

Package ‘CytobankAPI’

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Title Cytobank API Wrapper for R

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Description Tools to interface with Cytobank's API via R, organized by various endpoints that represent various areas of Cytobank functionality. Learn more about Cytobank at <<https://www.cytobank.org>>.

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License Artistic-2.0

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AdvancedAnalysis-class

S4 Advanced Analysis Class

Description

An Advanced Analysis object that is a parent class to all advanced analysis algorithms. This class should never be called explicitly. Its purpose is to act as a parent class for advanced analyses.

Value

An Advanced Analysis object

Slots

channels the channels selected for the advanced analysis, this can be either a list of short channel IDs (integer) OR long channel names (character)

compensation_id the compensation ID selected for the advanced analysis

name the name of the advanced analysis

source_experiment the source experiment ID the advanced analysis is associated with

.available_channels the list of available channels based off the [panels.list](#) function

.available_files the list of available files based off the [fcs_files.list](#) function

.available_populations the list of available populations based off the [populations.list](#) function

Description

Interact with attachments using these endpoints. Only FCS files can be analyzed in Cytobank, but any file can be uploaded as an attachment. Exported PDFs, statistics, and files also automatically attach themselves to the Experiment they are exported from. [Learn more about attachments in Cytobank.](#)

Usage

```
## S4 method for signature 'UserSession'
attachments.delete(UserSession, experiment_id,
  attachment_id, timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
attachments.download(UserSession, experiment_id,
  attachment_id, directory = getwd(), timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
attachments.download_zip(UserSession, experiment_id,
  directory = getwd(), timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
attachments.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
attachments.show(UserSession, experiment_id,
  attachment_id, output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
attachments.update(UserSession, attachment,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
attachments.upload(UserSession, experiment_id,
  file_path, output = "default", timeout = UserSession@long_timeout)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
attachment_id	integer representing an attachment ID
timeout	integer representing the request timeout time in seconds [optional]

directory	character representing a specific directory to which the file will be downloaded (optional ending directory slash), if left empty, the default will be the current working directory [optional]
output	character representing the output format [optional] - <i>attachments.list, attachments.show, attachments.update</i> : ("default", "raw")
attachment	dataframe representing an attachment (can retrieve via the attachments.show endpoint)
file_path	character representing a file path

Details

`attachments.delete` Permanently delete an attachment.

`attachments.download` Download an attachment from an experiment.

`attachments.download_zip` Download all attachments as a zip file from an experiment.

`attachments.list` List all attachments from an experiment. Outputs a dataframe [default] or raw list with all fields present.
- *Optional output parameter, specify one of the following*: ("default", "raw")

`attachments.show` Show attachment details from an experiment.
- *Optional output parameter, specify one of the following*: ("default", "raw")

`attachments.update` Update an attachment description from an experiment.

`attachments.upload` Upload an attachment to an experiment.
- *Optional output parameter, specify one of the following*: ("default", "raw")

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

attachments.delete(cyto_session, 22, attachment_id=2)

# Download an attachment to the current working directory
attachments.download(cyto_session, 22, attachment_id=2)

# Download an attachment to a new directory
attachments.download(cyto_session, 22, attachment_id=2, directory="/my/new/download/directory/")

# Download the attachment zip to the current working directory
attachments.download_zip(cyto_session, 22, attachment_id=2)

# Download the attachment zip to a new directory
attachments.download_zip(cyto_session, 22, attachment_id=2, directory="/my/new/download/directory/")

# Dataframe of all attachments with all fields present
attachments.list(cyto_session, 22)

# Raw list of all attachments with all fields present
```

```

attachments.list(cyto_session, 22, output="raw")

attachments.show(cyto_session, 22, attachment_id=2)

attachments.update(cyto_session, attachment=cyto_attachment)

attachments.upload(cyto_session, 22, file_path="/path/to/my_attachment.txt")

```

authentication *Authentication Endpoints*

Description

Interact with authentication endpoints. Every call to the Cytobank API must be accompanied by an authentication token. Tokens should be kept secure as they confer access to the data and analyses of an account. Tokens expire after 8 hours by default but this figure may change depending on custom configurations of an Enterprise Cytobank. Use the authentication.logout / authentication.revoke API endpoints to invalidate one or all tokens for a user account.

Usage

```

authenticate(site, username = NA, password = NA, auth_token = NA,
             short_timeout = 30, long_timeout = 60, timeout = 30)

## S4 method for signature 'UserSession'
authentication.logout(UserSession,
                      timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
authentication.revoke_all_tokens(UserSession,
                                 timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
authentication.revoke_all_tokens_user(UserSession,
                                       user_id, timeout = UserSession@short_timeout)

```

Arguments

site	character representing Cytobank user's site
username	character representing Cytobank user's username or email
password	character representing Cytobank user's password
auth_token	character representing Cytobank user's authentication token (expires in 8 hours)
short_timeout	numeric representing short request timeout times (default = 60s) [optional]
long_timeout	numeric representing long request timeout times (default = 30s) [optional]
timeout	integer representing the request timeout time in seconds [optional]
UserSession	Cytobank UserSession object
user_id	integer representing a Cytobank user's ID

Details

`authenticate` Authenticate a Cytobank user and returns a Cytobank `UserSession` object that is passed to all other Cytobank API endpoints.

`authentication.logout` Logout a Cytobank user.

`authentication.revoke_all_tokens` Invalidate all existing tokens for the user making this call.

`authentication.revoke_all_tokens_user` Revoke all tokens for a given user. This endpoint only works for admins of the Cytobank site being accessed.

