

Package ‘PhenotypeLibrary’

August 24, 2023

Type Package

Title The OHDSI Phenotype Library

Version 3.17.0

Date 2023-08-23

Author Gowtham Rao [aut, cre]

Maintainer Gowtham Rao <rao@ohdsi.org>

Description A repository to store the content of the OHDSI Phenotype library.

Imports checkmate,
readr,
dplyr,
rlang

Suggests reactable,
testthat,
knitr

License Apache License

RoxygenNote 7.2.3

Roxygen list(markdown = TRUE)

Encoding UTF-8

Language en-US

VignetteBuilder knitr

URL <https://ohdsi.github.io/PhenotypeLibrary/>, <https://github.com/OHDSI/PhenotypeLibrary>

BugReports <https://github.com/OHDSI/PhenotypeLibrary/issues>

R topics documented:

getPhenotypeLog	2
getPICohortDefinitionSet	2
listPhenotypes	3

Index	4
-------	---

getPhenotypeLog	<i>Get phenotype log</i>
-----------------	--------------------------

Description

Get phenotype log

Usage

```
getPhenotypeLog(cohortIds = listPhenotypes())$cohortId)
```

Arguments

cohortIds IDs of cohorts to extraction from the library.

Value

Returns a table with one row per cohort definitions with log information such as its release cycle. Example, this function gives us insight on when a cohort definition was added/updated/deprecated by the OHDSI PhenotypeLibrary.

A tibble.

Examples

```
getPhenotypeLog(cohortIds = c(1, 2))
```

getPlCohortDefinitionSet	<i>Get a cohort definition set</i>
--------------------------	------------------------------------

Description

Get a cohort definition set

Usage

```
getPlCohortDefinitionSet(cohortIds)
```

Arguments

cohortIds IDs of cohorts to extraction from the library.

Value

A tibble with the cohort ID, name, sql, and JSON for the provided cohort IDs. Can be used by the CohortGenerator package.

Examples

```
cohorts <- listPhenotypes()
subsetIds <- cohorts$cohortId[1:3]
getPlCohortDefinitionSet(subsetIds)
```

`listPhenotypes`*List all phenotypes in the library*

Description

List all phenotypes in the library

Usage

```
listPhenotypes()
```

Value

A tibble with the cohort ID and name.

Examples

```
listPhenotypes()
```

Index

`getPhenotypeLog`, [2](#)
`getPlCohortDefinitionSet`, [2](#)
`listPhenotypes`, [3](#)