

Package ‘Eunomia’

January 11, 2023

Type Package

Title Standard dataset manager for OMOP CDM sample datasets

Version 2.0

Date 2022-10-16

Maintainer Frank DeFalco <fdefalco@ohdsi.org>

Description Facilitates access to sample datasets from the EunomiaDatasets repository (<https://github.com/ohdsi/EunomiaDatasets>).

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URL <https://github.com/OHDSI/Eunomia>

BugReports <https://github.com/OHDSI/Eunomia/issues>

Depends DatabaseConnector (>= 2.2.0)

Imports readr,
rlang,
RSQLite,
SqlRender

Suggests testthat,
withr

Encoding UTF-8

LazyData true

RoxygenNote 7.2.1

R topics documented:

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createCohorts	<i>Construct cohorts</i>
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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.

downloadEunomiaData	<i>Download Eunomia data files Download the Eunomia data files from https://github.com/OHDSI/EunomiaDatasets</i>
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Description

Download Eunomia data files Download the Eunomia data files from <https://github.com/OHDSI/EunomiaData>

Usage

```
downloadEunomiaData(
  datasetName,
  cdmVersion = "5.3",
  pathToData = Sys.getenv("EUNOMIA_DATA_FOLDER"),
  overwrite = FALSE
)
```

Arguments

datasetName	The data set name as found on https://github.com/OHDSI/EunomiaDatasets . The data set name corresponds to the folder with the data set ZIP files
cdmVersion	The OMOP CDM version. This version will appear in the suffix of the data file, for example: <datasetName>_<cdmVersion>.zip. Default: '5.3'
pathToData	The path where the Eunomia data is stored on the file system., By default the value of the environment variable "EUNOMIA_DATA_FOLDER" is used.
overwrite	Control whether the existing archive file will be overwritten should it already exist.

Value

Invisibly returns the destination if the download was successful.

Examples

```
## Not run:
downloadEunomiaData("GiBleed")

## End(Not run)
```

extractLoadData	<i>Extract the Eunomia data files and load into a SQLite database Extract files from a .ZIP file and creates a SQLite OMOP CDM database that is then stored in the same directory as the .ZIP file.</i>
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Description

Extract the Eunomia data files and load into a SQLite database Extract files from a .ZIP file and creates a SQLite OMOP CDM database that is then stored in the same directory as the .ZIP file.

Usage

```
extractLoadData(dataFilePath)
```

Arguments

dataFilePath	The path to the .ZIP file that contains the data
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See Also

[downloadEunomiaData](#)

Examples

```
## Not run:
extractLoadData("c:/strategusData/GiBleed_5.3.zip")

## End(Not run)
```

getConnectionDetails *Get Eunomia Connection Details*

Description

Creates a copy of the default (GiBleed) Eunomia database, and provides details for connecting to that copy. Function provides backwards compatibility to prior releases of Eunomia default (GiBleed) dataset

Usage

```
getConnectionDetails(
  datasetName,
  cdmVersion = "5.3",
  pathToData = Sys.getenv("EUNOMIA_DATA_FOLDER"),
  dbms = "sqlite",
  autoDownload = TRUE
)
```

Arguments

datasetName	The data set name as found on https://github.com/OHDSI/EunomiaDatasets . The data set name corresponds to the folder with the data set ZIP files
cdmVersion	The OMOP CDM version. This version will appear in the suffix of the data file, for example: <datasetName>_<cdmVersion>.zip. Default: '5.3'
pathToData	The path where the Eunomia data is stored on the file system., By default the value of the environment variable "EUNOMIA_DATA_FOLDER" is used.
dbms	The DBMS to create a connection details object to support. Default is sqlite.
autoDownload	Controls if the CDM zip archive is automatically downloaded if the data is not currently available.

Value

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

getEunomiaConnectionDetails
 Get Default Eunomia Connection Details

Description

Creates a copy of the default (GiBleed) Eunomia database, and provides details for connecting to that copy. Function provides backwards compatibility to prior releases of Eunomia default (GiBleed) dataset

Usage

```
getEunomiaConnectionDetails()
```

Value

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

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