

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.

Depends R (>= 4.1.0)

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>

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

Get phenotype log

Usage

```
getPhenotypeLog(cohortIds = NULL)
```

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

```
getPlConceptDefinitionSet
```

Get conceptSets in cohorts

Description

Get conceptSets in cohorts

Usage

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

Arguments

cohortIds IDs of cohorts to extraction from the library.

Value

Returns a table with one row per concept set for given cohort definitions.
A tibble.

Examples

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

```
listPhenotypes
```

Deprecated. List all phenotypes in the library.

Description

Deprecated. List all phenotypes in the library.

Usage

```
listPhenotypes()
```

Value

A tibble with the cohort ID and name. Deprecated. Please use getPhenotypeLog

Examples

```
listPhenotypes()
```

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