Package 'PhenotypeLibrary'

December 5, 2022

Type Package
Title The OHDSI Phenotype library
Version 3.7.0
Date 2022-12-05
Author Gowtham Rao [aut, cre]
Maintainer Gowtham Rao <rao@ohdsi.org></rao@ohdsi.org>
Description A repository to store the content of the OHDSI Phenotype library.
Imports checkmate, readr, dplyr, rlang, stringr,
tidyr Suggests DatabaseConnector, reactable, testthat, rmarkdown, knitr
License Apache License
RoxygenNote 7.2.2
Roxygen list(markdown = TRUE)
Encoding UTF-8
Language en-US
VignetteBuilder knitr
<pre>URL https://ohdsi.github.io/PhenotypeLibrary/, https: //github.com/OHDSI/PhenotypeLibrary</pre>
<pre>BugReports https://github.com/OHDSI/PhenotypeLibrary/issues</pre>
R topics documented:
getPhenotypeLog getPlCohortDefinitionSet listPhenotypes updatePhenotypeLog
Index

 ${\tt getPhenotypeLog}$

Get phenotype log

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
```

Get a cohort definition set

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.

listPhenotypes 3

Examples

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

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()

updatePhenotypeLog

Update phenotype log

Description

Update phenotype log

Usage

updatePhenotypeLog(updates)

Arguments

updates

Data to update to the log. This is usually the output of ROhdsiWebApi::getCohortDefinitionsMetaData = baseUrl)

Value

Updates Phenotype Log related to added/updated/deprecated of the OHDSI PhenotypeLibrary.

A tibble.

Index

```
getPhenotypeLog, 2
getPlCohortDefinitionSet, 2
listPhenotypes, 3
updatePhenotypeLog, 3
```