

Package 'AsthmaCOPDTreatmentPatterns'

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Type Package

Title A package to analyse real-world treatment patterns for patients with asthma, COPD and Asthma-COPD Overlap.

Version 0.3.0

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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),
data.table,
dplyr

Imports Andromeda,
DatabaseConnector,
FeatureExtraction,
googleVis,
SqlRender,
stringr,
stringi,
readr,
rjson,
reshape2,
RJSONIO,
OhdsiSharing

Suggests ROhdsiWebApi

License Apache License 2.0

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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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,
  databaseId,
  targetCohortIds,
  minCellCount
)
```

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. 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.
<code>outputFolder</code>	Name of local folder to place results; make sure to use forward slashes (/).
<code>databaseId</code>	Unique identifier for database (can be the same as <code>databaseName</code>).

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.

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

This function will construct treatment pathways.

Usage

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

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 .</i>
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Description

This function will create the target and event cohorts following the definitions included in this package .

Usage

```
createCohorts(
  connection,
  connectionDetails,
  cdmDatabaseSchema,
  cohortDatabaseSchema,
  vocabularyDatabaseSchema = cdmDatabaseSchema,
  cohortTable,
  outputFolder,
  loadCohorts = FALSE,
  baseUrl = "...",
  generateCohorts = TRUE,
  detailedCount = 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. 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 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 extract specified target/event cohorts from database.
<code>detailedCount</code>	Setting to count which specific concepts occur in 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.

```
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(
  connection = NULL,
  connectionDetails = NULL,
  cdmDatabaseSchema,
  cohortDatabaseSchema = cdmDatabaseSchema,
  cohortTable = "cohort",
  outputFolder,
  databaseName = "Unknown",
  runCreateCohorts = TRUE,
  runCohortCharacterization = FALSE,
  runConstructPathways = TRUE,
  runGenerateResults = TRUE,
  study_settings
)
```

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. 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>databaseName</code>	Name of the database that will appear in the results.
<code>runCreateCohorts</code>	Setting to run part of the analysis where cohorts are created.
<code>runCohortCharacterization</code>	Setting to run part of the analysis where characterization of target cohorts is done.

`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.

`study_settings` Object that contains all study settings inputted by the user.

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

This function will generate all result files and plots.

Usage

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

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 (/).