Package ‘rbiouml’

May 9, 2026

Type Package

Title Interact with BioUML Server

Version 1.11

Date 2021-08-10

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

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Depends RCurl, RJSONIO

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-08-10 09:00:02 UTC

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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`

`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`) with row.names corresponding to parameter names and one column 'description' with parameter description

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`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

`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` *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', '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` *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', '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` *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)
```

`biouml.logout` *Logout from BioUML server*

Description

Logouts from BioUML server

Usage

```
biouml.logout()
```

`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)
```

`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)
```

`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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