

Package ‘TreatmentPatterns’

July 16, 2021

Type Package

Title A package to analyse real-world treatment patterns of a study population of interest.

Version 0.2.2

Author Aniek F Markus

Maintainer Aniek F Markus <a.markus@erasmusmc.nl>

Description This package gives insight in treatment patterns, the following tasks are performed sequentially:

1. Target/event cohorts of interest are created
2. Characterization of study/target population
3. Treatment pathways are constructed
4. Output is generated (sunburst plots and more)
5. Shiny application is available to visualize the results

Go to extras -> CodeToRun.R to execute package.

Depends R (≥ 3.6.1)

Imports Andromeda,
DatabaseConnector,
data.table,
dplyr,
SqlRender,
stringr,
stringi,
readr,
rjson,
reshape2,
googleVis,
RJSONIO,
FeatureExtraction,
OhdsiSharing,
R.utils

Suggests ROhdsiWebApi

License Apache License 2.0

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

VignetteBuilder knitr

R topics documented:

cohortCharacterization	2
constructPathways	3
createCohorts	3
createSunburstPlot	5
executeTreatmentPatterns	5
generateResults	7
importCohorts	8
launchShinyApplication	8

cohortCharacterization

This function will perform baseline characterization for the the target cohorts.

Description

This function will perform baseline characterization for the the target cohorts.

Usage

```
cohortCharacterization(
  connection,
  connectionDetails,
  cdmDatabaseSchema,
  cohortDatabaseSchema,
  cohortTable,
  outputFolder,
  instFolder,
  databaseId,
  targetCohortIds,
  minCellCount,
  standardCovariateSettings
)
```

Arguments

<code>connection</code>	Connection to database server.
<code>connectionDetails</code>	An object of type <code>connectionDetails</code> as created using the <code>createConnectionDetails</code> function in the <code>DatabaseConnector</code> package.
<code>cdmDatabaseSchema</code>	Schema name where your patient-level data resides if OMOP-CDM = TRUE. Note that for SQL Server, this should include both the database and schema name, for example <code>'cdm_data.dbo'</code> .
<code>cohortDatabaseSchema</code>	Schema name where intermediate data can be stored. You will need to have write privileges in this schema. Note that for SQL Server, this should include both the database and schema name, for example <code>'cdm_data.dbo'</code> .
<code>cohortTable</code>	The name of the table that will be created in the work database schema. This table will hold the target and event cohorts used in this study.

outputFolder	Name of local folder to place results; make sure to use forward slashes (/).
databaseId	Unique identifier for database (can be the same as databaseName).
targetCohortIds	IDs to refer to target cohorts.
minCellCount	Minimum number of persons with a specific treatment pathway for the pathway to be included in analysis.
standardCovariateSettings

constructPathways	<i>This function will construct treatment pathways.</i>
-------------------	---

Description

This function will construct treatment pathways.

Usage

```
constructPathways(
  all_data,
  study_settings,
  databaseName,
  studyName,
  outputFolder,
  tempFolder
)
```

Arguments

all_data	Datatable with all target and event cohorts.
study_settings	Object that contains all study settings inputted by the user.
databaseName	Name of the database that will appear in the results.
studyName	Name for the study corresponding to the current settings.
outputFolder	Name of local folder to place results; make sure to use forward slashes (/).

createCohorts	<i>This function will create the target and event cohorts following the definitions included in this package if OMOP-CDM = TRUE.</i>
---------------	--

Description

This function will create the target and event cohorts following the definitions included in this package if OMOP-CDM = TRUE.

Usage

```
createCohorts(
  connection,
  connectionDetails,
  cdmDatabaseSchema,
  cohortDatabaseSchema,
  cohortTable,
  outputFolder,
  instFolder,
  loadCohorts = FALSE,
  baseUrl,
  generateCohorts = TRUE,
  minCellCount,
  flowChart = TRUE
)
```

Arguments

<code>connection</code>	Connection to database server.
<code>connectionDetails</code>	An object of type <code>connectionDetails</code> as created using the createConnectionDetails function in the DatabaseConnector package.
<code>cdmDatabaseSchema</code>	Schema name where your patient-level data resides if OMOP-CDM = TRUE. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
<code>cohortDatabaseSchema</code>	Schema name where intermediate data can be stored. You will need to have write privileges in this schema. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
<code>cohortTable</code>	The name of the table that will be created in the work database schema. This table will hold the target and event cohorts used in this study.
<code>outputFolder</code>	Name of local folder to place results; make sure to use forward slashes (/).
<code>loadCohorts</code>	Setting to load cohorts from ATLAS.
<code>baseUrl</code>	The base URL for theWebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
<code>generateCohorts</code>	Setting to extract specified target/event cohorts from database.
<code>minCellCount</code>	Minimum number of persons with a specific treatment pathway for the pathway to be included in analysis.
<code>flowChart</code>	Setting to return numbers for flowchart with inclusion/exclusion criteria.

createSunburstPlot	<i>Function to create sunburst plot from CSV file.</i>
--------------------	--

Description

Function to create sunburst plot from CSV file.

