

Description of rbiouml package

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1 Introduction

The *rbiouml* package provides functions to interact with BioUML server from within R. BioUML is an open source integrated Java platform for analysis of data from omics sciences research and other advanced computational biology, for building the virtual cell and the virtual physiological human. It spans a comprehensive range of capabilities, including access to databases with experimental data, tools for formalized description of biological systems structure and functioning, as well as tools for their visualization, simulation, parameters fitting and analyses.

2 Getting started

2.1 Connecting to BioUML server

The first thing you need to do is load the package and login to the BioUML server. As an example we will connect to the free public BioUML server at <http://ie.biouml.org>. The function `biouml.login` connects to BioUML server and perform authentication.

```
> library(rbiouml)
> biouml.login("ie.biouml.org")
```

The `biouml.login` also accepts user and password, but we leave them empty in the example above for anonymous login. Alternatively you can install BioUML on your local computer and connect to it in the same way.

```
> biouml.login("localhost:8080")
```

See http://wiki.biouml.org/index.php/BioUML_server_installation for details on BioUML server installation.

2.2 Querying BioUML repository

The BioUML repository (or simply repository) is the central BioUML data storage place. Basically, all the data you work with in BioUML is stored in the repository. The repository has a hierarchical structure similar to file systems. On the top level the repository consists of several root folders. The most common ones are:

databases contains preinstalled or user-defined modules.

data contains user projects and public examples.

The `biouml.ls` function lists the contents of given folder in repository. The list of databases available in BioUML server:

```
> biouml.ls("databases")
```

```
[1] "Apoptosis model"
[2] "Biomodels"
[3] "Biopath"
[4] "Cardiovascular student"
[5] "DSMTS"
[6] "EHMN"
[7] "Ensembl"
[8] "EnsemblHuman52"
[9] "EnsemblMouse"
[10] "EnsemblRat"
[11] "GO"
[12] "GeneWays"
[13] "KEGG"
[14] "Patient-specific CVS models"
[15] "Reactome"
[16] "SBML tests"
[17] "The composite model of CD95 and NF-kB signaling"
[18] "Utils"
[19] "Virtual Human"
```

The list of data elements available in BioUML examples folder:

```
> biouml.ls("data/Examples/Optimization/Data/Experiments")
```

```
[1] "exp_data_1" "exp_data_2" "exp_data_3"
```

The `biouml.get` fetches a table from BioUML repository as R data.frame:

```
> x <- biouml.get("data/Examples/Optimization/Data/Experiments/exp_data_1")
> class(x)
```

```
[1] "data.frame"
```

```
> head(x)
```

```
  time      p43p41      pro8      casp8
0    0  0.05772537  59.96316  0.00000000
1   10  0.26814367  57.56464  0.04107502
2   20  4.76048117  58.58981  0.31611658
3   30  8.25193519  59.42156  1.39735609
4   45 16.14448337  48.18975  3.52037089
5   60 17.02060557  38.95027  3.94722894
```

This function allows to fetch not only true BioUML tables, but any data elements which have tabular representation, including profiles, user uploaded tracks and so on.

To store data.frame as a table into BioUML repository use `biouml.put` function:

```
> x[,5] <- x[,3] + x[,4]
> biouml.put("data/Collaboration/Demo/Data/Rtest/exp_data_1_sum", x)
> biouml.ls("data/Collaboration/Demo/Data/Rtest")
```

```
[1] "exp_data_1 filtered" "exp_data_1_sum"      "HIV-1"
[4] "matrix"              "Matrix library"    "test_df"
```

2.3 Using BioUML analyses

BioUML provides a set of analyses organized in groups. The list of analyses available in the current server can be fetched with `biouml.analysis.list` function.

```
> summary( biouml.analysis.list() )
```

	Group	Name	
BSA	:84	Adaptive simulated annealing:	1
Binding regions:	48	Add expression values	: 1
Import	:42	Add genes from CMA	: 1
Data	:39	Add reactants	: 1
RiboSeq	:24	Affymetrix normalization	: 1
GTRD	:22	Agilent normalization	: 1
(Other)	:70	(Other)	:323

Each biouml analysis has a set of parameters, `biouml.analysis.parameters` returns a `data.frame` with row names corresponding to parameter names and one column 'description'.

```
> biouml.analysis.parameters("Filter table")
```

	description
<code>inputPath</code>	Table to filter
<code>filterExpression</code>	Expression in JavaScript like 'ColumnName1 > 5 && ColumnName2 < 0'
<code>filteringMode</code>	Which rows to select
<code>outputPath</code>	Path to the filtered table

The `biouml.analysis` launches analysis with given parameters.

```
> biouml.analysis("Filter table", list(  
+   inputPath="data/Examples/Optimization/Data/Experiments/exp_data_1",  
+   filterExpression="time < 40",  
+   outputPath="data/Collaboration/Demo/Data/Rtest/exp_data_1 filtered"  
+ ))
```

```
0 %
```

```
INFO - Analysis 'Filter table' added to queue
```

```
70 %
```

```
INFO - Analysis 'Filter table' started
```

```
INFO - Filtering...
```

```
100 %
```

```
INFO - Writing result...
```

```
INFO - Analysis 'Filter table' finished (1.7 s)
```

```
[1] "RJOB574967581"
```

2.4 Importing files to and from BioUML

As described previously, `data.frames` can be fetched from and stored to BioUML repository using `biouml.get` and `biouml.put` functions. In addition, data can be imported from files and exported to files in various formats. The list of importers can be obtained with `biouml.importers` function.

```
> head( biouml.importers() )
```

```
[1] "BioNetGen language format (*.bngl)"
```

```
[2] "SDF file"
```

```
[3] "TRANSFAC matrices format (matrix*.dat)"
```

```
[4] "TRANSFAC profile (*.prf)"
```

```
[5] "Antimony"
```

```
[6] "Text output file generated by R (.Routput)"
```

As an example we will import fasta file to BioUML.

```
> hiv.genome <- system.file("extdata","HIV-1.fa", package="rbiouml")
> output.folder <- "data/Collaboration/Demo/Data/Rtest"
> biouml.import(hiv.genome, output.folder, importer="Fasta format (*.fasta)")

0 %
100 %
data/Collaboration/Demo/Data/Rtest/HIV-1[1] "data/Collaboration/Demo/Data/Rtest/HIV-1"

> biouml.ls(output.folder)

[1] "exp_data_1 filtered" "exp_data_1_sum"      "HIV-1"
[4] "matrix"              "Matrix library"    "test_df"
```

Similarly, we can use `biouml.export*` functions to export data from BioUML repository.

```
> head( biouml.exporters() )

[1] "Tab-separated text (*.txt)"
[2] "Match format (*.match)"
[3] "Portable Network Graphics (*.png)"
[4] "Archive containing exported elements (*.zip)"
[5] "SBN-ML"
[6] "SBML"

> biouml.export("data/Collaboration/Demo/Data/Rtest/HIV-1",
+ exporter="Fasta format (*.fasta)", target.file="HIV-1.fa")
> file.exists("HIV-1.fa")

[1] TRUE
```

2.5 Disconnecting from BioUML server

When you have finished with the BioUML server is recommended to do logout.

```
> biouml.logout()
```

```
NULL
```