

Package ‘TreatmentPatterns’

December 22, 2021

Type Package

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

Version 1.0.0

Author Aniek F Markus

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

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

1. Create target/event cohorts of interest
2. Optional, only for OMOP-CDM data: Perform baseline characterization of study/target population
3. Construct treatment pathways
4. Generate output (sunburst plots, Sankey diagrams and more)
5. Launch shiny application to visualize the results

Depends R (\geq 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:

addPathwaySettings	2
cohortCharacterization	3
constructPathways	4
createCharacterizationSettings	4
createCohorts	5
createCohortSettings	5
createDataSettings	6
createPathwaySettings	7
createSaveSettings	8
createSunburstPlot	9
executeTreatmentPatterns	9
generateOutput	10
launchResultsExplorer	11

addPathwaySettings	<i>Add set of pathway settings.</i>
--------------------	-------------------------------------

Description

Add set of pathway settings.

Usage

```
addPathwaySettings(
  studyName = "name_unknown",
  targetCohortId,
  eventCohortIds,
  includeTreatments = "startDate",
  periodPriorToIndex = 0,
  minEraDuration = 0,
  splitEventCohorts = "",
  splitTime = 30,
  eraCollapseSize = 30,
  combinationWindow = 30,
  minPostCombinationDuration = 30,
  filterTreatments = "First",
  maxPathLength = 5,
  minCellCount = 5,
  minCellMethod = "Remove",
  groupCombinations = 10,
  addNoPaths = FALSE
)
```

Arguments

studyName Name identifying the set of study parameters.

targetCohortId Target cohort ID of current study settings.

eventCohortIds Event cohort IDs of current study settings.

includeTreatments	Include treatments starting ('startDate') or ending ('endDate') after target cohort start date
periodPriorToIndex	Number of days prior to the index date of the target cohort that event cohorts are allowed to start
minEraDuration	Minimum time an event era should last to be included in analysis
splitEventCohorts	Specify event cohort to split in acute (i X days) and therapy ($i=$ X days)
splitTime	Specify number of days (X) at which each of the split event cohorts should be split in acute and therapy
eraCollapseSize	Window of time between which two eras of the same event cohort are collapsed into one era
combinationWindow	Window of time two event cohorts need to overlap to be considered a combination treatment
minPostCombinationDuration	Minimum time an event era before or after a generated combination treatment should last to be included in analysis
filterTreatments	Select first occurrence of ("First") / changes between ("Changes") / all event cohorts ("All")
maxPathLength	Maximum number of steps included in treatment pathway (max 5)
minCellCount	Minimum number of persons with a specific treatment pathway for the pathway to be included in analysis
minCellMethod	Select to completely remove / sequentially adjust (by removing last step as often as necessary) treatment pathways below minCellCount
groupCombinations	Select to group all non-fixed combinations in one category 'other' in the sunburst plot
addNoPaths	Select to include untreated persons without treatment pathway in the sunburst plot

cohortCharacterization

Optional, only for OMOP-CDM data: Perform baseline characterization of study/target population.

Description

Optional, only for OMOP-CDM data: Perform baseline characterization of study/target population.

Usage

```
cohortCharacterization(dataSettings, characterizationSettings, saveSettings)
```

Arguments

`dataSettings` Settings object as created by `createDataSettings()`.
`characterizationSettings`
 Settings object as created by `createCharcterizationSettings()`.
`saveSettings` Settings object as created by `createSaveSettings()`.

<code>constructPathways</code>	<i>Construct treatment pathways.</i>
--------------------------------	--------------------------------------

Description

Construct treatment pathways.

Usage

```
constructPathways(dataSettings, pathwaySettings, saveSettings)
```

Arguments

`dataSettings` Settings object as created by `createDataSettings()`.
`pathwaySettings`
 Settings object as created by `createPathwaySettings()`.
`saveSettings` Settings object as created by `createSaveSettings()`.

