

Package ‘cloudos’

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Title R Client Library for CloudOS

Version 0.2.0

Description The 'CloudOS' client library for R makes it easy to interact with CloudOS <<https://cloudos.lifebit.ai/>> in the R environment for analysis.

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Encoding UTF-8

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Imports httr, utils, methods, dplyr (>= 1.0.0), jsonlite, rappdirs, ggplot2, tibble

Suggests httpptest, kableExtra, knitr, lintr, rmarkdown, testthat

URL <https://github.com/lifebit-ai/cloudos>

BugReports <https://github.com/lifebit-ai/cloudos/issues>

NeedsCompilation no

Author Sangram Keshari Sahu [aut, cre],
Lifebit Biotech Ltd. [cph]

Maintainer Sangram Keshari Sahu <sangram@lifebit.ai>

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<code>.get_search_json</code>	<i>only used for v1 endpoint - creates v1 search json using the v2 style query</i>
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Description

only used for v1 endpoint - creates v1 search json using the v2 style query

Usage

```
.get_search_json(my_cohort)
```

Arguments

<code>my_cohort</code>	A cohort object
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<code>.v1_query_to_v2</code>	<i>Convert a v1 style query (moreFields) to v2 style (query). v2 queries are a superset of v1 queries. A list of v1 phenotype queries are equivalent to a set of nested v2 AND operators containing those phenotypes. This function builds the nested AND query from the flat list of v1 phenotypes.</i>
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Description

Convert a v1 style query (moreFields) to v2 style (query). v2 queries are a superset of v1 queries. A list of v1 phenotype queries are equivalent to a set of nested v2 AND operators containing those phenotypes. This function builds the nested AND query from the flat list of v1 phenotypes.

Usage

```
.v1_query_to_v2(cohort_more_fields)
```

Arguments

cohort_more_fields
query information ('moreFields') from `.get_cohort_info(cohort_id, cb_version="v1)`

cb_apply_filter_dry_run
Dry run for [cb_apply_query](#)

Description

This doesn't update the database but mimics [cb_apply_query](#)

Usage

```
cb_apply_filter_dry_run(cohort, simple_query)
```

Arguments

cohort A cohort object. (Required) See constructor function [cb_create_cohort](#) or [cb_load_cohort](#)

simple_query A phenotype query using the "simple query" list structure (see [cb_apply_query](#)).

Value

A data frame.

Examples

```
## Not run:  
my_cohort <- cb_load_cohort(cohort_id = "5f9af3793dd2dc6091cd17cd")  
cb_apply_filter_dry_run(my_cohort,  
  simple_query = list("22" = list("from" = "2015-05-13", "to" = "2016-04-29"),  
    "50" = c("Father", "Mother")) )  
  
## End(Not run)
```

cb_apply_query	<i>Apply a query to a cohort</i>
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Description

Updates a cohort by applying a new query.

Usage

```
cb_apply_query(
  cohort,
  simple_query,
  adv_query,
  column_ids,
  keep_query = TRUE,
  keep_columns = TRUE
)
```

Arguments

cohort	A cohort object. (Required) See constructor function cb_create_cohort or cb_load_cohort
simple_query	A phenotype query using the "simple query" list structure (see example).
adv_query	A phenotype query using the "advanced query" nested list structure (see example). Advanced queries can include logical operators: 'AND', 'OR', 'NOT'.
column_ids	Phenotype IDs to be added as columns in the participant table.
keep_query	If True, combines the newly supplied query with the pre-existing query. Otherwise, pre-existing query is overwritten. (Default: TRUE)
keep_columns	If True, pre-existing columns are retained and newly supplied columns are added. Otherwise, pre-existing columns are overwritten. (Default: TRUE)

Value

A confirmation string.

