Package 'TreatmentPatterns'

August 3, 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:
0. If input arguments given, use these to create study settings
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. Launch shiny application to visualize the results

Depends R (¿= 3.6.1)

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

Suggests testthat (¿= 3.0.0),
ROhdsiWebApi

License Apache License 2.0

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

VignetteBuilder knitr

Config/testthat/edition 3

R topics documented:

---

cohortCharacterization

> *Only for OMOP-CDM TRUE: Perform baseline characterization for the the target cohorts.*

Description

Only for OMOP-CDM TRUE: Perform baseline characterization for the the target cohorts.

Usage

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

Arguments

connection   Connection to database server.

connectionDetails

>   Only for OMOP-CDM TRUE: An object of type connectionDetails as
>   created using the createConnectionDetails function in the DatabaseCon-
>   nector package.

cdmDatabaseSchema

>   Only for OMOP-CDM TRUE: Schema name where your patient-level
>   data resides. Note that for SQL Server, this should include both the
>   database and schema name, for example 'cdm_data.dbo'.

cohortDatabaseSchema

>   Only for OMOP-CDM TRUE: Schema name where intermediate data can
>   be stored. You will need to have write priviliges in this schema. Note that
>   for SQL Server, this should include both the database and schema name,
>   for example 'cdm_results.dbo'.

cohortTable	Only for OMOP-CDM TRUE: The name of the table that will be created in the cohortDatabaseSchema. This table will hold the target and event cohorts used in this study.
instFolder	Name of local folder to place all settings and cohorts; make sure to use forward slashes (/).
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).
standardCovariateSettings	
	An object of type covariateSettings as created using the createCovariate-Settings function in the FeatureExtraction package.

---

constructPathways	*Load already created cohorts and construct pathways based on pathway settings.*

Description

Load already created cohorts and construct pathways based on pathway settings.

Usage

```
constructPathways(
  OMOP_CDM,
  connection,
  connectionDetails,
  cohortTable,
  cohortDatabaseSchema,
  cohortLocation,
  databaseName,
  studyName,
  outputFolder,
  tempFolder
)
```

Arguments

OMOP_CDM	Format of database 'Observational Medical Outcomes Partnership Common Data Model' = TRUE or 'Other' = FALSE.
connection	Connection to database server.
connectionDetails	
	Only for OMOP-CDM TRUE: An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package.
cohortTable	Only for OMOP-CDM TRUE: The name of the table that will be created in the cohortDatabaseSchema. This table will hold the target and event cohorts used in this study.

cohortDatabaseSchema

> Only for OMOP-CDM TRUE: Schema name where intermediate data can be stored. You will need to have write priviliges in this schema. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_results.dbo'.

cohortLocation   Only for OMOP-CDM FALSE: Location from where cohorts can be loaded.

databaseName   Name of the database that will appear in the results.

studyName   Name for the study corresponding to the current pathway settings.

outputFolder   Name of local folder to place results; make sure to use forward slashes (/).

tempFolder   Name of local folder to place intermediate results (not to be shared); make sure to use forward slashes (/).

---

createCohorts   *Only for OMOP-CDM TRUE: Extract target and event cohorts from the database using the definitions included in the package. Cohorts can be defined 1) in ATLAS (recommended) or 2) by creating custom concept sets in combination with a SQL cohort template (advanced).*

Description

Only for OMOP-CDM TRUE: Extract target and event cohorts from the database using the definitions included in the package. Cohorts can be defined 1) in ATLAS (recommended) or 2) by creating custom concept sets in combination with a SQL cohort template (advanced).

Usage

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

Arguments

connection   Connection to database server.

connectionDetails

> An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package.

cdmDatabaseSchema

        Schema name where your patient-level data resides. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.

cohortDatabaseSchema

        Only for OMOP-CDM TRUE: Schema name where intermediate data can be stored. You will need to have write priviliges in this schema. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_results.dbo'.

cohortTable   The name of the table that will be created in the cohortDatabaseSchema. This table will hold the target and event cohorts used in this study.

instFolder   Name of local folder to place all settings and cohorts; make sure to use forward slashes (/).

outputFolder   Name of local folder to place results; make sure to use forward slashes (/).

loadCohorts   etting to retrieve cohort definitions from ATLAS WebApi.

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 (re)generate cohortTable in the database.

flowChart   Setting to return numbers for flowchart with inclusion/exclusion criteria for ATLAS cohorts.

---

createStudySettings	*Transforms and saves input arguments given by user in inst-Folder/settings.*

Description

Transforms and saves input arguments given by user in instFolder/settings.

Usage

```
createStudySettings(
  instFolder,
  targetCohorts = NULL,
  eventCohorts = NULL,
  characterizationSettings = NULL,
  pathwaySettings = NULL
)
```

Arguments

instFolder   Name of local folder to place all settings and cohorts; make sure to use forward slashes (/).

targetCohorts   Data frame containing the study population of interest (cohortId, atlasId, cohortName).

eventCohorts   Data frame containing the events of interest (cohortId, atlasId, cohort-
                   Name).

characterizationSettings
                   Data frame containing the baseline characteristics of interest (covariate-
                   Name, covariateId).

pathwaySettings
                   Data frame containing all pathway settings.

