

# Package ‘TestGenerator’

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**Type** Package

**Title** Integration Unit Tests for Pharmacoepidemiological Studies

**Version** 0.3.1

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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** 7.3.1

**Depends** R (>= 4.1.0)

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

**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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**Repository** CRAN

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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 <a href="https://github.com/darwin-eu/EunomiaDatasets">https://github.com/darwin-eu/EunomiaDatasets</a> . 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)
```



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patientsCDM                      *Pushes test population into a blank CDM.*

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### Description

Pushes test population into a blank CDM.

### Usage

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

### 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".

### 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())
```

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

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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_ocurrence, 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())
```

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readPatients.csv	<i>Converts a sample of patients in CSV format into a Unit Testing Definition JSON file.</i>
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**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_ocurrence.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())
```

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