

Package ‘Cohort2Trajectory’

September 5, 2022

Type Package

Title Package for creating patient orientated treatment trajectories from cohorts defined in OHDSI ATLAS

Version 1.0

Date 2022-01-11

Author Markus Haug

Maintainer Markus Haug <markus.haug@ut.ee>

Description Package Cohort2Trajectory creates patient orientated treatment trajectories from cohorts defined in OHDSI ATLAS. The package can be used with access to OMOP CDM database. The package creates discrete and continuous time trajectories (and outputs them as .csv file) which describe patients' treatment through time. Package can be run with GUI or CLI.

License GPL (>= 2)

Imports Rcpp (>= 1.0.7),

shiny,
shinydashboard,
shinycssloaders,
DT,
stringi,
dplyr,
RColorBrewer,
ggplot2,
plyr,
utils,
sortable,
RJSONIO

Remotes OHDSI/CirceR,
OHDSI/CohortGenerator,
OHDSI/DatabaseConnector,
OHDSI/SqlRender,
OHDSI/ParallelLogger,
OHDSI/Eunomia,
OHDSI/ROhdsiWebApi

Suggests testthat (>= 3.0.0),
pheatmap
LinkingTo Rcpp
RoxygenNote 7.1.2
Config/testthat/edition 3

R topics documented:

Cohort2Trajectory-package	2
Cohort2Trajectory	3
runGUI	5
Index	8

Cohort2Trajectory-package
<i>Package for creating patient orientated treatment trajectories from cohorts defined in OHDSI ATLAS</i>

Description

Package Cohort2Trajectory creates patient orientated treatment trajectories from cohorts defined in OHDSI ATLAS. The package can be used with access to OMOP CDM database. The package creates discrete and continuous time trajectories (and outputs them as .csv file) which describe patients’ treatment through time. Package can be run with GUI or CLI.

Details

This package can be used in two ways 1) Running with GUI 2) Running with CLI

Author(s)

Markus Haug, haugmarkus@protonmail.com.
Maintainer: Markus Haug haugmarkus@protonmail.com

References

This optional section can contain literature or other references for background information.

See Also

HealthInformaticsUT/TrajectoryMarkovAnalysis, HealthInformaticsUT/TrajectoryViz

Examples

```
## Not run:
## Optional simple examples of the most important functions
## These can be in \dontrun{} and \donttest{} blocks.

## End(Not run)
```

Cohort2Trajectory	<i>This function creates patient treatment trajectories</i>
-------------------	---

Description

This function creates patient treatment trajectories

Usage

```
Cohort2Trajectory(
  dbms = "postgresql",
  connection,
  cdmSchema = "ohdsi_cdm",
  cdmTmpSchema = "ohdsi_temp",
  cdmResultsSchema = "ohdsi_results",
  studyName = "Cohort2Trajectory",
  baseUrl = "http://localhost:8080/WebAPI",
  atlasTargetCohort,
  atlasStateCohorts,
  stateCohortLabels,
  stateCohortPriorityOrder,
  stateCohortMandatory,
  stateCohortAbsorbing,
  stateSelectionType,
  trajectoryType,
  lengthOfStay,
  outOfCohortAllowed,
  runSavedStudy = FALSE,
  pathToResults = getwd()
)
```

Arguments

dbms	The type of DBMS running on the server. Valid values are: 'oracle', 'postgresql', 'redshift', 'sql server', 'pdw', 'netezza', 'bigquery', 'sqlite', 'sqlite extended', 'spark'
connection	Connection to database
cdmSchema	Schema which contains the OHDSI Common Data Model.
cdmTmpSchema	Schema for temporary tables, will be deleted.

```

cdmResultsSchema
    Schema which has the information about the cohorts created in Atlas
atlasTargetCohort
    The id of the target cohort defined in OHDSI tool ATLAS
atlasStateCohorts
    The ids of the state cohorts defined in OHDSI tool ATLAS
stateCohortLabels
    Vector of the customized labels of the state cohorts
stateCohortPriorityOrder
    Vector of the customized labels of the state cohorts in priority order
stateCohortMandatory
    Vector of the customized labels of the state cohorts which are mandatory in
    trajectory
stateCohortAbsorbing
    Vector of the customized labels of the state cohorts which are absorbing
stateSelectionType
    The type of state selection (1 - First occurring, 2 - Max overlap, 3 - Priority)
trajectoryType
    The type of the trajectory (0 - Discrete time, 1 - Continuous time)
lengthOfStay
    The length of stay (days) in one state (Effect only in discrete case)
outOfCohortAllowed
    boolean whether the patient trajectory can surpass the target cohort's observation-
    period