---

createSunburstPlot   *Function to create sunburst plot from CSV file.*

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 parts of the treatment pathways analysis. The following tasks are performed sequentially: 0) If input arguments given, use these to create study settings 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) Launch shiny application to visualize the results*

Description

This is the main function which runs all parts of the treatment pathways analysis. The following tasks are performed sequentially: 0) If input arguments given, use these to create study settings 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) Launch shiny application to visualize the results

Usage

```
executeTreatmentPatterns(
  OMOP_CDM = TRUE,
  connectionDetails = NULL,
  cdmDatabaseSchema,
  cohortDatabaseSchema,
  databaseName = "unknown_name",
  cohortTable = "treatmentpatterns_cohorts",
  rootFolder = getwd(),
  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,
  pathwaySettings = NULL,
  loadCohorts = FALSE,
  baseUrl = NULL,
  generateCohorts = TRUE,
  flowChart = TRUE,

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

Arguments

connectionDetails
            Only for OMOP-CDM TRUE: An object of type connectionDetails as
            created using the createConnectionDetails function in the DatabaseCon-
            nector package.

cdmDatabaseSchema
            Only for OMOP-CDM TRUE: Schema name where your patient-level
            data resides. Note that for SQL Server, this should include both the
            database and schema name, for example 'cdm_data.dbo'.

cohortDatabaseSchema
            Only for OMOP-CDM TRUE: Schema name where intermediate data can
            be stored. You will need to have write priviliges in this schema. Note that
            for SQL Server, this should include both the database and schema name,
            for example 'cdm_results.dbo'.

databaseName   Name of the database that will appear in the results.

cohortTable   Only for OMOP-CDM TRUE: The name of the table that will be created
            in the cohortDatabaseSchema. This table will hold the target and event
            cohorts used in this study.

rootFolder   Name of local folder to place all package output (instFolder, outputFolder,
            tempFolder if not given).

instFolder   Name of local folder to place all settings and cohorts; make sure to use
            forward slashes (/).

outputFolder   Name of local folder to place results; make sure to use forward slashes
            (/).

tempFolder   Name of local folder to place intermediate results (not to be shared); make
            sure to use forward slashes (/).

cohortLocation Only for OMOP-CDM FALSE: Location from where cohorts can be loaded.

targetCohorts   Data frame containing the study population of interest (cohortId, atlasId,
            cohortName).

eventCohorts   Data frame containing the events of interest (cohortId, atlasId, cohort-
            Name).

characterizationSettings
            Only for OMOP-CDM TRUE: Data frame containing the baseline char-
            acteristics of interest (covariateName, covariateId).

pathwaySettings
            Data frame containing all pathway settings.

loadCohorts   Only for OMOP-CDM TRUE: Setting to retrieve cohort definitions from
            ATLAS WebApi.

baseUrl   Only for OMOP-CDM TRUE: 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
            Only for OMOP-CDM TRUE: Setting to (re)generate cohortTable in the
            database.

flowChart   Only for OMOP-CDM TRUE: Setting to return numbers for flowchart
            with inclusion/exclusion criteria for ATLAS cohorts.

standardCovariateSettings

>An object of type covariateSettings as created using the createCovariate-Settings function in the FeatureExtraction package.

runCreateCohorts

>Setting to run 1) Target/event cohorts of interest are created.

runCohortCharacterization

>Only for OMOP-CDM TRUE: Setting to run 2) Characterization of study/target population.

runConstructPathways

>Setting to run 3) Treatment pathways are constructed.

runGenerateResults

>Setting to run 4) Output is generated (sunburst plots and more).

launchShiny   Setting to run 5) Launch shiny application to visualize the results.

OMOP-CDM   Format of database 'Observational Medical Outcomes Partnership Common Data Model' = TRUE or 'Other' = FALSE.

---

generateResults   *Generate all result files and plots from constructed pathways.*

Description

Generate all result files and plots from constructed pathways.

Usage

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

Arguments

databaseName   Name of the database that will appear in the results.

studyName   Name for the study corresponding to the current pathway settings.

outputFolder   Name of local folder to place results; make sure to use forward slashes (/).

tempFolder   Name of local folder to place intermediate results (not to be shared); make sure to use forward slashes (/).

---

importCohorts   *Only for OMOP-CDM FALSE: Import the target and event cohorts from a csv file in which the cohorts are stored.*

Description

Only for OMOP-CDM FALSE: Import the target and event cohorts from a csv file in which the cohorts are stored.

Usage

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

Arguments

cohortLocation   Location from where cohorts can be loaded.

outputFolder   Name of local folder to place results; make sure to use forward slashes
                 (/).

---

launchShinyApplication

> *Processes the zipped result folder(s) and launch the shiny application.*

Description

Processes the zipped result folder(s) and launch the shiny application.

Usage

```
launchShinyApplication(zipFolder)
```

Arguments

zipFolder   Name of local folder containing zip file(s).