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rock!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

authentication.logout(cyto_session)

authentication.revoke_all_tokens(cyto_session)

authentication.revoke_all_tokens_user(cyto_session)
```

 citrus

CITRUS Endpoints

Description

Interact with CITRUS advanced analyses using these endpoints.

Usage

```
## S4 method for signature 'UserSession,CITRUS'
citrus.copy_settings(UserSession, citrus,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,CITRUS'
citrus.delete(UserSession, citrus,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,CITRUS'
citrus.download(UserSession, citrus,
  directory = getwd(), timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
citrus.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)
```

```

## S4 method for signature 'UserSession'
citrus.new(UserSession, experiment_id, citrus_name,
  timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession,CITRUS'
citrus.rename(UserSession, citrus, citrus_name,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,CITRUS'
citrus.run(UserSession, citrus,
  output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
citrus.show(UserSession, experiment_id, citrus_id,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,CITRUS'
citrus.status(UserSession, citrus,
  output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession,CITRUS'
citrus.update(UserSession, citrus,
  timeout = UserSession@long_timeout)

```

Arguments

UserSession	Cytobank UserSession object
citrus	Cytobank CITRUS object
output	character representing the output format [optional] - <i>citrus.list</i> , <i>citrus.run</i> , <i>citrus.status</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds [optional]
directory	character representing a specific directory to which the file will be downloaded (optional ending directory slash), if left empty, the default will be the current working directory [optional]
experiment_id	integer representing an experiment ID
citrus_name	character representing a new CITRUS name
citrus_id	integer representing a CITRUS ID

Details

`citrus.copy_settings` Copy CITRUS advanced analysis settings from an experiment and returns a CITRUS object.

`citrus.delete` Delete a CITRUS advanced analysis from an experiment.

`citrus.download` Download a CITRUS analysis from an experiment.

`citrus.list` List all CITRUS advanced analyses from an experiment. Outputs a dataframe [default] or list with all fields present.

- *Optional output parameter, specify one of the following: ("default", "raw")*

`citrus.new` Create a new CITRUS advanced analysis from an experiment and returns a CITRUS object.

`citrus.rename` Rename a CITRUS advanced analysis from an experiment and returns a CITRUS object.

`citrus.run` Run a CITRUS advanced analysis from an experiment.

`citrus.show` Show CITRUS advanced analysis details from an experiment and returns a CITRUS object.

`citrus.status` Show the status of a CITRUS advanced analysis from an experiment.

`citrus.update` Update a CITRUS advanced analysis from an experiment and returns the new CITRUS object.

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# cyto_citrus refers to a CITRUS object that is created from CITRUS endpoints
# examples: citrus.new, citrus.show (see details section for more)

citrus.copy_settings(cyto_session, citrus=cyto_citrus)

citrus.delete(cyto_session, citrus=cyto_citrus)

# Download a CITRUS analysis to the current working directory
citrus.download(cyto_session, citrus)

# Download a CITRUS analysis to a new directory
citrus.download(cyto_session, citrus, directory="/my/new/download/directory/")

# Dataframe of all CITRUS advanced analyses with all fields present
citrus.list(cyto_session, 22)

# Raw list of all CITRUS advanced analyses with all fields present
citrus.list(cyto_session, 22, output="raw")

citrus.new(cyto_session, 22, citrus_name="My new CITRUS analysis")

citrus.rename(cyto_session, citrus=cyto_citrus, citrus_name="My updated CITRUS name")

citrus.run(cyto_session, citrus=cyto_citrus)

citrus.show(cyto_session, 22, citrus_id=2)

citrus.status(cyto_session, citrus=cyto_citrus)
```



```
citrus.update(cyto_session, citrus=cyto_citrus)
```

CITRUS-class

S4 CITRUS Class

Description

A CITRUS object that holds pertinent CITRUS advanced analysis run information, [learn more about CITRUS](#). This class should never be called explicitly. If a user would like to create a new Cytobank CITRUS object, utilize the [citrus.new](#) function, or any other [CITRUS endpoints that return CITRUS objects documented in the 'Details' section](#).

Value

A CITRUS advanced analysis object

Slots

`associated_models` list representing statistical methods used to discover stratifying signatures from clustered data features that explain differences between sample groups, [learn more about CITRUS association models](#)
- choose from the following : ("sam", "pamr" [default], "glmnet")

`attachment_id` numeric representing the CITRUS attachment ID

`cross_validation_folds` numeric representing the regulation threshold, controlling the number of features in the model (only applies to PAM, LASSO), [learn more about CITRUS cross validation folds](#)

`citrus_id` numeric representing the CITRUS analysis ID

`cluster_characterization` character representing the principle for analyzing and quantifying individual samples, [learn more about CITRUS cluster characterization](#)
- choose one of the following : ("abundance" [default], "medians")

`event_sampling_method` character representing the sampling method, [learn more about CITRUS event sampling methods](#)
- choose one of the following : ("equal" [default], "max-per-file")

`events_per_file` numeric representing the number of events taken from each sample

`false_discovery_rate` numeric representing the false discovery rate (only applies to PAM, SAM), [learn more about CITRUS false discovery rate](#)

`file_grouping` numeric dataframe representing which group samples belong to, [learn more about CITRUS file grouping, the core functionality of CITRUS](#)

`minimum_cluster_size` numeric representing the number of nodes, [learn more about CITRUS minimum cluster size](#)

`normalize_scales` logical representing whether or not to normalize channels, [learn more about normalizing CITRUS scales](#)

plot_theme character representing the background color of images and figures within the CITRUS results
 - choose one of the following : ("white" [default], "black")

population_id dataframe representing a population **gate set ID**

statistics_channels list representing the statistics channels used for the 'median' cluster characterization, these channels should not be selected for clustering

 compensations

Compensation Endpoints

Description

Interact with compensation endpoints. Get information about compensations stored in Cytobank. For information about file-internal compensation for an individual FCS file, consult the [FCS files endpoints](#). [Learn more about compensation in Cytobank](#).

Usage

```
## S4 method for signature 'UserSession'
compensations.upload_csv(UserSession, experiment_id,
  file_path, timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
compensations.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
compensations.show(UserSession, experiment_id,
  compensation_id, output = "default", timeout = UserSession@short_timeout)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
file_path	character representing a file path
timeout	integer representing the request timeout time in seconds [optional]
output	character representing the output format [optional] - <i>compensations.list</i> : ("default", "raw") - <i>compensations.show</i> : ("default", "dataframe", "raw") - dataframe: <i>converts the compensation matrix output to a dataframe</i>
compensation_id	integer representing a compensation ID

Details

`compensations.upload_csv` Upload a compensation CSV to an experiment.

`compensations.list` List all compensations from an experiment. Outputs a formatted list [default] or raw list with all fields present.

- *Optional output parameter, specify one of the following:* ("default", "raw")

`compensations.show` Show compensation details from an experiment.

- *Optional output parameter, specify one of the following:* ("default", "dataframe", "raw")
- *dataframe: converts the compensation matrix output to a dataframe*

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocksl!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

compensations.upload_csv(cyto_session, 22, file_path="/path/to/my_compensation.csv")

# List of all compensations with all fields present, with a compensation matrix dataframe list item
compensations.list(cyto_session, 22)

# Raw list of all compensations with all fields present
compensations.list(cyto_session, 22, output="raw")

# List form of a compensation
compensations.show(cyto_session, 22, compensation_id=2)

# Compensation dataframe only
compensations.show(cyto_session, 22, compensation_id=2, output="dataframe")
```

drop

DROP File Endpoints

Description

Upload DROP file(s) into Cytobank. A DROP file consists of any CSV, TSV, TXT, or FCS file. If the DROP file is of the type CSV, TSV, or TXT, the file will be converted to an FCS file to be used within Cytobank. [Learn more about DROP.](#)

