

Package ‘rbiouml’

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

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biouml.analysis	<i>Run BioUML analysis</i>
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Description

Run BioUML analysis optionally 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](#)

biouml.analysis.list	<i>List available BioUML analyses</i>
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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](#)) 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

<code>path</code>	path to data element in BioUML repository to export
<code>exporter</code>	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	<i>Fetch BioUML table</i>
------------	---------------------------

Description

biouml.get fetches table data from BioUML server

Usage

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

Arguments

path	Path to table in BioUML repository
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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	<i>Import file to BioUML</i>
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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 possible values
importer.params	list of parameters to exporter

Value

Resulting path in BioUML repository

```
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

```
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	<i>Fetch BioUML job info</i>
-----------------	------------------------------

Description

biouml.job.info fetches info about BioUML job

Usage

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

Arguments

jobID	ID of job usually returned from biouml.analysis
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Value

A list with following entries

status	job status, one of 'CREATED', 'RUNNING', 'PAUSED', 'COMPLETED', 'TERMINATED_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	<i>Wait for job completion</i>
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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', 'TERMINATED_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.login	<i>Login to BioUML server</i>
--------------	-------------------------------

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)
```

biouml.logout	<i>Logout from BioUML server</i>
---------------	----------------------------------

Description

Logouts from BioUML server

Usage

```
biouml.logout()
```

biouml.ls	<i>List data elements by path</i>
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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)
```

biouml.put	<i>Put data.frame to BioUML repository</i>
------------	--

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)
```

biouml.workflow	<i>Run BioUML workflow</i>
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Description

Run BioUML workflow optionally 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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