Package 'Eunomia'

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Title A Standard Dataset in the OMOP Common Data Model

Type Package

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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
<pre>URL https://github.com/OHDSI/Eunomia</pre>
BugReports https://github.com/OHDSI/Eunomia/issues
Depends DatabaseConnector (>= 2.2.0)
Imports SqlRender, RSQLite (> 2.1.1), rJava
Suggests testthat
Encoding UTF-8
LazyData true
RoxygenNote 7.1.1
R topics documented:
createCohorts
inuex

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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)</pre>
```

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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

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Connection details for the Eunomia database. Defaults to a fresh Eunomia database.

Examples

```
# For this example we'll create a temp folder:
folder <- tempfile()</pre>
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"
                                                                  \hbox{\tt "CONCEPT\_SYNONYM.csv"}
 # [7] "CONCEPT_CLASS.csv"
                                     "CONCEPT_RELATIONSHIP.csv"
                                                                  "COST.csv"
 # [10] "CONDITION_ERA.csv"
                                     "CONDITION_OCCURRENCE.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"
                                   "RELATIONSHIP.csv"
 # [31] "PROVIDER.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)
```

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```
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)</pre>
```

supportsJava8

Determine if Java virtual machine supports Java

Description

Tests Java virtual machine (JVM) java.version system property to check if version >= 8.

Usage

```
supportsJava8()
```

Value

Returns TRUE if JVM supports Java >= 8.

Examples

```
supportsJava8()
```

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