

Package ‘CytobankBridgeR’

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Title Bridging and Extending the CytobankAPI Package in R to the
Cytobank Web Application

Version 1.0.0

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Description A collection of tools that leverage the CytobankAPI R package <<https://cran.r-project.org/web/packages/CytobankAPI/vignettes/cytobank-quickstart.html>> to complete more complex workflows, and add/extend various Cytobank features.

Depends CytobankAPI (>= 1.0.0), stats

License Artistic-2.0

LazyData FALSE

RoxygenNote 5.0.1

Suggests rmarkdown

NeedsCompilation no

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fcs_files.download_fcs_files_stable
FCS Files

Description

FCS File High Level Functions

Usage

```
fcs_files.download_fcs_files_stable(UserSession, experiment_id, fcs_files,  
  directory = getwd(), zip_download = TRUE, timeout = 300)
```

Arguments

UserSession	Cytobank UserSession object
experiment_id	integer representing an experiment ID
fcs_files	vector/list of integers representing a list of FCS file IDs
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]
zip_download	logical representing whether or not to download each file one by one via ZIP download [default] or normal FCS download [optional]
timeout	integer representing the request timeout time in seconds [optional]

Details

fcs_files.download_fcs_files_stable Apply cluster gate(s) to specific clusters via an integer vector

Examples

```
fcs_files.download_fcs_files_stable(cyto_session, 22, fcs_files=c(1,2,3),  
  directory="/my/new/download/directory/")  
  
# 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.apply_cluster_gates
Gates

Description

Gates High Level Functions

Usage

```
gates.apply_cluster_gates(UserSession, experiment_id, name, clusters,
    channel_name, integer_min = 1, integer_max = max(clusters),
    grouped = FALSE, timeout = 60)
```

Arguments

UserSession	Cytobank UserSession object (created via the authenticate function)
experiment_id	integer representing an experiments ID
name	character representing a cluster prefix (if grouped=FALSE) or multicluster gate name
clusters	integer vector representing the clusters to gate - There are 2 modes of operation: 1) grouped=FALSE: clusters represent individual integer clusters to gate, this will create multiple gates that represents multiple individual populations 2) grouped=TRUE: clusters represent a multi-integer cluster to gate, this will create one gate that represents one population around the integer clusters specified
channel_name	character representing the channel short name
integer_min	integer representing the minimum cluster integer for setting scales [optional] - The default is set to 1, this assumes clusters begin at 1, but can be changed if there is any +/- offset - The minimum scale will be set to integer_min-1 (0 by)
integer_max	integer representing the maximum cluster integer for setting scales [optional] - The default is the maximum number presented within the clusters vector, but can be set to any integer - The max scale will be set to integer_max+1
grouped	logical representing whether to gate a vector of integer clusters as individual integer clusters (grouped=FALSE), or together as a single multicluster (grouped=TRUE)
timeout	integer representing the request timeout time in seconds [optional]

Details

gates.apply_cluster_gates Apply cluster gate(s) to specific clusters via an integer vector

Examples

```
gates.apply_cluster_gates(cyto_session, 22, name="cluster_names",
  clusters=c(1,5,9), channel_name="cluster_id")
```

news	<i>News</i>
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Description

Get news on CytobankR updates

Usage

```
CytobankBridgeR_news()
```

Details

CytobankR_news View a log of CytobankR updates and release notes.

spade.bubble_spade_nodes	<i>SPADE</i>
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Description

SPADE High Level Functions

Usage

```
spade.bubble_spade_nodes(UserSession, spade, prefix = "cluster_")
```

Arguments

UserSession	Cytobank UserSession object (created via the authenticate function)
spade	Cytobank spade object
prefix	character representing a prefix to be used before each node number

Details

spade.bubble_spade_nodes Bubble each individual node on a SPADE tree as their own bubble, with a specific prefix.

Examples

```
# Using the prefix "bubble_" will provide bubbles in the form:
# "bubble_1", "bubble_2", "bubble_n", etc...
spade.bubble_spade_nodes(cyto_session, spade=cyto_spade, prefix="bubble_")
```

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