

Package ‘TreatmentPatterns’

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Type Package

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

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Description This package gives insight in treatment patterns, 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

Depends R ($i=$ 3.6.1)

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

Suggests testthat ($i=$ 3.0.0),
ROhdsiWebApi

License Apache License 2.0

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

VignetteBuilder knitr

Config/testthat/edition 3

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

Add set of pathway settings.

Usage

```
addPathwaySettings(
  studyName = "name_unknown",
  targetCohortId,
  eventCohortIds,
  includeTreatmentsPriorToIndex = 0,
  minEraDuration = 0,
  splitEventCohorts = "",
  eraCollapseSize = 0,
  combinationWindow = 30,
  minStepDuration = 30,
  filterTreatments = "First",
  maxPathLength = 5,
  minCellCount = 0,
  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.
includeTreatmentsPriorToIndex	Number of days prior to the index date of the target cohort that event cohorts are allowed to start

<code>minEraDuration</code>	Minimum time an event era should last to be included in analysis
<code>splitEventCohorts</code>	Specify event cohort to split in acute ($i \leq 30$ days) and therapy ($i > 30$ days)
<code>eraCollapseSize</code>	Window of time between which two eras of the same event cohort are collapsed into one era
<code>combinationWindow</code>	Window of time two event cohorts need to overlap to be considered a combination treatment
<code>minStepDuration</code>	Minimum time an event era before or after a generated combination treatment should last to be included in analysis
<code>filterTreatments</code>	Select first occurrence of / changes between / all event cohorts
<code>maxPathLength</code>	Maximum number of steps included in treatment pathway (max 5)
<code>minCellCount</code>	Minimum number of persons with a specific treatment pathway for the pathway to be included in analysis
<code>minCellMethod</code>	Select to completely remove / sequentially adjust (by removing last step as often as necessary) treatment pathways below minCellCount
<code>groupCombinations</code>	Select to group all non-fixed combinations in one category 'other' in the sunburst plot
<code>addNoPaths</code>	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

<code>dataSettings</code>	Settings object as created by <code>createDataSettings()</code> .
<code>characterizationSettings</code>	Settings object as created by <code>createCharacterizationSettings()</code> .
<code>saveSettings</code>	Settings object as created by <code>createSaveSettings()</code> .

constructPathways	<i>Construct treatment pathways.</i>
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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().

```
createCharacterizationSettings
```

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

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),
  minCellCount = 5
)
```

Arguments

baselineCovariates_location	Optional: Location of saved baselineCovariates object.
baselineCovariates	Data frame containing the baseline characteristics of interest (covariateName = "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.

Value

Object `characterizationSettings`.

<code>createCohorts</code>	<i>Create target/event cohorts of interest.</i>
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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()`.

<code>createCohortSettings</code>	<i>Create cohort settings.</i>
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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 (<code>cohortId</code> = "Unique ID number", <code>cohortName</code> = "Descriptive name cohort", optional: <code>atlasId</code> = "Cohort ID ATLAS", optional: <code>conceptSet</code> = "Concept set to use with SQL template").
<code>eventCohorts</code>	Data frame containing the events of interest (<code>cohortId</code> = "Unique ID number", <code>cohortName</code> = "Descriptive name cohort", optional: <code>atlasId</code> = "Cohort ID ATLAS", optional: <code>conceptSet</code> = "Concept set to use with SQL template").
<code>loadCohorts</code>	Setting to retrieve cohort definitions with <code>atlasId</code> 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 <code>conceptSet</code> .

Value

Object `cohortSettings`.

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

Create data settings.

Usage

```
createDataSettings(
  OMOP_CDM = "TRUE",
  connectionDetails = DatabaseConnector::createConnectionDetails(dbms =
    Sys.getenv("dbms"), server = Sys.getenv("server"), user = Sys.getenv("user"),
    password = Sys.getenv("password"), port = Sys.getenv("port")),
  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.

createSaveSettings	<i>Create save settings.</i>
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Description

Create save settings.

Usage

```
createSaveSettings(
  databaseName = "unknown_name",
  rootFolder = getwd(),
  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>
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Description

Function to create sunburst plot from CSV file.

Usage

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


Arguments

<code>data</code>	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.
<code>outcomes</code>	Character vector containing all event cohorts.
<code>folder</code>	Root folder to store the results.
<code>file_name</code>	File name for the results.
<code>shiny</code>	Set to TRUE if HTML file is generated for shiny application, FALSE will generate a standalone HTML with title and legend.
<code>title</code>	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 = FALSE
)
```

Arguments

<code>dataSettings</code>	Settings object as created by <code>createDataSettings()</code> .
<code>cohortSettings</code>	Settings object as created by <code>createCohortSettings()</code> .
<code>characterizationSettings</code>	Optional, only for OMOP-CDM data: Settings object as created by <code>createCharacterizationSettings()</code> .
<code>pathwaySettings</code>	Settings object as created by <code>createPathwaySettings()</code> .
<code>saveSettings</code>	Settings object as created by <code>createSaveSettings()</code> .
<code>runCreateCohorts</code>	Setting to run 1) <code>createCohorts()</code> .
<code>runCohortCharacterization</code>	Optional, only for OMOP-CDM data: Setting to run 2) <code>cohortCharacterization()</code> .
<code>runConstructPathways</code>	Setting to run 3) <code>constructPathways()</code> .
<code>runGenerateOutput</code>	Setting to run 4) <code>generateOutput()</code> .
<code>launchShiny</code>	Setting to run 5) <code>launchResultsExplorer()</code> .

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

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

Usage

```
generateOutput(saveSettings)
```

Arguments

<code>saveSettings</code>	Settings object as created by <code>createSaveSettings()</code> .
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<code>launchResultsExplorer</code>	<i>Processes the zipped result folder(s) and launch the shiny application.</i>
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Description

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

Usage

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

Arguments

<code>saveSettings</code>	Settings object as created by <code>createSaveSettings()</code> .
<code>zipFolder</code>	Name of local folder containing zip file(s).