Usage

```
## S4 method for signature 'UserSession'
drop.upload(UserSession, experiment_id, file_path,
  data_matrix_start_row = 2, data_matrix_start_column = 1,
  skipped_columns = c(), output = "default",
  timeout = UserSession@long_timeout)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
file_path	character representing a file path
data_matrix_start_row	integer representing the start row of the DROP file(s)
data_matrix_start_column	integer representing the start column of the DROP file(s)
skipped_columns	integer vector representing the channels to skip within the DROP file(s)
output	character representing the output format [optional] - <i>drop.upload</i> : ("default", "raw") - <i>dataframe</i> : <i>converts the file internal compensation matrix output to a dataframe</i>
timeout	integer representing the request timeout time in seconds [optional]

Details

`drop.upload` Upload a DROP file (CSV, TSV, TXT, FCS) to an experiment. - *Optional output parameter, specify one of the following: ("default", "raw")*

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

drop.upload(cyto_session, 22, file_path="/path/to/my_drop_file.type",
  data_matrix_start_row=2, data_matrix_start_column=1, skipped_columns=c(4,8))
```

experiments

Experiment Endpoints

Description

Interact with experiment endpoints. An Experiment is a container for data and analyses in Cytobank. If data are on Cytobank, they must be within an Experiment. Configurations such as [gates](#), [compensations](#), [scales](#), Sample Tags, and illustrations are also linked to an individual Experiment. Within the Cytobank interface, the [Experiment Summary Page](#) is a useful integration point for information about an Experiment.

Usage

```
## S4 method for signature 'UserSession'
experiments.clone_full(UserSession, experiment_id,
  output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
experiments.clone_selective(UserSession, experiment_id,
  experiment_name, fcs_files = c(-1), primary_researcher = NA,
  principal_investigator = NA, clone_gates = FALSE,
  clone_annotations = FALSE, clone_attachments = FALSE,
  clone_reagents = FALSE, clone_compensations = FALSE,
  clone_panels = FALSE, clone_illustrations = FALSE,
  clone_project = FALSE, clone_user_access = FALSE,
  allow_full_access_pi = FALSE, output = "default",
  timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
experiments.delete(UserSession, experiment_id,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
experiments.full_access_users_list(UserSession,
  experiment_id, output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
experiments.full_access_users_add(UserSession,
  experiment_id, user_id = NA, user_email = NA, username = NA,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
experiments.full_access_users_remove(UserSession,
  experiment_id, user_id = NA, user_email = NA, username = NA,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
experiments.list(UserSession, output = "default",
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
experiments.new(UserSession, experiment_name, purpose,
  comments = NA, primary_researcher = NA, principal_investigator = NA,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
experiments.show(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
```

```

experiments.trash(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
experiments.update(UserSession, experiment,
  output = "default", timeout = UserSession@short_timeout)

```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
output	character representing the output format [optional] - <i>experiments.clone_full</i> , <i>experiments.clone_selective</i> , <i>experiments.full_access_users_list</i> , <i>experiments.list</i> , <i>experiments.new</i> , <i>experiments.show</i> , <i>experiments.trash</i> , <i>experiments.update</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds [optional]
experiment_name	character representing an experiment name
fcs_files	vector/list of integers representing a list of FCS file IDs [optional]
primary_researcher	integer representing a primary researcher ID [optional]
principal_investigator	integer representing a principal investigator ID [optional]
clone_gates	boolean denoting cloning gates option [optional]
clone_annotations	boolean denoting cloning annotations option [optional]
clone_attachments	boolean denoting cloning attachments option [optional]
clone_reagents	boolean denoting cloning reagents option [optional]
clone_compensations	boolean denoting cloning compensations option [optional]
clone_panels	boolean denoting cloning panels option [optional]
clone_illustrations	boolean denoting cloning illustrations option [optional]
clone_project	boolean denoting cloning project option [optional]
clone_user_access	boolean denoting cloning user access option [optional]
allow_full_access_pi	boolean denoting to allow full access to PI option [optional]
user_id	integer representing a user's ID
user_email	character representing a user's email
username	character representing a username
purpose	character representing an experiment purpose
comments	character representing an experiment comment [optional]
experiment	dataframe representing an experiment

Details

`experiments.clone_full` Full clone an experiment. [Learn more about the full clone functionality.](#)
 - *Optional output parameter, specify one of the following: ("default", "raw")*

`experiments.clone_selective` Selectively clone an experiment. [Learn more about the selective clone functionality](#)
 - *Optional output parameter, specify one of the following: ("default", "raw")*

`experiments.delete` Permanently delete an experiment and all analyses (including SPADE, viSNE, etc.) permanently. This is not reversible.

`experiments.list` List all full access users from an experiment.
 - *Optional output parameter, specify one of the following: ("default", "raw")*

`experiments.list` Add a full access user to an experiment. A full access user can be added by a user ID, email, or username.

`experiments.list` Remove a full access user from an experiment. A full access user can be removed by a user ID, email, or username.

`experiments.list` List all inbox experiments. Outputs a dataframe [default] or raw list with all fields present.
 - *Optional output parameter, specify one of the following: ("default", "raw")*

`experiments.new` Create a new experiment.
 - *Optional output parameter, specify one of the following: ("default", "raw")*

`experiments.show` Show experiment details.
 - *Optional output parameter, specify one of the following: ("default", "raw")*

`experiments.trash` Trash an experiment. This is reversible and not to be confused with permanent deletion.

