

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,
stringr,
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, showHidden = FALSE)
```

Arguments

cohortIds	IDs of cohorts to extraction from the library.
showHidden	Some cohorts in the library are designed to be hidden. They are not retrieved by default. To retrieve such cohorts, please set showHidden as TRUE. Examples of hidden cohorts are withdrawn, deprecated, referrent cohorts.

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.
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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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