Package 'CohortExplorer'

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Type Package

Title An R package with a Shiny viewer to explore profiles of patients in a cohort

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Description An R package with a Shiny viewer to explore profiles of patients in a cohort.

Depends DatabaseConnector (>= 5.0.0),
R (>= 4.1.0)

Imports checkmate,
clock,
dplyr,
lifecycle,
ParallelLogger,
rlang,
stats

Suggests rmarkdown,
testthat,
knitr,
withr

License Apache License

RoxygenNote 7.2.2

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

Encoding UTF-8

Language en-US

URL https://ohdsi.github.io/CohortExplorer/, https://github.com/OHDSI/CohortExplorer

BugReports https://github.com/OHDSI/CohortExplorer/issues

R topics documented:

createCohortExplorerApp

Create Cohort explorer shiny app with person level data

Description

Export person level data from omop cdm tables for eligible persons in the cohort. Creates a folder with files that are part of the Cohort Explorer Shiny app. This app may then be run to review person level profiles.

Usage

```
createCohortExplorerApp(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema = "cohort",
  cdmDatabaseSchema,
  vocabularyDatabaseSchema = cdmDatabaseSchema,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),
  cohortTable = "cohort",
  cohortDefinitionId,
  cohortName = NULL,
  doNotExportCohortData = FALSE,
  sampleSize = 25,
  personIds = NULL,
  exportFolder,
  databaseId,
  shiftDates = FALSE,
  assignNewId = FALSE
)
```

Arguments

connectionDetails

An object of type connectionDetails as created using the [createConnectionDetails](#) function in the DatabaseConnector package. Can be left NULL if connection is provided.

connection An object of type connection as created using the [connect](#) function in the DatabaseConnector package. Can be left NULL if connectionDetails is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes.

cohortDatabaseSchema

Schema name where your cohort tables reside. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.

cdmDatabaseSchema

Schema name where your omop cdm tables with person level data reside. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.

vocabularyDatabaseSchema

            Schema name where your omop vocabulary tables reside. It maybe the cdmDatabaseSchema. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.

tempEmulationSchema

            Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.

cohortTable   The name of the cohort table.

cohortDefinitionId

            The cohort id to extract records.

cohortName   (optional) Cohort Name

doNotExportCohortData

            (Optional) Do you want to not export cohort data? If set to true, parameters cohortDefinitionId, cohort, cohortDatabaseSchema, cohortName will be ignored. The persons entire observation period would be considered the cohort. Cohort Name will be 'Observation Period', cohort id will be set to 0.

sampleSize   (Optional, default = 20) The number of persons to randomly sample. Ignored, if personId is given.

personIds   (Optional) An array of personId's to look for in Cohort table and CDM.

exportFolder   The folder where the output will be exported to. If this folder does not exist it will be created.

databaseId   A short string for identifying the database (e.g. 'Synpuf'). This will be displayed in shiny app to toggle between databases. Should not have space or underscore (_).

shiftDates   (Default = FALSE) Do you want to shift dates? This will help further de-identify data. The shift is the process of recalibrating dates such that all persons min(observation_period_start_date) is 2000-01-01.

assignNewId   (Default = FALSE) Do you want to assign a newId for persons. This will replace the personId in the source with a randomly assigned newId.

Examples

```
## Not run:
connectionDetails <- createConnectionDetails(
  dbms = "postgresql",
  server = "ohdsi.com",
  port = 5432,
  user = "me",
  password = "secure"
)

createCohortExplorerApp(
  connectionDetails = connectionDetails,
  cohortDefinitionId = 1234
)

## End(Not run)
```

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