`experiments.update` Update an experiment. (all parameters are optional, except for `experiment_id`)
 - *Optional output parameter, specify one of the following: ("default", "raw")*

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

experiments.clone_full(cyto_session, 22)

experiments.clone_selective(cyto_session, 22,
  experiment_name="My New Experiment Name", fcs_files=c(12, 13, 14, 15, 16))

experiments.delete(cyto_session, 22)

# Dataframe of all full access users
experiments.full_access_users_list(cyto_session, 22)

# List of all full access users
experiments.full_access_users_list(cyto_session, 22, output="raw")

# Add a user as a full access user by user's ID
```

```

experiments.full_access_users_add(cyto_session, 22, user_id=2)

# Add a user as a full access user by user's email
experiments.full_access_users_add(cyto_session, 22, user_email="sammy_cytometry@cytobank.org")

# Add a user as a full access user by user's username
experiments.full_access_users_add(cyto_session, 22, username="sammy_cytometry")

# Remove a user as a full access user by user's ID
experiments.full_access_users_remove(cyto_session, 22, user_id=2)

# Remove a user as a full access user by user's email
experiments.full_access_users_remove(cyto_session, 22, user_email="sammy_cytometry@cytobank.org")

# Remove a user as a full access user by user's username
experiments.full_access_users_remove(cyto_session, 22, username="sammy_cytometry")

# Dataframe of all inbox experiments with all fields present
experiments.list(cyto_session)

# Raw list of all inbox experiments with all fields present
experiments.list(cyto_session, output="raw")

experiments.new(cyto_session, "My New Experiment Name", "My experiment purpose",
               "An optional comment")

experiments.show(cyto_session, 22)

experiments.trash(cyto_session, 22)

experiments.update(cyto_session, experiment=cyto_experiment)

```

fcs_files

FCS File Endpoints

Description

Interact with FCS file endpoints.

Usage

```

## S4 method for signature 'UserSession'
fcs_files.download(UserSession, experiment_id,
                  fcs_file_id, directory = getwd(), timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
fcs_files.download_zip(UserSession, experiment_id,
                      fcs_files, directory = getwd(), timeout = UserSession@long_timeout)

```



```

## S4 method for signature 'UserSession'
fcs_files.file_internal_comp_show(UserSession,
  experiment_id, fcs_file_id, output = "default",
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
fcs_files.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
fcs_files.show(UserSession, experiment_id, fcs_file_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
fcs_files.upload(UserSession, experiment_id, file_path,
  output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
fcs_files.upload_zip(UserSession, experiment_id,
  file_path, output = "default", timeout = UserSession@long_timeout)

```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
fcs_file_id	integer representing an FCS file ID
directory	character representing a specific directory to which the file will be downloaded (optional ending directory slash), if left empty, the default will be the current working directory [optional]
timeout	integer representing the request timeout time in seconds [optional]
fcs_files	vector/list of integers representing a list of FCS file IDs
output	character representing the output format [optional] - <i>fcs_files.file_internal_comp_show</i> : ("default", "dataframe", "raw") - <i>fcs_files.list, fcs_files.show, fcs_files.upload, fcs_files.upload_zip</i> : ("default", "raw") - dataframe: <i>converts the file internal compensation matrix output to a dataframe</i>
file_path	character representing a file path

Details

`fcs_files.download` Download an FCS file from an experiment.

`fcs_files.download_zip` Download all or a select set of FCS files as a zip file from an experiment.

`fcs_files.file_internal_comp_show` Show FCS file internal compensation (aka spillover matrix, spill matrix, spill string) details from an experiment.

- *Optional output parameter, specify one of the following*: ("default", "dataframe", "raw")

`fcs_files.list` List all FCS files from an experiment. Outputs a dataframe [default] or raw full list with all fields present.

- *Optional output parameter, specify one of the following: ("default", "raw")*

`fcs_files.show` Show FCS file details from an experiment. - *Optional output parameter, specify one of the following: ("default", "raw")*

`fcs_files.upload` Upload an FCS file to an experiment. - *Optional output parameter, specify one of the following: ("default", "raw")*

`fcs_files.upload_zip` Upload a zip of FCS file(s) to an experiment. - *Optional output parameter, specify one of the following: ("default", "raw")*

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rock!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# Download an FCS file to the current working directory
fcs_files.download(cyto_session, 22, fcs_file_id=2)

# Download an FCS file to a new directory
fcs_files.download(cyto_session, 22, fcs_file_id=2, directory="/my/new/download/directory/")

# Download all files, to the current directory
fcs_files.download_zip(cyto_session, 22)

# Download specific files, to a new directory
fcs_files.download_zip(cyto_session, 22, fcs_files=c(22, 23, 24, 25),
  directory="/my/new/download/directory/")

# List of a file internal compensation, containing a file internal compensation matrix
fcs_files.file_internal_comp_show(cyto_session, 22, fcs_file_id=2)

# Dataframe only of a file internal compensation
fcs_files.file_internal_comp_show(cyto_session, 22, fcs_file_id=2, output="dataframe")

# Raw list of a file internal compensation
fcs_files.file_internal_comp_show(cyto_session, 22, fcs_file_id=2, output="raw")

# Dataframe of all FCS files with all fields present
fcs_files.list(cyto_session, 22)

# Raw list of all FCS files with all fields present
fcs_files.list(cyto_session, 22, output="raw")

fcs_files.show(cyto_session, 22, fcs_file_id=2)

fcs_files.upload(cyto_session, 22, file_path="/path/to/my_fcs_file.fcs")

fcs_files.upload_zip(cyto_session, 22, file_path="/path/to/my_fcs_files.zip")
```

Description

Interact with gate endpoints. In Cytobank there is a distinction between gates and populations. A gate is simply a shape drawn on a plot. A [population](#) is a set of gates and can have parents and children. [Learn more about gates and populations](#). Currently gate and population information can only be read and not written to Cytobank via the JSON API. To write gates and populations to Cytobank via the API, the `gates.gatingML_upload` endpoint should be used.

Usage

```
## S4 method for signature 'UserSession'
gates.gatingML_download(UserSession, experiment_id,
  directory = getwd(), timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
gates.gatingML_upload(UserSession, experiment_id,
  file_path, timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
gates.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
gates.show(UserSession, experiment_id, gate_id,
  output = "default", timeout = UserSession@short_timeout)
```

Arguments

<code>UserSession</code>	Cytobank <code>UserSession</code> object
<code>experiment_id</code>	integer representing an experiment ID
<code>directory</code>	character representing a specific directory to which the file will be downloaded (optional ending directory slash), if left empty, the default will be the current working directory [optional]
<code>timeout</code>	integer representing the request timeout time in seconds [optional]
<code>file_path</code>	character representing a file path
<code>output</code>	character representing the output format [optional] - <code>gates.list</code> , <code>gates.show</code> : ("default", "raw")
<code>gate_id</code>	integer representing a gate ID

Details

`gates.gatingML_download` Download the gatingML from an experiment. [Learn more about Gating-ML.](#)

`gates.gatingML_upload` Upload a gatingML to an experiment. [Learn more about Gating-ML.](#)

`gates.list` List all gates from an experiment. Outputs a dataframe [default] or raw list with all fields present. Currently only the Scratch Gates from the gating interface are returned. These have a version of -1. This is to be contrasted with Experiment Gates, which will have a version number that is a positive integer equal to the number of times the version has been incremented in the gating interface. [Learn more about gate versioning in Cytobank.](#)

- *Optional output parameter, specify one of the following:* ("default", "raw")

`gates.show` Show gate details from an experiment.

