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 (¿= 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

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Encoding UTF-8

LazyData true

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VignetteBuilder knitr

Config/testthat/edition 3

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addPathwaySettings *Add set of pathway settings.*

Description

Add set of pathway settings.

Usage

```
addPathwaySettings(
  studyName = c("default"),
  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

`minEraDuration` # Minimum time an event era should last to be included in analysis

`splitEventCohorts` # Specify event cohort to split in acute (¡ 30 days) and therapy (¿= 30 days)

`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

`minStepDuration` # Minimum time an event era before or after a generated combination treatment should last to be included in analysis

`filterTreatments` # Select first occurrence of / changes between / all event cohorts

`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

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`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().

constructPathways *Construct treatment pathways.*

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 baselieCovariates object.

`baselineCovariates` Data frame containing the baseline characteristics of interest (covariateName, covariateId).

`standardCovariateSettings` An object of type covariateSettings as created using the createCovariateSettings function in the FeatureExtraction package.

`createCohorts` *Create target/event cohorts of interest.*

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` *Create cohort settings.*

Description

Create cohort settings.

Usage

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

Arguments

`cohortsToCreate_location`	Optional: Location of saved cohortsToCreate object.
`targetCohorts`	Data frame containing the study population of interest (cohortId, cohortName, atlasId, conceptSet).
`eventCohorts`	Data frame containing the events of interest (cohortId, cohortName, atlasId, conceptSet).
`loadCohorts`	Setting to retrieve cohort definitions with atlasId 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.

`includeDescendants`
: Whether to include all descendants of Custom cohorts defined using conceptSet.

`createDataSettings` *Create data settings.*

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 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.

`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.

`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.

`createSaveSettings` *Create save settings.*

Description

Create save settings.

Usage

```
createSaveSettings(
  databaseName = "unknown_name",
  rootFolder = getwd(),
  outputFolder = paste0(rootFolder, "/output"),
  tempFolder = paste0(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 (/).

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: 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

`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) cohortCharacterization().

`runConstructPathways` Setting to run 3) constructPathways().

`runGenerateOutput`	Setting to run 4) generateOutput().
`launchShiny`	Setting to run 5) launchResultsExplorer().

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

Description

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

Usage

```
generateOutput(saveSettings)
```

Arguments

`saveSettings`	Settings object as created by createSaveSettings().

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

Description

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

Usage

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

Arguments

`saveSettings`	Settings object as created by createSaveSettings().
`zipFolder`	Name of local folder containing zip file(s).