<code>createCharacterizationSettings</code>	<i>Create characterization settings (optional, only for OMOP-CDM data).</i>
---	--

Description

Create characterization settings (optional, only for OMOP-CDM data).

Usage

```
createCharacterizationSettings(
  baselineCovariates_location = NULL,
  baselineCovariates = data.frame(covariateName = c("Male", "Age",
    "Charlson comorbidity index score"), covariateId = c(8507001, 1002, 1901)),

  standardCovariateSettings = FeatureExtraction::createCovariateSettings(useDemographicsAge
    = TRUE, useDemographicsGender = TRUE, useDemographicsTimeInCohort = TRUE,
    useDemographicsPostObservationTime = TRUE, useConditionGroupEraAnyTimePrior = TRUE,
    useConditionGroupEraLongTerm = TRUE, useCharlsonIndex = TRUE),
  returnCovariates = "all",
  minCellCount = 5
)
```

Arguments

- baselineCovariates_location** Optional: Location of saved baselineCovariates object.
- baselineCovariates** Data frame containing the baseline characteristics of interest (covariate-Name = "Descriptive name covariate", covariateId = "Unique ID number referring to covariate from FeatureExtraction or 'Custom' (see explanation below)"), covariateId can be "custom" if SQL code is
- standardCovariateSettings** An object of type covariateSettings as created using the createCovariateSettings function in the FeatureExtraction package.
- returnCovariates** Return "all" features or only "selection" of features
- minCellCount** Minimum number of persons with a specific baseline covariate to be included in analysis

Value

Object characterizationSettings.

createCohorts	<i>Create target/event cohorts of interest.</i>
---------------	---

Description

Create target/event cohorts of interest.

Usage

```
createCohorts(dataSettings, cohortSettings, saveSettings)
```

Arguments

- dataSettings** Settings object as created by createDataSettings().
- cohortSettings** Settings object as created by createCohortSettings().
- saveSettings** Settings object as created by createSaveSettings().

createCohortSettings	<i>Create cohort settings.</i>
----------------------	--------------------------------

Description

Create cohort settings.

Usage

```
createCohortSettings(
  cohortsToCreate_location = NULL,
  targetCohorts = NULL,
  eventCohorts = NULL,
  loadCohorts = FALSE,
  cohortsFolder = NULL,
  baseUrl = NULL,
  generateCohorts = TRUE,
  includeDescendants = TRUE
)
```

Arguments

<code>cohortsToCreate_location</code>	Optional: Location of saved cohortsToCreate object.
<code>targetCohorts</code>	Data frame containing the study population of interest (cohortId = "Unique ID number", cohortName = "Descriptive name cohort", optional: atlasId = "Cohort ID ATLAS", optional: conceptSet = "Concept set to use with SQL template").
<code>eventCohorts</code>	Data frame containing the events of interest (cohortId = "Unique ID number", cohortName = "Descriptive name cohort", optional: atlasId = "Cohort ID ATLAS", optional: conceptSet = "Concept set to use with SQL template").
<code>loadCohorts</code>	Setting to retrieve cohort definitions with atlasId from ATLAS WebApi.
<code>cohortsFolder</code>	Location where cohort definitions are stored (SQL/JSON files).
<code>baseUrl</code>	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.
<code>generateCohorts</code>	Setting to (re)generate cohortTable in the database.
<code>includeDescendants</code>	Whether to include all descendants of Custom cohorts defined using conceptSet.

Value

Object cohortSettings.

<code>createDataSettings</code>	<i>Create data settings.</i>
---------------------------------	------------------------------

Description

Create data settings.

Usage

```
createDataSettings(
  OMOP_CDM = "TRUE",
  connectionDetails = NULL,
  cdmDatabaseSchema = NULL,
  cohortDatabaseSchema = NULL,
  cohortTable = "treatmentpatterns_cohorts",
  cohortLocation = NULL
)
```

Arguments

connectionDetails

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

cohortLocation

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

OMOP-CDM

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

Value

Object dataSettings.

createPathwaySettings *Create pathway settings.*

Description

Create pathway settings.