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

gates.gatingML_download(cyto_session, 22, directory="/my/new/download/directory/")

gates.gatingML_upload(cyto_session, 22, file_path="/path/to/my_gatingML.xml")

# Dataframe of all gates with all fields present
gates.list(cyto_session, 22)

# Raw list of all gates with all fields present
gates.list(cyto_session, 22, output="raw")

gates.show(cyto_session, 22, gate_id=2)
```

 helper_functions

Helper Functions

Description

Various helper functions to utilize within the Cytobank API.

Usage

```
helper.filter_names_to_ids_from_df(ids_names_df, names_array = c("*"))

helper.channel_ids_from_long_names(panels_list, long_channel_names,
  fcs_files = c())
```

Arguments

<code>ids_names_df</code>	dataframe containing both IDs and their associated names
<code>names_array</code>	vector or list of character regular expressions to use
<code>panels_list</code>	list provided from the panels.list endpoint
<code>long_channel_names</code>	vector of character representing long channel names
<code>fcs_files</code>	vector of integers representing a list of FCS file IDs

Details

`helper.filter_names_to_ids_from_df` Compile a vector of IDs from an array of regular expressions.

`helper.channel_ids_from_long_names` Compile a vector of IDs based on long channel names for specific FCS files from an experiment. If no FCS files are provided, IDs will be retrieved based on unique short channel / long channel combinations across all FCS files.

Examples

```
helper.filter_names_to_ids_from_df(id_and_names_dataframe, names_list=c("CD.*", "Time", "pp38"))

helper.channel_ids_from_long_names(panels.list(cyto_session, 22),
  long_channel_names=c("long_channel1", "long_channel2"), fcs_files=c(1,2,3,4,5))
```

news

News

Description

Get news on CytobankAPI updates

Usage

```
CytobankAPI_news()
```

Details

`CytobankAPI_news` View a log of CytobankAPI updates and release notes.

panels

Panel Endpoints

Description

Interact with panel endpoints. A collection of channels, the markers being studied on them, and the FCS files this applies to form a panel. [Learn more about panels in Cytobank.](#)

Usage

```
## S4 method for signature 'UserSession'
panels.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
panels.show(UserSession, experiment_id, panel_id,
  output = "default", timeout = UserSession@short_timeout)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
output	character representing the output format [optional] - <i>panels.list, panels.show</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds [optional]
panel_id	integer representing a panel ID

Details

`panels.list` List all panels from an experiment. Outputs a formatted list [default] or raw list with all fields present.

- *Optional output parameter, specify one of the following: ("default", "raw")*

`panels.show` Show panel details from an experiment. Outputs a full list with all fields present, or an IDs/names list (See [attachments](#) examples section for IDs/names list example).

- *Optional output parameter, specify one of the following: ("default", "raw")*

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# Full panel list with all fields present, with a dataframe of channels
panels.list(cyto_session, 22)
```

```
# Raw list of all panels with all fields present
panels.list(cyto_session, 22, output="raw")

# Full panel info with all fields present
panels.show(cyto_session, 22, panel_id=2)
```

populations	<i>Population Endpoints</i>
-------------	-----------------------------

Description

Interact with population (aka gate sets) endpoints. A population is a set of [gates](#) and can have parents and children. [Learn more about gates and populations.](#)

Usage

```
## S4 method for signature 'UserSession'
populations.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
populations.show(UserSession, experiment_id,
  population_id, output = "default", timeout = UserSession@short_timeout)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
output	character representing the output format [optional] - <i>populations.list, populations.show</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds
population_id	integer representing a population ID

Details

`populations.list` List all populations from an experiment. Outputs a dataframe [default] or raw list with all fields present.

- *Optional output parameter, specify one of the following: ("default", "raw")*

`populations.show` Show population details from an experiment. - *Optional output parameter, specify one of the following: ("default", "raw")*

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# Dataframe of all populations with all fields present
populations.list(cyto_session, 22)

# Raw list of all populations with all fields present
populations.list(cyto_session, 22, output="raw")

populations.show(cyto_session, 22, population_id=2)
```

sample_tags

Sample Tag Endpoints

Description

Interact with sample tag endpoints. Download and upload sample tags to save time during the annotation process. [Learn more about sample tags here.](#)

Usage

```
## S4 method for signature 'UserSession'
sample_tags.download(UserSession, experiment_id,
  directory = getwd(), timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
sample_tags.upload(UserSession, experiment_id,
  file_path, timeout = UserSession@long_timeout)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
directory	character representing a specific directory to which the file will be downloaded (optional ending directory slash), if left empty, the default will be the current working directory [optional]
timeout	integer representing the request timeout time in seconds
file_path	character representing a file path

Details

sample_tags.download Download the sample tags from an experiment.

sample_tags.upload Upload sample tag annotation data TSV to an experiment.

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# Download the experiment sample tags TSV to the current working directory
sample_tags.download(cyto_session, 22)

# Download the experiment sample tags TSV to a new directory
sample_tags.download(cyto_session, 22, directory="/my/new/download/directory/")

sample_tags.upload(cyto_session, 22, file_path="/path/to/my_annotations.tsv")
```

scales

Scale Endpoints

Description

Interact with scale endpoints. Data are rarely presented exactly as they were acquired on the instrument. [Learn more about data scaling.](#)

Usage

```
## S4 method for signature 'UserSession'
scales.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
scales.show(UserSession, experiment_id, scale_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
scales.update(UserSession, scale, output = "default",
  timeout = UserSession@short_timeout)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
output	character representing the output format [optional] - <i>scales.list</i> , <i>scales.show</i> , <i>scales.update</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds
scale_id	integer representing a scale ID
scale	dataframe representing a scale

Details

`scales.list` List all scales from an experiment. Outputs a dataframe [default] or raw list with all fields present.

