Package 'Eunomia'

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Type Package

Title A Standard Common Data Model Dataset

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Description A standard CDM dataset 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)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

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)
```

Eunomia *Eunomia*

Description

Eunomia

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

```
## Not run:
exportToCsv("c:/temp/csv")

## End(Not run)
```

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 dataabase 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