Package 'PhenotypeLibrary'

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Type Package

Title The OHDSI Phenotype library

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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 7.2.0

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:

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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))
```

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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.

Examples

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

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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()
```

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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.

Examples

```
updatePhenotypeLog(updates)
```

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