- *Optional output parameter, specify one of the following:* ("default", "raw")

`scales.show` Show scale details from an experiment. - *Optional output parameter, specify one of the following:* ("default", "raw")

`scales.update` Update a single scale from an experiment. (all parameters are optional, except for `experiment_id` and `scale_id`)

- *Scale Types* – 1: Linear, 2: Log, 4: Arcsinh

- *Optional output parameter, specify one of the following:* ("default", "raw")

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# Dataframe of all scales with all fields present
scales.list(cyto_session, 22)

# Raw list of all scales with all fields present
scales.list(cyto_session, 22, output="raw")

scales.show(cyto_session, 22, scale_id=2)

# Update any number of parameters (scale_type, cofactor, minimum, maximum)
# Scale Types -- 1: Linear, 2: Log, 4: Arcsinh
scales.update(cyto_session, scale=cyto_scale)
```

 spade

SPADE Endpoints

Description

Interact with SPADE advanced analyses using these endpoints.

Usage

```
## S4 method for signature 'UserSession,SPADE'
spade.bubbles_export(UserSession, spade, bubbles,
  output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession,SPADE'
spade.bubbles_set(UserSession, spade, bubbles,
  output = "default", timeout = UserSession@long_timeout)
```

```
## S4 method for signature 'UserSession,SPADE'  
spade.bubbles_show(UserSession, spade,  
  output = "default", timeout = UserSession@short_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.copy_results(UserSession, spade,  
  output = "default", timeout = UserSession@short_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.copy_settings(UserSession, spade,  
  output = "default", timeout = UserSession@short_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.delete(UserSession, spade,  
  timeout = UserSession@short_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.download_all(UserSession, spade,  
  directory = getwd(), timeout = UserSession@long_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.download_clusters_table(UserSession, spade,  
  directory = getwd(), timeout = UserSession@long_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.download_global_boundaries_table(UserSession,  
  spade, directory = getwd(), timeout = UserSession@long_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.download_gml(UserSession, spade,  
  directory = getwd(), timeout = UserSession@long_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.download_layout_table(UserSession, spade,  
  directory = getwd(), timeout = UserSession@long_timeout)  
  
## S4 method for signature 'UserSession,SPADE'  
spade.download_statistics_tables(UserSession,  
  spade, directory = getwd(), timeout = UserSession@long_timeout)  
  
## S4 method for signature 'UserSession'  
spade.list(UserSession, experiment_id,  
  output = "default", timeout = UserSession@short_timeout)  
  
## S4 method for signature 'UserSession'  
spade.new(UserSession, experiment_id, spade_name,
```

```

    timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession,SPADE'
spade.rename(UserSession, spade, spade_name,
             timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,SPADE'
spade.run(UserSession, spade,
          output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
spade.show(UserSession, experiment_id, spade_id,
           timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,SPADE'
spade.status(UserSession, spade,
             output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession,SPADE'
spade.update(UserSession, spade,
             timeout = UserSession@long_timeout)

```

Arguments

UserSession	Cytobank UserSession object
spade	Cytobank SPADE object
bubbles	vector/list of characters representing bubbles within a SPADE analysis, learn more about SPADE bubbles
output	character representing the output format [optional] - <i>spade.list</i> , <i>spade.run</i> , <i>spade.status</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds [optional]
directory	character representing a specific directory (optional ending directory slash), default will be current working directory [optional]
experiment_id	integer representing an experiment ID
spade_name	character representing a new SPADE name
spade_id	integer representing a SPADE ID

Details

`spade.bubbles_export` Export SPADE advanced analysis bubbles from an experiment to a new experiment.

`spade.bubbles_set` Set SPADE advanced analysis bubbles from an experiment.

`spade.bubbles_show` Show SPADE advanced analysis bubbles from an experiment.

`spade.copy_results` Copy SPADE advanced analysis results from an experiment to a new experiment.

`spade.copy_settings` Copy SPADE advanced analysis settings from an experiment.
`spade.delete` Delete a SPADE advanced analysis from an experiment.
`spade.download_all` Download a SPADE advanced analysis with all data included from an experiment.
`spade.download_clusters_table` Download a SPADE advanced analysis global clusters table from an experiment.
`spade.download_global_boundaries_table` Download a SPADE advanced analysis global boundaries table from an experiment.
`spade.download_gml` Download a SPADE advanced analysis GML from an experiment.
`spade.download_layout_table` Download a SPADE advanced analysis layout table from an experiment.
`spade.download_statistics_tables` Download a SPADE advanced analysis statistics table from an experiment.
`spade.list` List all SPADE advanced analyses from an experiment. Outputs a dataframe [default] or list with all fields present.
- Optional output parameter, specify one of the following: ("default", "raw")
`spade.new` Create a new SPADE advanced analysis from an experiment and returns a SPADE object.
`spade.rename` Rename a SPADE advanced analysis from an experiment and returns a SPADE object.
`spade.run` Run a SPADE advanced analysis from an experiment.
`spade.show` Show SPADE advanced analysis details from an experiment and returns a SPADE object.
`spade.status` Show the status of a SPADE advanced analysis from an experiment.
`spade.update` Update a SPADE advanced analysis from an experiment and returns the new SPADE object.

Examples

```

# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# cyto_spade refers to a SPADE object that is created from SPADE endpoints
# examples: spade.new, spade.show (see details section for more)

spade.bubbles_export(cyto_session, spade=cyto_spade, bubbles=c("bubble1", "bubble2"))

named_bubble_list_of_node_vectors <- list("bubble_1"=c(1,2,4), "bubble_2"=8, "bubble_4"=c(10,12))
spade.bubbles_set(cyto_session, spade=cyto_spade, bubbles=named_bubble_list_of_node_vectors)

spade.bubbles_show(cyto_session, spade=cyto_spade)

spade.copy_results(cyto_session, spade=cyto_spade)
  
```

```
spade.copy_settings(cyto_session, spade=cyto_spade)

spade.delete(cyto_session, spade=cyto_spade)

spade.download_all(cyto_session, spade=cyto_spade, directory="/my/new/download/directory/")

spade.download_clusters_table(cyto_session, spade=cyto_spade,
  directory="/my/new/download/directory/")

spade.download_global_boundaries_table(cyto_session,
  spade=cyto_spade, directory="/my/new/download/directory/")

spade.download_gml(cyto_session, spade=cyto_spade, directory="/my/new/download/directory/")

spade.download_layout_table(cyto_session, spade=cyto_spade, directory="/my/new/download/directory/")

spade.download_statistics_tables(cyto_session, spade=cyto_spade,
  directory="/my/new/download/directory/")

