

Package ‘PhenotypeLibrary’

August 15, 2022

Type Package

Title The OHDSI Phenotype library

Version 3.1.6

Date 2022-08-15

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

Imports checkmate,

readr,

dplyr,

rlang

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>

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getPhenotypeLog	<i>Get phenotype log</i>
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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>
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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	<i>List all phenotypes in the library</i>
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Description

List all phenotypes in the library

Usage

```
listPhenotypes()
```

Value

A tibble with the cohort ID and name.

Examples

```
listPhenotypes()
```

updatePhenotypeLog	<i>Update phenotype log</i>
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Description

Update phenotype log

Usage

```
updatePhenotypeLog(updates)
```

Arguments

updates	Data to update to the log
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Value

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

Examples

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

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