Package ‘Eunomia’

November 4, 2020

Type Package
Title A Standard Dataset in the OMOP Common Data Model
Version 1.0.1
Date 2020-10-21
Maintainer Frank DeFalco <fdefalco@ohdsi.org>
Description A sample dataset in the OMOP (Observational Medical Outcomes Partnership) Common Data Model (CDM) format. The CDM enables uniform storage of observational health care data, and is widely used for health care analytics. 'Eunomia' contains simulated data as well as a subset of the OMOP Vocabulary, and enables testing of additional packages and is used for educational and demonstration purposes.
License Apache License 2.0
URL https://github.com/OHDSI/Eunomia
BugReports https://github.com/OHDSI/Eunomia/issues
Depends DatabaseConnector (>= 2.2.0)
Imports SqlRender, RSQLite (> 2.1.1)
Suggests testthat
Encoding UTF-8
LazyData true
RoxygenNote 7.1.1
NeedsCompilation no
Author Frank DeFalco [aut, cre],
       Martijn Schuemie [aut],
       Observational Health Data Science and Informatics [cph]
Repository CRAN
Date/Publication 2020-11-04 08:50:02 UTC

R topics documented:

createCohorts ................................................................. 2
exportToCsv ................................................................. 3
getEunomiaConnectionDetails ............................................. 4
createCohorts

Description

Creates a set of predefined cohorts in a cohort table. WARNING: this will delete all existing cohorts in the table!

Usage

createCohorts(
  connectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)

Arguments

connectionDetails
  The connection details to connect to the (Eunomia) database.
cdmDatabaseSchema
  The name of the database schema holding the CDM data.
cohortDatabaseSchema
  The name of the database schema where the cohorts will be written.
cohortTable
  The name of the table in the cohortDatabaseSchema where the cohorts will be written.

Value

A data frame listing all created cohorts.

Examples

connectionDetails <- getEunomiaConnectionDetails()
createCohorts(connectionDetails)

connection <- connect(connectionDetails)

sql <- "SELECT COUNT(*)
FROM main.cohort
WHERE cohort_definition_id = 1;"

renderTranslateQuerySql(connection, sql)

disconnect(connection)
exportToCsv  Extract the Eunomia database to CSV files

Description

Extract the Eunomia database to CSV files

Usage

```r
exportToCsv(
  outputFolder = file.path(getwd(), "csv"),
  connectionDetails = getEunomiaConnectionDetails()
)
```

Arguments

- `outputFolder`: A folder where the CSV files will be written.
- `connectionDetails`: Connection details for the Eunomia database. Defaults to a fresh Eunomia database.

Examples

```r
# For this example we'll create a temp folder:
folder <- tempfile()
dir.create(folder)

exportToCsv(folder)

list.files(folder)

# [1] "CARE_SITE.csv" "CDM_SOURCE.csv" "COHORT.csv"
# [4] "COHORT_ATTRIBUTE.csv" "CONCEPT.csv" "CONCEPT_ANCESTOR.csv"
# [7] "CONCEPT_CLASS.csv" "CONCEPT_RELATIONSHIP.csv" "CONCEPT_SYNONYM.csv"
# [10] "CONDITION_ERA.csv" "CONDITION_OCCURRENCE.csv" "COST.csv"
# [13] "DEATH.csv" "DEVICE_EXPOSURE.csv" "DOMAIN.csv"
# [16] "DOSE_ERA.csv" "DRUG.csv" "DRUG_EXPOSURE.csv"
# [19] "DRUG_STRENGTH.csv" "FACT_RELATIONSHIP.csv" "LOCATION.csv"
# [22] "MEASUREMENT.csv" "METADATA.csv" "NOTE.csv"
# [25] "NOTE_NLP.csv" "OBSERVATION.csv" "OBSERVATION_PERIOD.csv"
# [28] "PAYER_PLAN_PERIOD.csv" "PERSON.csv" "PROCEDURE_OCCURRENCE.csv"
# [31] "PROVIDER.csv" "RELATIONSHIP.csv" "SOURCE_TO_CONCEPT_MAP.csv"
# [34] "SPECIMEN.csv" "VISIT_DETAIL.csv" "VISIT_OCCURRENCE.csv"
# [37] "VOCABULARY.csv"

# Cleaning up the temp folder used in this example:
unlink(folder, recursive = TRUE)
```
getEunomiaConnectionDetails

Get Eunomia Connection Details

Description

Creates a copy of the Eunomia database, and provides details for connecting to that copy.

Usage

getEunomiaConnectionDetails(databaseFile = tempfile(fileext = ".sqlite"))

Arguments

databaseFile  The path where the database file will be copied to. By default, the database will be copied to a temporary folder, and will be deleted at the end of the R session.

Value

A ConnectionDetails object, to be used with the DatabaseConnector package.

Examples

connectionDetails <- getEunomiaConnectionDetails()
connection <- connect(connectionDetails)
querySql(connection, "SELECT COUNT(*) FROM person;")
disconnect(connection)
Index

createCohorts, 2
exportToCsv, 3
getEunomiaConnectionDetails, 4