# Dataframe of all SPADE advanced analyses with all fields present
spade.list(cyto_session, 22)

# Raw list of all SPADE advanced analyses with all fields present
spade.list(cyto_session, 22, output="raw")

spade.new(cyto_session, 22, spade_name="My new SPADE analysis")

spade.rename(cyto_session, spade=cyto_spade, spade_name="My updated SPADE name")

spade.run(cyto_session, spade=cyto_spade)

spade.show(cyto_session, 22, spade_id=2)

spade.status(cyto_session, spade=cyto_spade)

spade.update(cyto_session, spade=cyto_spade)
```

SPADE-class

S4 SPADE Class

Description

A SPADE object that holds pertinent SPADE advanced analysis run information. This class should never be called explicitly. If a user would like to create a new Cytobank SPADE object, utilize the [spade.new](#) function, or any other [SPADE endpoints that return SPADE objects documented in the 'Details' section](#).

Value

A SPADE advanced analysis object

Slots

`created_experiment` numeric representing the experiment that gets created from the SPADE analysis

`down_sampled_events_target` numeric representing the percent OR absolute number (depends on 'down_sampled_events_type' slot) for downsampling occurring within the SPADE analysis, [learn more about SPADE density-dependent downsampling](#)

`down_sampled_events_type` character representing the downsampling type for `down_sampled_events_target`, [learn more about SPADE density-dependent downsampling types - choose one of the following](#): ("percent" [default], "absolute_number")

`fold_change_groups` dataframe representing the fold change groups within a SPADE analysis, [learn more about SPADE fold change groups](#)

`population_id` numeric representing the population to run the SPADE analysis on, [learn more about choosing a population for SPADE](#)

`spade_id` numeric representing the SPADE analysis ID

`target_number_nodes` numeric representing how many population nodes SPADE will seek out within the given data, [learn more about target number of nodes for SPADE](#)

 statistics

Statistic Endpoints

Description

Interact with statistic endpoints. Gather data about event counts and general channel statistics. Create dataframes of statistics to help with visualization and downstream analysis.

Usage

```
## S4 method for signature 'UserSession'
statistics.event_counts(UserSession, experiment_id,
  gate_version = -1, compensation_id, fcs_files, populations = c(),
  output = "dataframe", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
statistics.general(UserSession, experiment_id,
  gate_version = -1, compensation_id, fcs_files, channels,
  populations = c(), output = "dataframe_row",
  timeout = UserSession@long_timeout)
```

Arguments

`UserSession` Cytobank UserSession object

`experiment_id` integer representing an [experiment](#) ID

gate_version	integer representing an experiment gate version, an integer of -1 corresponds to the state of gates and populations in the gating interface. Faster performance can be achieved by using the maximum gate version from the experiment (learn more about gate versions). Maximum gate version can be seen as the gateVersion attribute returned from a call to the Show Experiment Details endpoint [optional]
compensation_id	integer representing a compensation ID (use -2 for file-internal compensation, -1 for uncompensated)
fcs_files	vector/list of integers representing a list of FCS file IDs
populations	vector/list of integers representing a list of population IDs to calculate statistics for. This is the gateSetId attribute of a population object. Another term for a population is a "gate set". If not specified, all population statistics will be fetched [optional]
output	character representing the output format [optional] <ul style="list-style-type: none"> - <i>statistics.event_counts</i>: ("default" [default], "dataframe") - <i>statistics.general</i>: ("default", "dataframe_col", "dataframe_row") - dataframe: <i>converts the output to a dataframe for the event count statistics</i> - dataframe_col: <i>for statistics data on multiple channels, proliferate channel statistics as columns</i> - dataframe_row: <i>for statistics data on multiple channels, proliferate channel statistics as rows</i>
timeout	integer representing the request timeout time in seconds
channels	vector/list of integers or character representing a list of channel IDs (integers) or long channel names (character)

Details

`statistics.event_counts` Get event count statistics from an experiment. In the absence of channel information, only event count data are returned. If only event count data are needed, this approach can be faster than retrieving all statistics by avoiding unnecessary computation.

- *Optional output parameter, specify one of the following:* ("full", "dataframe" [default])
- *dataframe: converts the output to a dataframe for the event count statistics*

`statistics.general` Get a batch of common statistics for specific channels on populations from an experiment.

- *Optional output parameter, specify one of the following:* ("full", "dataframe_col", "dataframe_row" [default])
- *dataframe_col: for statistics data on multiple channels, proliferate channel statistics as columns*
- *dataframe_row: for statistics data on multiple channels, proliferate channel statistics as rows*

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")
```



```

statistics.event_counts(cyto_session, 22, compensation_id=-2,
  fcs_files=c(12, 13, 14), channels=c(53, 54, 55), populations=c(32, 33, 34))

# Full list with all fields present
statistics.general(cyto_session, 22, compensation_id=-2,
  fcs_files=c(12, 13, 14), channels=c(53, 54, 55), populations=c(32, 33, 34))

# Statistics list transformed into a dataframe, proliferating channel statistics by column
statistics.general(cyto_session, 22, compensation_id=-2,
  fcs_files=c(12, 13, 14), channels=c(53, 54, 55), populations=c(32, 33), output="dataframe_col")

# Statistics list transformed into a dataframe, proliferating channel statistics by row
statistics.general(cyto_session, 22, compensation_id=-2,
  fcs_files=c(12, 13, 14), channels=c(53, 54, 55), populations=c(32, 33), output="dataframe_row")

# Statistics list transformed into a dataframe, using helper functions (names_to_ids)
# Get FCS files that match 'pbmc' in their filename
fcs_files <- fcs_files.list(cyto_session, 22)
fcs_files <- fcs_files[,c("id", "filename")]
fcs_files <- unlist(fcs_files$id[grep("pbmc", fcs_files$filename)])

# Get channels that match 'pp' or 'pStat' as their longName
channels <- panels.list(cyto_session, 22)$`Panel 1`$channels
channels <- channels[,c("normalizedShortNameId", "shortName", "longName")]
channels <- channels$normalizedShortNameId[grep("pp.*|pStat.*", channels$longName)]

# Get populations that match 'CD' as their population name
populations <- populations.list(cyto_session, 22)
populations <- populations[,c("gateSetId", "name")]
populations <- populations$id[grep("CD.*", populations$name)]

statistics.general(cyto_session, 22, compensation_id=-2,
  fcs_files=fcs_files, channels=channels, populations=populations, output="dataframe_row")

```

 users

User Endpoints

Description

Interact with user endpoints. One should never analyze alone...

