

Package ‘TestGenerator’

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Type Package

Title Integration Unit Tests for Pharmacoepidemiological Studies

Version 0.3.3

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Description Push a sample population for unit testing on data mapped to the Observational Medical Outcomes Partnership (OMOP) Common Data Model.

License Apache License (>= 2)

Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 4.1.0)

Imports jsonlite, readxl, readr, CDMConnector, DBI, dplyr, checkmate,
glue, duckdb, cli, rlang, withr, ggplot2, tibble, testthat,
arrow, openxlsx

Suggests knitr, rmarkdown

Config/testthat/edition 3

URL <https://github.com/darwin-eu/TestGenerator>,
<https://darwin-eu.github.io/TestGenerator/>

BugReports <https://github.com/darwin-eu/TestGenerator/issues>

NeedsCompilation no

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downloadTestData	<i>Download Test Data Files</i>
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Description

Download Test Data Files

Usage

```
downloadTestData(
  datasetName = "mimicIV",
  cdmVersion = "5.3",
  pathToData = Sys.getenv("STUDY_DATASETS"),
  overwrite = FALSE
)
```

Arguments

datasetName	The data set name as found on https://github.com/darwin-eu/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: synpuf_5.3.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:
downloadTestData()

## End(Not run)
```

generateTestTables	<i>Generates an Excel file with sheets that correspond to an OMOP-CDM tables.</i>
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Description

Generates an Excel file with sheets that correspond to an OMOP-CDM tables.

Usage

```
generateTestTables(
  tableNames,
  cdmVersion,
  outputFolder,
  filename = paste0("test_cdm_", cdmVersion)
)
```

Arguments

tableNames	A list specifying the table names to include in the Excel file.
cdmVersion	The CDM version to use for creating the requested tables (either 5.3 or 5.4).
outputFolder	The folder where the Excel file will be saved.
filename	The name of the Excel file. It does not include the extension .xlsx.

Value

An Excel file with the tables requested.

graphCohort	<i>'graphCohort()' aids in the visualisation of cohorts timelines, useful to get a grip on intersections.</i>
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Description

'graphCohort()' aids in the visualisation of cohorts timelines, useful to get a grip on intersections.

Usage

```
graphCohort(subject_id, cohorts = list())
```

Arguments

subject_id	Only one subject id per visualisation
cohorts	List of cohorts

Value

A ggplot graph

Examples

```

hospitalised <- tibble::tibble(cohort_definition_id = 2,
                              subject_id = 1,
                              cohort_start_date = "2018-01-01",
                              cohort_end_date = "2018-01-10")

icu_patients <- tibble::tibble(cohort_definition_id = 5,
                              subject_id = 1,
                              cohort_start_date = "2018-01-02",
                              cohort_end_date = "2018-01-04")

drugs_treatment <- tibble::tibble(cohort_definition_id = 5,
                                  subject_id = 1,
                                  cohort_start_date = "2018-01-07",
                                  cohort_end_date = "2018-01-09")

TestGenerator::graphCohort(subject_id = 1, cohorts = list("hospitalised" = hospitalised,
                                                         "icu_patients" = icu_patients,
                                                         "drugs_treatment" = drugs_treatment))

```

patientsCDM

Pushes test population into a blank CDM.

Description

Pushes test population into a blank CDM.

Usage

```

patientsCDM(
  pathJson = NULL,
  testName = NULL,
  cdmVersion = "5.3",
  cdmName = NULL
)

```

Arguments

pathJson	Directory where the sample populations in json are located. If NULL, gets the default inst/testCases directory.
testName	Name of the sample population JSON file. If NULL it will push the first sample population in the testCases directory.
cdmVersion	cdm version, default "5.3".
cdmName	Name of the cdm, default NULL.

Value

A CDM reference object with a sample population.

Examples

```
filePath <- system.file("extdata", "testPatientsRSV.xlsx", package = "TestGenerator")
TestGenerator::readPatients(filePath = filePath, outputPath = tempdir())
cdm <- TestGenerator::patientsCDM(pathJson = tempdir(), testName = "test")
duckdb::duckdb_shutdown(duckdb::duckdb())
```

readPatients	<i>Converts a sample of patients into Unit Testing Definition JSON file.</i>
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Description

Converts a sample of patients into Unit Testing Definition JSON file.

Usage

```
readPatients(
  filePath = NULL,
  testName = "test",
  outputPath = NULL,
  cdmVersion = "5.3"
)
```

Arguments

filePath	Path to the test patient data in Excel format. The Excel has sheets that represent tables from the OMOP-CDM, e.g. person, drug_exposure, condition_occurrence, etc.
testName	A name of the test population in character.
outputPath	Path of the output file, if NULL, a folder will be created in the project folder inst/testCases.
cdmVersion	cdm version, default "5.3".

Value

A JSON file with sample patients inside the project directory.

Examples

```
filePath <- system.file("extdata", "testPatientsRSV.xlsx", package = "TestGenerator")
readPatients(filePath = filePath, outputPath = tempdir())
```

readPatients.csv	<i>Converts a sample of patients in CSV format into a Unit Testing Definition JSON file.</i>
------------------	--

Description

Converts a sample of patients in CSV format into a Unit Testing Definition JSON file.

Usage

```
readPatients.csv(  
  filePath = NULL,  
  testName = "test",  
  outputPath = NULL,  
  cdmVersion = "5.3",  
  reduceLargeIds = FALSE  
)
```

Arguments

filePath	Path to the test patient data in CSV format. Multiple CSV files representing tables from the OMOP-CDM must be provided, e.g. person.csv, drug_exposure.csv, condition_occurrence.csv, etc.
testName	Name for the test population file in character.
outputPath	Path of the output file, if NULL, a folder will be created in the project folder inst/testCases.
cdmVersion	cdm version, default "5.3".
reduceLargeIds	Reduces the length of very long ids generally in int64 format, such as those found in the MIMIC-IV database.

Value

A JSON file with sample patients inside the project directory.

Examples

```
filePath <- system.file("extdata", "mimic_sample", package = "TestGenerator")  
readPatients.csv(filePath = filePath, outputPath = tempdir())
```

readPatients.xl	<i>Converts a sample of patients in XLSX format into Unit Testing Definition JSON file.</i>
-----------------	---

Description

Converts a sample of patients in XLSX format into Unit Testing Definition JSON file.

Usage

```
readPatients.xl(  
  filePath = NULL,  
  testName = "test",  
  outputPath = NULL,  
  cdmVersion = "5.3"  
)
```

Arguments

filePath	Path to the test patient data in Excel format. The Excel has sheets that represent tables from the OMOP-CDM, e.g. person, drug_exposure, condition_occurrence, etc.
testName	A name of the test population in character.
outputPath	Path to write the test JSON files. If NULL, the files will be written at the project's testthat folder, i.e. tests/testthat/testCases.
cdmVersion	cdm version, default "5.3".

Value

A directory with the test JSON files with sample patients inside the project directory.

Examples

```
filePath <- system.file("extdata", "testPatientsRSV.xlsx", package = "TestGenerator")  
readPatients.xl(filePath = filePath, outputPath = tempdir())
```

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