



Iobion

Stratagene Analysis Software

Connecting R to GeneTraffic™ User Guide

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GeneTraffic R Integration Install Notes

Install the GeneTraffic R Integration package with the following command:

Unix Systems

```
R INSTALL GeneTraffic_1.0.1.tar.gz
```

Windows Systems

```
Rcmd INSTALL GeneTraffic_1.0.1.zip
```

~Or~

Select the “install package from local zip” from the Packages menu of the R GUI

Dependencies

- XML ($\geq 0.95.6$) (<http://www.omegahat.org/RXML/>)
(for Windows http://www.iobion.com/web_services/R/Win32/XML_0.95-6.zip)
- SSOAP ($\geq 0.1.2$) (<http://www.omegahat.org/SSOAP/>)
(for Windows http://www.iobion.com/web_services/R/Win32/SSOAP_0.1-2.zip)
- affy ($\geq 1.3.28$) (<http://www.bioconductor.org/>)
- marray ($\geq 1.2.3$) (<http://www.bioconductor.org/>)
- BioBase ($\geq 1.4.0$) (<http://www.bioconductor.org/>)
- digest ($\geq 0.1.1$) (<http://cran.r-project.org/src/contrib/Descriptions/digest.html>)

GTServer {GeneTraffic}

Create a GeneTraffic server object

Description

This is a constructor for the GTServer class which is used to identify the host, port, username and password of a GeneTraffic server.

Usage

```
GTServer(host, username, password, port = 80)
```

Arguments

- host* The name of the GeneTraffic machine.
- username* The username used to connect to the GeneTraffic server.
- password* The password used to connect to the GeneTraffic server.
- port* The port used to connect to the GeneTraffic server.
If not specified, by default port 80 is used.

Value

An object of class GTServer.

Examples

```
gt <- GTServer(host = "genetraffic", username="demo", password="pass",  
port = 80)
```

GTLogin {GeneTraffic}

Login into a GeneTraffic server

Description

This is the function to login into a GeneTraffic server using the GeneTraffic Web Services API.

Usage

```
session <- GTLogin(gt)
```

Arguments

gt a GTServer object.

Value

The session id required further on to interact with a GeneTraffic server.

Examples

```
gt <- GTServer(host = "genetraffic", username="demo", password="pass",  
port = 80)  
session <- GTLogin(gt)
```

GTLogout {GeneTraffic}

Logout from a GeneTraffic server

Description

This is the function to logout from a GeneTraffic server using the GeneTraffic Web Services API.

Usage

```
GTLogout(gt, session)
```

Arguments

gt a GTServer object.

session the session id returned by the GTLogin function.

Value

The logical value representing success or failure trying to logout from a GeneTraffic server.

Examples

```
gt <- GTServer(host = "genetraffic", username="demo", password="pass",  
port = 80)  
session <- GTLogin(gt)  
GTLogout(gt, session)
```

GTGetProjectList {GeneTraffic}

Get a project list from a GeneTraffic server

Description

This is the function that retrieves a project list from a GeneTraffic server using the GeneTraffic Web Services API.

Usage

```
GTGetProjectList(gt, session)
```

Arguments

gt a GTServer object.

session the session id returned by the GTLogin function.

Value

The list of projects from a GeneTraffic server.

Examples

```
gt <- GTServer(host = "genetraffic", username="demo", password="pass",  
port = 80)  
session <- GTLogin(gt)  
pl <- GTGetProjectList(gt, session)  
pl
```

GTGetProjectSummary {GeneTraffic}

Get a project summary zip from a GeneTraffic server

Description

This is the function that retrieves a project summary zip file from a GeneTraffic server using the GeneTraffic Web Services API.

Usage

```
GTGetProjectSummary(gt, session)
```

Arguments

gt a GTServer object.

session the session id returned by the GTLogin function.

Value

The file name of the project summary zip file retrieved from a GeneTraffic server.

Examples

```
gt <- GTServer(host = "genetraffic", username="demo", password="pass",  
port = 80)  
session <- GTLogin(gt)  
pl <- GTGetProjectList(gt, session)  
filename <- GTGetProjectSummary(gt, session, pl[[1]]$"project_id")
```

GTLoadExpression {GeneTraffic}

Reads from a GeneTraffic project summary file

Description

A GeneTraffic project summary is read from a file which contains the summarize data for that project.

Usage

```
GTLoadExpression(filename = "Project.zip")
```

Arguments

filename Name of the file containing the GeneTraffic project summary in zip format.

Value

The return value depends on how many chip types the project summary file contains. If it has only one, it returns one `exprSet` object, otherwise it returns a list of `exprSet` objects (for 1 color projects). For two color projects, if it has only one chip type, it returns one `marray` object, otherwise it returns a list of `marray` objects.

Examples

From a file:

```
eset <- GTLoadExpression(filename="Project.zip")
eset
```

From a GeneTraffic server:

```
gt <- GTServer(host = "genetraffic", username="demo", password="pass",
port = 80)
session <- GTLogin(gt)
pl <- GTGetProjectList(gt, session)
filename <- GTGetProjectSummary(gt, session, pl[[1]]$"project_id")
GTLogout(gt, session)
eset <- GTLoadExpression(filename)
eset
```


For further information regarding all aspects of the program's functionality please contact Iobion Informatics, LLC at:

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