Package ‘clinicalomicsdbR’

June 26, 2024

Title Interface with the 'ClinicalOmicsDB' API, Allowing for Easy Data Downloading and Importing

Version 1.0.5

Description Provides an interface to the 'ClinicalOmicsDB' API, allowing for easy data downloading and importing. 'ClinicalOmicsDB' is a database of clinical and 'omics' data from cancer patients. The database is accessible at <`http://trials.linkedomics.org`>.

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Encoding UTF-8

RoxygenNote 7.3.1

Imports httr2, R6, dplyr, utils, jsonlite

BugReports `https://github.com/bzhanglab/clinicalomicsdbR/issues`

URL `https://github.com/bzhanglab/clinicalomicsdbR`

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-06-26 12:50:05 UTC

Contents

`clinicalomicsdbR` *clinicalomicsdbR object*

Description

clinicalomicsdbR object

clinicalomicsdbR object

Value

Returns a new clinicalomicsdbR object

Public fields

`hostname` The url of the API to connect to. Only change if you are using a custom service.

`study_list` The list of all the studies that are a result of filtering.

`verbosity` The level of messages wanted for downloads (defaults to 0: No Output). Follows httr2 documentatation for `req_perform`

Methods

Public methods:

- `clinicalomicsdbR$filter()`
- `clinicalomicsdbR$get_download_url()`
- `clinicalomicsdbR$download()`
- `clinicalomicsdbR$download_from_id()`
- `clinicalomicsdbR$dataframe()`
- `clinicalomicsdbR$dataframe_from_id()`
- `clinicalomicsdbR$clone()`

Method `filter()`**:** filter objects according to the specified drugs and cancers

Usage:

```
clinicalomicsdbR$filter(drugs = c(), cancers = c())
```

Arguments:

`drugs` list or vector containing drugs that studies need to contain at least one of

`cancers` list of vector of cancer types to consider. Leave empty to consider all cancer types

Returns: new clinicalomicsdbR object with the filtered results in `$study_list`

Method `get_download_url()`**:** Get download url for a study at specified `study_id`

Usage:

```
clinicalomicsdbR$get_download_url(study_id)
```

Arguments:

`study_id` String of the ID of the study to get the download url of

Returns: String of the download url

Method `download()`**:** Download all files of the studies in `self$study_list`. Use `filter` function first

Usage:

```
clinicalomicsdbR$download(output_dir)
```

Arguments:

`output_dir` Directory to download files to.

Returns: unmodifed clinicalomicsdbR object

Method `download_from_id()`**:** Download all file from `study_id` into `output_dir` directory

Usage:

```
clinicalomicsdbR$download_from_id(study_id)
```

Arguments:

`study_id` String containing the ID of the study to download

`output_dir` Directory to download files to.

Returns: unmodifed clinicalomicsdbR object

Method `dataframe()`**:** Get all files of the studies in `self$study_list` and load into data frame. Use `filter` function first.

Usage:

```
clinicalomicsdbR$dataframe()
```

Returns: list with `study_list` element to display all studies and list `df` with each dataframe in the list

Method `dataframe_from_id()`**:** Get file from `study_id` and convert into dataframe.

Usage:

```
clinicalomicsdbR$dataframe_from_id(study_id)
```

Arguments:

`study_id` String containing the ID of the study to get dataframe of

Returns: data frame containing data of study

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
clinicalomicsdbR$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
clinicalomicsdbR$new()$filter(drugs = c("ipilimumab", "rituximab"))$study_list # downloads all files
```

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