Examples

```
## Not run:
my_cohort <- cb_load_cohort(cohort_id = "5f9af3793dd2dc6091cd17cd", cb_version = "v1")
cb_apply_query(my_cohort,
  simple_query = list("22" = list("from" = "2015-05-13", "to" = "2016-04-29"),
    "50" = c("Father", "Mother")) )

my_cohort <- cb_load_cohort(cohort_id = "5f9af3793dd2dc6091cd17cd", cb_version = "v2")
adv_query <- list(
  "operator" = "AND",
  "queries" = list(
```

```

    list("id" = 22, "value" = list("from"="2015-05-13", "to"="2016-04-29")),
  list(
    "operator" = "OR",
    "queries" = list(
      list("id" = 32, "value" = c("Cancer", "Rare Diseases")),
      list("id" = 14, "value" = "Yes")
    )
  )
)
)
)
cb_apply_query(my_cohort, adv_query = adv_query)

## End(Not run)

```

cb_create_cohort	<i>Create Cohort</i>
------------------	----------------------

Description

Creates a new Cohort

Usage

```
cb_create_cohort(cohort_name, cohort_desc, filters = "", cb_version = "v2")
```

Arguments

cohort_name	New cohort name to be created. (Required)
cohort_desc	New cohort description to be created. (Optional)
filters	WIP - details will be added.
cb_version	cohort browser version. ["v1" "v2"] (Optional) Default - "v2"

Value

A [cohort](#) object.

See Also

[cb_load_cohort](#) for loading a available cohort.

Examples

```

## Not run:
my_cohort <- cb_create_cohort(cohort_name = "Cohort-R",
                             cohort_desc = "This cohort is for testing purpose, created from R.")

## End(Not run)

```

cb_extract_samples *Extract participants - WIP*

Description

Extracts selected participants.

Usage

```
cb_extract_samples(raw_data)
```

Arguments

raw_data A JSON string for selected participants. (Required)

Value

A dataframe.

cb_get_cohort_phenotypes
Get data for phenotypes associated with a cohort

Description

Get a dataframe with distribution data for each phenotype associated with a cohort. Associated phenotypes are those found in the "Overview" section of the Cohort Browser Web UI.

Usage

```
cb_get_cohort_phenotypes(cohort)
```

Arguments

cohort A cohort object. (Required) See constructor function [cb_create_cohort](#) or [cb_load_cohort](#)

Value

A list of data frames.

`cb_get_genotypic_table`*Get genotypic table*

Description

Get Genotypic table in a dataframe. Optionally genotypic filters can be applied as well.

Usage

```
cb_get_genotypic_table(cohort, size = 10, geno_filters_query)
```

Arguments

cohort	A cohort object. (Required) See constructor functions cb_create_cohort or cb_load_cohort
size	Number of entries from database. (Optional) Default - 10 (Optional)
geno_filters_query	Genotypic filter query (Optional)

Value

A dataframe.

`cb_get_participants_table`*Get participant data table*

Description

Get participant data table in a dataframe.

Usage

```
cb_get_participants_table(cohort, page_number = 0, page_size = 10)
```

Arguments

cohort	A cohort object. (Required) See constructor functions cb_create_cohort or cb_load_cohort
page_number	Number of page. (Optional) Default - 0
page_size	Number of entries in a page. (Optional) Default - 10

Value

A dataframe.

`cb_get_phenotype_metadata`*Phenotype metadata*

Description

Get the metadata of a phenotype in the cohort browser

Usage

```
cb_get_phenotype_metadata(pheno_id, cb_version = "v2")
```

Arguments

<code>pheno_id</code>	A phenotype ID. (Required)
<code>cb_version</code>	cohort browser version. (Default: "v2") ["v1" "v2"]

Value

A data frame.

`cb_get_phenotype_statistics`*Get distribution of a phenotype in a cohort*

Description

Retrieve a data frame containing the distribution data for a specific phenotype within a cohort.