Usage

```
createPathwaySettings(
  pathwaySettings_location = NULL,
  pathwaySettings_list = NULL,
  targetCohortId = NULL,
  eventCohortIds = NULL,
  ...
)
```

Arguments

- `pathwaySettings_location` Optional: Location of saved pathwaySettings object.
- `pathwaySettings_list` Create (list of pathway settings) with `addPathwaySettings()` (e.g. `pathwaySettings_list = addPathwaySettings()` or `pathwaySettings_list = list(addPathwaySettings(), addPathwaySettings())`).
- `targetCohortId` Target cohort ID of current study settings.
- `eventCohortIds` Event cohort IDs of current study settings.

Value

Object `pathwaySettings`.

<code>createSaveSettings</code>	<i>Create save settings.</i>
---------------------------------	------------------------------

Description

Create save settings.

Usage

```
createSaveSettings(
  databaseName = "unknown_name",
  rootFolder,
  outputFolder = file.path(rootFolder, "output"),
  tempFolder = file.path(rootFolder, "temp")
)
```

Arguments

- `databaseName` Name of the database that will appear in the results.
- `rootFolder` Name of local folder to place all package output (`outputFolder`, `tempFolder` if not given).
- `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 (/).

Value

Object `saveSettings`.

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 parts of the treatment pathways analysis. The following tasks are performed sequentially: 1) Create target/event cohorts of interest, 2) Optional, only for OMOP-CDM data: Perform baseline characterization of study/target population, 3) Construct treatment pathways, 4) Generate output (sunburst plots, Sankey diagrams 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: 1) Create target/event cohorts of interest, 2) Optional, only for OMOP-CDM data: Perform baseline characterization of study/target population, 3) Construct treatment pathways, 4) Generate output (sunburst plots, Sankey diagrams and more), 5) Launch shiny application to visualize the results.

Usage

```
executeTreatmentPatterns(
  dataSettings,
  cohortSettings,
  characterizationSettings = NULL,
  pathwaySettings,
  saveSettings,
  runCreateCohorts = TRUE,
  runCohortCharacterization = TRUE,
  runConstructPathways = TRUE,
  runGenerateOutput = TRUE,
  launchShiny = TRUE
)
```

Arguments

dataSettings Settings object as created by createDataSettings().

cohortSettings Settings object as created by createCohortSettings().

characterizationSettings
Optional, only for OMOP-CDM data: Settings object as created by createCharcterizationSettings().

pathwaySettings
Settings object as created by createPathwaySettings().

saveSettings Settings object as created by createSaveSettings().

runCreateCohorts
Setting to run 1) createCohorts().

runCohortCharacterization
Optional, only for OMOP-CDM data: Setting to run 2) cohortCharac-
terization().

runConstructPathways
Setting to run 3) constructPathways().

runGenerateOutput
Setting to run 4) generateOutput().

launchShiny Setting to run 5) launchResultsExplorer().

generateOutput	<i>Generate output (sunburst plots, Sankey diagrams and more).</i>
----------------	--

Description

Generate output (sunburst plots, Sankey diagrams and more).

Usage

```
generateOutput(saveSettings)
```

Arguments

saveSettings Settings object as created by createSaveSettings().

launchResultsExplorer	<i>Processes the zipped result folder(s) and launch the shiny application.</i>
-----------------------	--

Description

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

Usage

```
launchResultsExplorer(  
  saveSettings = NULL,  
  zipFolder = NULL,  
  outputFolder = NULL  
)
```

Arguments

saveSettings	Settings object as created by createSaveSettings().
zipFolder	Name of local folder containing zip file(s) to move to outputFolder.
outputFolder	Name of local folder containing output.