

# GeneTraffic

October 25, 2011

---

GTGetProjectList *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(server, session)
```

## Arguments

<code>server</code>	a <code>GTServer</code> object.
<code>session</code>	the session id returned by the <code>GTLogin</code> function.

## Value

The list of projects from a GeneTraffic server.

## Examples

```
## Not run:  
gt <- GTServer(host = "genetraffic", username="demo", password="pass", port = 80)  
session <- GTLogin(gt)  
pl <- GTGetProjectList(gt, session)  
pl  
  
## End(Not run)
```

GTGetProjectSummary

*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(server, session, project, dest)
```

### Arguments

server	a GTServer object.
session	the session id returned by the GTLogin function.
project	the project id returned by the GTGetProjectList function.
dest	the destination file name where the project summary should be retrieved.

### Value

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

### Examples

```
## Not run:
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")

## End(Not run)
```

---

GTLoadExpression    *Reads from a GeneTraffic project summary file*

---

### Description

A GeneTraffic project summary is read from a file representing the experiment interpretation 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 `ExpressionSet` object, otherwise it returns a list of `ExpressionSet` objects (for 1 color projects). For two color projects, if it has only one chip type, it returns one `marrayRaw` object, otherwise it returns a list of `marrayRaw` objects.

**Examples**

```
#From a file:
eset <- GTLoadExpression(filename="Project.zip")
eset

#From a GeneTraffic server:
## Not run:
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

## End(Not run)
```

---

 GTLogin

*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(server)
```

**Arguments**

`server` a `GTServer` object.

**Value**

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

**Examples**

```
## Not run:
gt <- GTServer(host = "genetraffic", username="demo", password="pass", port = 80)
session <- GTLogin(gt)

## End(Not run)
```

---

GTLogout	<i>Logout from a GeneTraffic server</i>
----------	---

---

**Description**

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

**Usage**

```
GTLogout(server, session)
```

**Arguments**

<code>server</code>	a GTServer object.
<code>session</code>	the session id returned by the GTLogin function.

**Value**

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

**Examples**

```
## Not run:
gt <- GTServer(host = "genetraffic", username="demo", password="pass", port = 80)
session <- GTLogin(gt)
GTLogout(gt, session)

## End(Not run)
```

---

GTServer-class	<i>Create a GeneTraffic server object - class</i>
----------------	---

---

**Description**

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

**Examples**

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

---

`GTServer`*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)
```

**Arguments**

<code>host</code>	the name of the GeneTraffic machine.
<code>username</code>	the username used to connect to the GeneTraffic server.
<code>password</code>	the password used to connect to the GeneTraffic server.
<code>port</code>	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)
```

# Index

## \*Topic **IO**

- GTGetProjectList, [1](#)
- GTGetProjectSummary, [2](#)
- GTLoadExpression, [2](#)
- GTLogin, [3](#)
- GTLogout, [4](#)
- GTServer, [5](#)
- GTServer-class, [4](#)

- GTGetProjectList, [1](#)
- GTGetProjectSummary, [2](#)
- GTLoadExpression, [2](#)
- GTLogin, [3](#)
- GTLogout, [4](#)
- GTServer, [5](#)
- GTServer-class, [4](#)