Usage

```
cb_get_phenotype_statistics(cohort, pheno_id)
```

Arguments

<code>cohort</code>	A cohort object. (Required) See constructor function cb_create_cohort or cb_load_cohort
<code>pheno_id</code>	A phenotype ID. (Required)

Value

A data frame holding distribution data.

cb_list_cohorts	<i>List cohorts</i>
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Description

Extracts the data frame with limited cohort data columns.

Usage

```
cb_list_cohorts(size = 10, cb_version = "v2")
```

Arguments

size	Number of cohort entries from database. (Optional) Default - 10
cb_version	cohort browser version. ["v1" "v2"] (Optional) Default - "v2"

Value

A data frame with available cohorts.

Examples

```
## Not run:  
cohorts_list()  
  
## End(Not run)
```

cb_load_cohort	<i>Get cohort information</i>
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Description

Get all the details about a cohort including applied query.

Usage

```
cb_load_cohort(cohort_id, cb_version = "v2")
```

Arguments

cohort_id	Cohort id (Required)
cb_version	cohort browser version (Optional) ["v1" "v2"]

Value

A [cohort](#) object.

See Also

[cb_create_cohort](#) for creating a new cohort.

cb_participant_count *Participant Count*

Description

Returns the number of participants in a cohort if the supplied query were to be applied.

Usage

```
cb_participant_count(cohort, simple_query, adv_query, keep_query = TRUE)
```

Arguments

cohort	A cohort object. (Required) See constructor function cb_create_cohort or cb_load_cohort
simple_query	A phenotype query using the "simple query" list structure (see cb_apply_query).
adv_query	A phenotype query using the "advanced query" nested list structure (see cb_apply_query).
keep_query	Apply newly specified query on top of existing query (Default: TRUE)

Value

A list with count of participants in the cohort and the total no. of participants in the dataset.

cb_plot_filters *Plot filters*

Description

Get a list of ggplot objects, each plot having one filter.

Usage

```
cb_plot_filters(cohort)
```

Arguments

cohort	A cohort object. (Required) See constructor function cb_create_cohort or cb_load_cohort
--------	---

Value

A list of ggplot objects

Examples

```
## Not run:
my_cohort <- cb_load_cohort(cohort_id = "5f9af3793dd2dc6091cd17cd")
plot_list <- cb_plot_filters(cohort = my_cohort)

plot_list[[1]]

library(ggpubr)
ggpubr::ggarrange(plotlist = plot_list)

## End(Not run)
```

cb_search_phenotypes *Search available phenotypes*

Description

Search for phenotypes in the Cohort Browser that match your term and return a tibble containing the metadata information for each matching phenotype. Use 'term = ""' to return all phenotypes.

Usage

```
cb_search_phenotypes(term, cb_version = "v2")
```

Arguments

term	A term to search. (Required)
cb_version	cohort browser version (Optional) ["v1" "v2"]

Value

A tibble with phenotype metadata

Examples

```
## Not run:
cancer_phenos <- cb_search_phenotypes(term = "cancer")

all_phenos <- cb_search_phenotypes(term = "")

## End(Not run)
```

cloudos_configure	<i>Configure cloudos</i>
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Description

On a system for the first time the cloudos configuration needed to be done. This function can help do that.

Usage

```
cloudos_configure(base_url, token, team_id)
```

Arguments

base_url	Base URL for cloudos
token	API key or token
team_id	team/workspace ID

Value

None

cloudos_whoami	<i>whoami</i>
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Description

To check the current configuration

Usage

```
cloudos_whoami()
```

Value

None

cohort-class	<i>cohort class</i>
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Description

This class creates a cohort object, which holds the information related to a cohort: cohort ID, name, description, query, table columns. This class is used in functions which carry out operations related to specific cohorts. A cohort class object can be created using constructor functions [cb_create_cohort](#) or [cb_load_cohort](#).

Slots

id cohort ID.

name cohort name.

desc cohort description.

phenotype_filters phenotypes displayed in the cohort overview.

query applied query.

columns All the columns

cb_version cohort browser version

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