Usage

```
createSunburstPlot(
  data,
  outcomes = NULL,
  folder = NULL,
  file_name = NULL,
  shiny = FALSE,
  title = ""
)
```

Arguments

data	A data frame containing two columns: 1) column "path" should specify the event cohorts separated by dashes - (combinations can be indicated using &) and 2) column "freq" should specify how often that (unique) path occurs.
outcomes	Character vector containing all event cohorts.
folder	Root folder to store the results.
file_name	File name for the results.
shiny	Set to TRUE if HTML file is generated for shiny application, FALSE will generate a standalone HTML with title and legend.
title	Optional if shiny = FALSE: add descriptive title in sunburst plot for standalone HTML.

executeTreatmentPatterns

This is the main function which runs all different parts of the treatment pathways analysis.

Description

This is the main function which runs all different parts of the treatment pathways analysis.

Usage

```
executeTreatmentPatterns(
  OMOP_CDM = TRUE,
  connectionDetails = NULL,
  cdmDatabaseSchema,
  cohortDatabaseSchema = cdmDatabaseSchema,
  databaseName = "unknown",
  cohortTable = "cohort",
  rootFolder,
  instFolder = paste0(rootFolder, "/inst"),
  outputFolder = paste0(rootFolder, "/output/", databaseName),
  tempFolder = paste0(rootFolder, "/temp/", databaseName),
  cohortLocation = paste0(instFolder, "/cohorts/input_cohorts.csv"),
  targetCohorts = NULL,
  eventCohorts = NULL,
  characterizationSettings = NULL,
  studySettings = NULL,
  loadCohorts = FALSE,
  baseUrl = NULL,
  generateCohorts = TRUE,
  flowChart = TRUE,
  runCreateCohorts = TRUE,
  runCohortCharacterization = TRUE,

  standardCovariateSettings = FeatureExtraction::createCovariateSettings(useDemographicsAge
    = TRUE, useDemographicsGender = TRUE, useDemographicsTimeInCohort = TRUE,
    useDemographicsPostObservationTime = TRUE, useConditionGroupEraAnyTimePrior = TRUE,
    useConditionGroupEraLongTerm = TRUE, useCharlsonIndex = TRUE),
  runConstructPathways = TRUE,
  runGenerateResults = TRUE
)
```

Arguments

connectionDetails	An object of type <code>connectionDetails</code> as created using the createConnectionDetails function in the <code>DatabaseConnector</code> package.
cdmDatabaseSchema	Schema name where your patient-level data resides if OMOP-CDM = TRUE. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
cohortDatabaseSchema	Schema name where intermediate data can be stored. You will need to have write privileges in this schema. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
databaseName	Name of the database that will appear in the results.
cohortTable	The name of the table that will be created in the work database schema. This table will hold the target and event cohorts used in this study.
rootFolder	...
instFolder	...

outputFolder	Name of local folder to place results; make sure to use forward slashes (/).
tempFolder	...
cohortLocation	Location where cohorts are saved if OMOP-CDM = FALSE.
targetCohorts	...
eventCohorts	...
characterizationSettings	...
studySettings	...
loadCohorts	Setting to load cohorts from ATLAS.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
generateCohorts	Setting to extract specified target/event cohorts from database.
flowChart	Setting to return numbers for flowchart with inclusion/exclusion criteria.
runCreateCohorts	Setting to run part of the analysis where cohorts are created.
runCohortCharacterization	Setting to run part of the analysis where characterization of target cohorts is done.
standardCovariateSettings
runConstructPathways	Setting to run part of the analysis where treatment pathways are constructed.
runGenerateResults	Setting to run part of the analysis where final result files and plots are generated.
OMOP-CDM	Format of 'Observational Medical Outcomes Partnership Common Data Model' = TRUE or 'Other' = FALSE
study_settings	Object that contains all study settings inputted by the user.

generateResults	<i>This function will generate all result files and plots.</i>
-----------------	--

Description

This function will generate all result files and plots.

Usage

```
generateResults(
  study_settings,
  databaseName,
  studyName,
  outputFolder,
  tempFolder
)
```

Arguments

study_settings	Object that contains all study settings inputted by the user.
databaseName	Name of the database that will appear in the results.
studyName	Name for the study corresponding to the current settings.
outputFolder	Name of local folder to place results; make sure to use forward slashes (/).

importCohorts	<i>This function will import the target and event cohorts following the path included in this package if OMOP-CDM = FALSE.</i>
---------------	--

Description

This function will import the target and event cohorts following the path included in this package if OMOP-CDM = FALSE.

Usage

```
importCohorts(cohortLocation, outputFolder)
```

Arguments

cohortLocation	Location where cohorts are saved if OMOP-CDM = FALSE.
outputFolder	Name of local folder to place results; make sure to use forward slashes (/).

launchShinyApplication	<i>This function processes the zipped result folder(s) and launches the shiny application.</i>
------------------------	--

Description

This function processes the zipped result folder(s) and launches the shiny application.

Usage

```
launchShinyApplication(rootFolder)
```

Arguments

rootFolder
