Package 'CohortExplorer'

November 14, 2022

Type Package

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

Version 0.0.1

Date 2022-11-14

Maintainer Gowtham Rao <rao@ohdsi.org>

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,
dplyr,
lifecycle,
ParallelLogger,
SqlRender

Suggests Eunomia,
testthat

Remotes ohdsi/Eunomia,
ohdsi/ParallelLogger

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:

exportPersonLevelData   *Export person level data for cohort*

Description

Export person level data from omop cdm tables from eligible persons in the cohort.

Usage

```
exportPersonLevelData(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema = "cohort",
  cdmDatabaseSchema,
  vocabularyDatabaseSchema = cdmDatabaseSchema,
  tempEmulationSchema = NULL,
  cohortTable = "cohort",
  cohortDefinitionId,
  cohortName = NULL,
  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

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"
)

exportPersonLevelData(
  connectionDetails = connectionDetails,
  cohortDefinitionId = 1234
)

## End(Not run)
```

Index