Usage

```

## S4 method for signature 'UserSession'
users.list(UserSession, output = "default",
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'

```

```
users.show(UserSession, user_id, output = "default",
           timeout = UserSession@short_timeout)
```

Arguments

UserSession	Cytobank UserSession object
output	character representing the output format [optional] - <i>users.list, users.show</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds [optional]
user_id	integer representing a user ID

Details

`users.list` List all users from an experiment. Outputs a dataframe [default] or raw list with all fields present.

- *Optional output parameter, specify one of the following*: ("default", "raw")

`users.show` Show user details from an experiment. - *Optional output parameter, specify one of the following*: ("default", "raw")

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rock!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# Dataframe of all users with all fields present
users.list(cyto_session)

# Raw list of all users with all fields present
users.list(cyto_session, output="raw")

users.show(cyto_session, user_id=2)
```

UserSession-class *S4 Cytobank UserSession Class*

Description

A Cytobank UserSession object that holds pertinent user information, used to make calls to various Cytobank endpoints. This class should never be called explicitly. If a user would like to create a new Cytobank UserSession object, utilize the [authenticate](#) function.

Value

A Cytobank UserSession object

Slots

auth_token character representing Cytobank user's authentication token (expires in 8 hours)
 long_timeout numeric representing long request timeout times
 short_timeout numeric representing short request timeout times
 site character representing Cytobank user's site

Examples

```
cytobank_user <- new("UserSession", auth_token="my_auth_token", site="premium")
```

visne	<i>viSNE Endpoints</i>
-------	------------------------

Description

Interact with viSNE advanced analyses using these endpoints.

Usage

```

## S4 method for signature 'UserSession,viSNE'
visne.copy_settings(UserSession, visne,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,viSNE'
visne.delete(UserSession, visne,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
visne.list(UserSession, experiment_id,
  output = "default", timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession'
visne.new(UserSession, experiment_id, visne_name,
  timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession,viSNE'
visne.rename(UserSession, visne, visne_name,
  timeout = UserSession@short_timeout)

## S4 method for signature 'UserSession,viSNE'
visne.run(UserSession, visne,
  output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession'
visne.show(UserSession, experiment_id, visne_id,
  timeout = UserSession@short_timeout)

```

```
## S4 method for signature 'UserSession,viSNE'
visne.status(UserSession, visne,
  output = "default", timeout = UserSession@long_timeout)

## S4 method for signature 'UserSession,viSNE'
visne.update(UserSession, visne,
  timeout = UserSession@long_timeout)

visne.helper.set_populations(visne, population_id = NA, fcs_files = NA)
```

Arguments

UserSession	Cytobank UserSession object
visne	Cytobank viSNE object
output	character representing the output format [optional] - <i>visne.list</i> , <i>visne.run</i> , <i>visne.status</i> : ("default", "raw")
timeout	integer representing the request timeout time in seconds [optional]
experiment_id	integer representing an experiment ID
visne_name	character representing a new viSNE name
visne_id	integer representing a viSNE ID
population_id	integer representing a population gate set ID
fcs_files	vector/list of integers representing a list of FCS file IDs

Details

`visne.copy_settings` Copy viSNE advanced analysis settings from an experiment and returns a viSNE object.

`visne.delete` Delete a viSNE advanced analysis from an experiment.

`visne.list` List all viSNE advanced analyses from an experiment. Outputs a dataframe [default] or list with all fields present.
- *Optional output parameter, specify one of the following:* ("default", "raw")

`visne.new` Create a new viSNE advanced analysis from an experiment and returns a viSNE object.

`visne.rename` Rename a viSNE advanced analysis from an experiment and returns a viSNE object.

`visne.run` Run a viSNE advanced analysis from an experiment.

`visne.show` Show viSNE advanced analysis details from an experiment and returns a viSNE object.

`visne.status` Show the status of a viSNE advanced analysis from an experiment.

`visne.update` Update a viSNE advanced analysis from an experiment and returns the new viSNE object.

`visne.helper.set_populations` Set viSNE advanced analysis populations to be selected from an experiment and returns the new viSNE object with the new population selections. The population provided will be overwritten by the newly selected FCS files provided.

Examples

```
# Authenticate via username/password
cyto_session <- authenticate(site="premium", username="cyril_cytometry", password="cytobank_rocks!")
# Authenticate via auth_token
cyto_session <- authenticate(site="premium", auth_token="my_secret_auth_token")

# cyto_visne refers to a viSNE object that is created from viSNE endpoints
# examples: visne.new, visne.show (see details section for more)

visne.copy_settings(cyto_session, visne=cyto_visne)

visne.delete(cyto_session, visne=cyto_visne)

# Dataframe of all viSNE advanced analyses with all fields present
visne.list(cyto_session, 22)

# Raw list of all viSNE advanced analyses with all fields present
visne.list(cyto_session, 22, output="raw")

visne.new(cyto_session, 22, visne_name="My new viSNE analysis")

visne.rename(cyto_session, visne=cyto_visne, visne_name="My updated viSNE name")

visne.run(cyto_session, visne=cyto_visne)

visne.show(cyto_session, 22, visne_id=2)

visne.status(cyto_session, visne=cyto_visne)

visne.update(cyto_session, visne=cyto_visne)

visne.helper.set_populations(visne=cyto_visne, population_id=1, fcs_files=c(1,2,3))
```

viSNE-class

S4 viSNE Class

Description

A viSNE object that holds pertinent viSNE advanced analysis run information. This class should never be called explicitly. If a user would like to create a new Cytobank viSNE object, utilize the [visne.new](#) function, or any other [viSNE endpoints that return viSNE objects documented in the 'Details' section](#).

Value

A viSNE advanced analysis object

Slots

- `created_experiment` numeric representing the experiment that gets created from the viSNE analysis
- `iterations` numeric representing the number of times viSNE processes the dataset using its step-wise optimization algorithm, [learn more about how iterations affect viSNE results](#)
- `perplexity` dataframe representing a rough guess for the number of close neighbors any given cellular event will have, [learn more about viSNE perplexity](#)
- `population_selections` dataframe representing which population(s) data will be sourced, [learn more about selecting populations for viSNE](#)
- `visne_id` numeric representing the viSNE analysis ID
- `sampling_total_count` numeric representing the total number of events to sample for the viSNE analysis
- `sampling_target_type` character representing the event sampling type
- choose one of the following : ("proportional", "equal")
- `seed` character representing the seed, viSNE picks a random seed each run, but if users want reproducible data, setting the same seed will allow them to do this
- `theta` numeric representing the balance of speed and accuracy in the viSNE run compared to the original tSNE algorithm, [learn more about viSNE theta](#)

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