```
biouml.import.parameters(path, importer)
```

Arguments

path   path to data element in BioUML repository to import

importer   name of BioUML importer, use `biouml.importers` to get the list of possible
                values

Value

A data frame (`data.frame`) with row.names corresponding to parameter names and one column
'description' with parameter description

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biouml.importers   *List BioUML importers*

Description

`biouml.importers` fetches the list of importers from BioUML server, these importers can be used
in `biouml.import` function

Usage

```
biouml.importers()
```

Value

Character vector of BioUML importers.

---

biouml.job.info *Fetch BioUML job info*

Description

`biouml.job.info` fetches info about BioUML job

Usage

```
biouml.job.info(jobID)
```

Arguments

jobID   ID of job usually returned from biouml.analysis

Value

A list with following entries

status	job status, one of 'CREATED','RUNNING', 'PAUSED', 'COMPLETED', 'TER-MINATED_BY_REQUEST', 'TERMINATED_BY_ERROR'
results	a list of resulting paths in BioUML repository
values	character vector of messages from job
percent	percent complete

---

biouml.job.wait *Wait for job completion*

Description

`biouml.job.wait` waits for BioUML job completion

Usage

```
biouml.job.wait(jobID, verbose=T)
```

Arguments

jobID	ID of job usually returned from biouml.analysis
verbose	print messages and progress from BioUML job

Value

A list with following entries

status	job status, one of 'CREATED','RUNNING', 'PAUSED', 'COMPLETED', 'TER-MINATED_BY_REQUEST', 'TERMINATED_BY_ERROR'
results	a list of resulting paths in BioUML repository
values	character vector of messages from job
percent	percent complete

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biouml.login	*Login to BioUML server*

Description

Login to BioUML server. The connection will be saved in global options under name biouml_connection for future reuse.

Usage

```
biouml.login(url='http://localhost:8080/biouml', user='', pass='')
```

Arguments

url	URL of running biouml server
user	BioUML user, empty string for anonymous login
pass	password

Value

Invisible connection to BioUML server, connection is a list with following items:

user	the name of user used for connection
pass	password in plain text
url	URL of biouml server
sessionId	session id returned by BioUML server

Examples

```
## Not run:
## connect to public BioUML server at https://ict.biouml.org
biouml.login("https://ict.biouml.org")
getOption("biouml_connection")
biouml.logout()

## End(Not run)
```

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biouml.logout *Logout from BioUML server*

Description

Logouts from BioUML server

Usage

```
biouml.logout()
```

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biouml.ls *List data elements by path*

Description

`biouml.ls` lists children data elements by path in BioUML repository

Usage

```
biouml.ls(path, extended=F)
```

Arguments

path	Path to data collection in BioUML repository
extended	whether to return additional attributes for each children

Value

If extended is FALSE a character vector with child names, otherwise a data frame (data.frame) with row.names corresponding to child names and columns hasChildren and type.

Examples

```
## Not run:
## list databases available in public BioUML server
biouml.login("https://ict.biouml.org")
biouml.ls("databases")
biouml.logout()

## End(Not run)
```

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biouml.put   *Put data.frame to BioUML repository*

Description

biouml.put stores data.frame in BioUML repository

Usage

```
biouml.put(path, value)
```

Arguments

path	Path in BioUML repository
value	data.frame to store

Examples

```
## Not run:
## put data.frame into BioUML repository
x <- data.frame(A=1:10,B=LETTERS[1:10])
biouml.login("https://ict.biouml.org")
biouml.put("data/Collaboration/Demo/Data/Rtest/test_df", x)
biouml.logout()

## End(Not run)
```

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biouml.workflow   *Run BioUML workflow*

Description

Run BioUML workflow optionaly tracking progress

Usage

```
biouml.workflow(path, parameters=list(), wait=T, verbose=T)
```

Arguments

path	path to BioUML workflow
parameters	list of parameters to BioUML workflow
wait	whether to wait for workflow completion or return immediately
verbose	print messages and progress from BioUML workflow, only meaningful if wait is TRUE

Value

Job id that can be passed to `biouml.job.info` and `biouml.job.wait`

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