

# 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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**License** GPL-2

**Depends** RCurl, RJSONIO

**NeedsCompilation** no

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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 <a href="#">biouml.analysis.list</a> to get the list of possible values
parameters	list of parameters to BioUML analysis, use <a href="#">biouml.analysis.parameters</a> 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	<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*

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**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 <a href="#">biouml.exporters</a> 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*

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**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>
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**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("ie.biouml.org")  
x <- biouml.get("data/Examples/Optimization/Data/Experiments/exp_data_1")  
head(x)  
  
## 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 <a href="#">biouml.importers</a> 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>
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**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

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biouml.login	<i>Login to BioUML server</i>
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**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 ie.biouml.org
biouml.login("ie.biouml.org")
getOption("biouml_connection")

## End(Not run)
```



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biouml.logout	<i>Logout from BioUML server</i>
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**Description**

Logouts from BioUML server

**Usage**

```
biouml.logout()
```

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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("ie.biouml.org")  
biouml.ls("databases")  
  
## End(Not run)
```

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biouml.put	<i>Put data.frame to BioUML repository</i>
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**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("ie.biouml.org")
biouml.put("data/Collaboration/Demo/Data/Rtest/test_df", x)

## End(Not run)
```

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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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