```

Examples

```

#####
#
# Example on Eunomia
#
#####

studyName = "TestCohort2Trajectory" #TODO
pathToResults <-getwd() #TODO

#####
#
# Database credentials
#
#####
pathToDriver = './Drivers'
dbms <- "sqlite" #TODO

cdmSchema = "main" #TODO # Schema which contains the OHDSI Common Data Model
cdmTmpSchema = "main" #TODO # Schema for temporary tables, will be deleted # should be ohdsi_temp
cdmResultsSchema = "main" #TODO # Schema which will contain the final results

baseUrl = NULL #TODO # WebAPI URL is not needed when jsons' are already imported

```

```
#####
#
# Initiate the database connection
#
#####
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
conn <- DatabaseConnector::connect(connectionDetails)
Eunomia::createCohorts(connectionDetails)

#####
#
# Run the study
#
#####

Cohort2Trajectory::Cohort2Trajectory(
  dbms = dbms,
  connection = conn,
  cdmSchema = cdmSchema,
  cdmTmpSchema = cdmTmpSchema,
  cdmResultsSchema = cdmResultsSchema,
  studyName = studyName,
  baseUrl = baseUrl,
  atlasTargetCohort = 1,
  atlasStateCohorts = c(3,4),
  stateCohortLabels = c("TestState1", "TestState2"),
  stateCohortPriorityOrder = c("TestState1", "TestState2"),
  stateCohortMandatory = c("TestState2"),
  stateCohortAbsorbing = c("TestState2"),
  #####
  # stateSelectionTypes
  # 1 - First occurring
  # 2 - Largest overlap
  # 3 - Priority ordering
  #####
  stateSelectionType = 3,
  #####
  # trajectoryType
  # 0 - Discrete time
  # 1 - Continuous time
  #####
  trajectoryType = 0,
  lengthOfStay = 30,
  outOfCohortAllowed = TRUE,
  runSavedStudy = FALSE,
  pathToResults = pathToResults
)
```

runGUI

This function initiates the connection with database and starts Shiny application

Description

This function initiates the connection with database and starts Shiny application

Usage

```
runGUI(
  conn,
  connectionDetails,
  pathToDriver = "./Drivers",
  pathToResults = NULL,
  dbms = "postgresql",
  cdmSchema = "ohdsi_cdm",
  cdmTmpSchema = "ohdsi_temp",
  cdmResultsSchema = "ohdsi_results",
  studyName = "Cohort2Trajectory",
  baseUrl = "http://localhost:8080/WebAPI"
)
```

Arguments

pathToDriver	Path to a folder containing the JDBC driver JAR files. See downloadJdbcDrivers for instructions on how to download the relevant drivers.
pathToResults	Path to target directory where results will be saved
dbms	The type of DBMS running on the server. Valid values are: 'oracle', 'postgresql', 'redshift', 'sql server', 'pdw', 'netezza', 'bigquery', 'sqlite', 'sqlite extended', 'spark'
cdmSchema	Schema which contains the OHDSI Common Data Model.
cdmTmpSchema	Schema for temporary tables
cdmResultsSchema	Schema which has the information about the cohorts created in Atlas
user	The user name used to access the server.
pw	The password for that user.
server	The name of the server.
port	The port on the server to connect to.

Examples

```
#####
#
# Example on Eunomia
#
#####
```

```

studyName = "TestCohort2Trajectory" # TODO
pathToResults <- getwd() # TODO # default value: paste(getwd(), "/tmp", sep = "")

#####
#
# Database credentials
#
#####
pathToDriver = './Drivers'
dbms <- "sqlite" #TODO

cdmSchema = "main" #TODO # Schema which contains the OHDSI Common Data Model
cdmTmpSchema = "main" #TODO # Schema for temporary tables, will be deleted # should be ohdsi_temp
cdmResultsSchema = "main" #TODO # Schema which will contain the final results

baseUrl = NULL #TODO # WebAPI URL is not needed when jsons' are already imported

#####
#
# Initiate the database connection
#
#####
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
conn <- DatabaseConnector::connect(connectionDetails)
Eunomia::createCohorts(connectionDetails)

Cohort2Trajectory::runGUI(
  conn,
  connectionDetails,
  pathToDriver = pathToDriver,
  pathToResults = pathToResults,
  dbms = dbms,
  cdmSchema = cdmSchema,
  cdmTmpSchema = cdmTmpSchema,
  cdmResultsSchema = cdmResultsSchema,
  studyName = studyName,
  baseUrl = baseUrl
)

```

Index

* **package**

Cohort2Trajectory-package, [2](#)

Cohort2Trajectory, [3](#)

Cohort2Trajectory

(Cohort2Trajectory-package), [2](#)

Cohort2Trajectory-package, [2](#)

runGUI, [5](#)