

Package ‘Eunomia’

September 18, 2020

Type Package

Title A Standard Dataset in the OMOP Common Data Model

Version 1.0.1

Date 2019-11-18

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Description A standard dataset in the 'OMOP' ('Observational Medical Outcomes Partnership') 'Common Data Model', for testing and demonstration purposes.

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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

R topics documented:

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`createCohorts`*Construct cohorts*

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

```
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

```
# 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_ERA.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

<code>databaseFile</code>	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.
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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)
```

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