

Package ‘TreatmentPatterns’

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Type Package

Title Analyzes Real-World Treatment Patterns of a Study Population of Interest

Version 2.6.5

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Description Computes treatment patterns within a given cohort using the Observational Medical Outcomes Partnership (OMOP) common data model (CDM). As described in Markus, Verhamme, Kors, and Rijnbeek (2022) <[doi:10.1016/j.cmpb.2022.107081](https://doi.org/10.1016/j.cmpb.2022.107081)>.

URL <https://github.com/darwin-eu-dev/TreatmentPatterns>

BugReports <https://github.com/darwin-eu-dev/TreatmentPatterns/issues>

Language en-US

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CharacterizationPlots *CharacterizationPlots*

Description

Class to handle the characterization plots.

Super class

[TreatmentPatterns::Module](#) -> CharacterizationPlots

Methods**Public methods:**

- [CharacterizationPlots\\$uiMenu\(\)](#)
- [CharacterizationPlots\\$uiBody\(\)](#)
- [CharacterizationPlots\\$server\(\)](#)
- [CharacterizationPlots\\$clone\(\)](#)

Method [uiMenu\(\)](#): Method to include a [menuItem](#) to link to the body.

Usage:

```
CharacterizationPlots$uiMenu(
  label = "Characteristics",
  tag = "characteristics"
)
```

Arguments:

```
label (character(1))
  Label to show for the menuItem.
tag (character(1))
  Tag to use internally in input.
```

Returns: (menuItem)

Method `uiBody()`: Method to include a [tabItem](#) to include the body.

Usage:

```
CharacterizationPlots$uiBody()
```

Returns: (tabItem)

Method `server()`: Method to handle the back-end.

Usage:

```
CharacterizationPlots$server(input, output, session, inputHandler)
```

Arguments:

`input` (input)

Input from the server function.

`output` (output)

Output from the server function.

`session` (session)

Session from the server function.

`inputHandler` (inputHandler)

[InputHandler](#) class.

Returns: (NULL)

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
CharacterizationPlots$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

computePathways

computePathways

Description

Compute treatment patterns according to the specified parameters within specified cohorts.

Usage

```
computePathways(  
  cohorts,  
  cohortTableName,  
  cdm = NULL,  
  connectionDetails = NULL,  
  cdmSchema = NULL,  
  resultSchema = NULL,  
  tempEmulationSchema = NULL,
```

```

includeTreatments = "startDate",
periodPriorToIndex = 0,
minEraDuration = 0,
splitEventCohorts = NULL,
splitTime = NULL,
eraCollapseSize = 30,
combinationWindow = 30,
minPostCombinationDuration = 30,
filterTreatments = "First",
maxPathLength = 5
)

```

Arguments

cohorts	(data.frame()) Data frame containing the following columns and data types: cohortId numeric(1) Cohort ID's of the cohorts to be used in the cohort table. cohortName character(1) Cohort names of the cohorts to be used in the cohort table. type character(1) ["target", "event", "exit"] Cohort type, describing if the cohort is a target, event, or exit cohort
cohortTableName	(character(1)) Cohort table name.
cdm	(CDMConnector::cdm_from_con()): NULL Optional; Ignores connectionDetails, cdmSchema, and resultSchema.
connectionDetails	(DatabaseConnector::createConnectionDetails(): NULL) Optional; In congruence with cdmSchema and resultSchema. Ignores cdm.
cdmSchema	(character(1): NULL) Optional; In congruence with connectionDetails and resultSchema. Ignores cdm.
resultSchema	(character(1): NULL) Optional; In congruence with connectionDetails and cdmSchema. Ignores cdm.
tempEmulationSchema	Schema used to emulate temp tables
includeTreatments	(character(1): "startDate") "startDate" Include treatments after the target cohort start date and onwards. "endDate" Include treatments before target cohort end date and before.
periodPriorToIndex	(integer(1): 0) Number of days prior to the index date of the target cohort that event cohorts are allowed to start

minEraDuration (integer(1): 0)
 Minimum time an event era should last to be included in analysis

splitEventCohorts
 (character(n): "")
 Specify event cohort to split in acute (< X days) and therapy (>= X days)

splitTime (integer(1): 30)
 Specify number of days (X) at which each of the split event cohorts should be split in acute and therapy

eraCollapseSize
 (integer(1): 30)
 Window of time between which two eras of the same event cohort are collapsed into one era

combinationWindow
 (integer(1): 30)
 Window of time two event cohorts need to overlap to be considered a combination treatment

minPostCombinationDuration
 (integer(1): 30)
 Minimum time an event era before or after a generated combination treatment should last to be included in analysis

filterTreatments
 (character(1): "First" ["first", "Changes", "all"])
 Select first occurrence of ('First'); changes between ('Changes'); or all event cohorts ('All').

maxPathLength (integer(1): 5)
 Maximum number of steps included in treatment pathway

Value

(Andromeda::andromeda()) [andromeda](#) object containing non-sharable patient level data outcomes.

Examples

```

library(TreatmentPatterns)
library(CDMConnector)
library(dplyr)

if (require("CirceR", character.only = TRUE, quietly = TRUE)) {
  withr::local_envvar(
    EUNOMIA_DATA_FOLDER = Sys.getenv("EUNOMIA_DATA_FOLDER", unset = tempfile())
  )

  downloadEunomiaData(overwrite = TRUE)

  con <- DBI::dbConnect(duckdb::duckdb(), dbdir = eunomia_dir())
  cdm <- cdmFromCon(con, cdmSchema = "main", writeSchema = "main")

  cohortSet <- readCohortSet(

```

```

  path = system.file(package = "TreatmentPatterns", "exampleCohorts")
)

cdm <- generateCohortSet(
  cdm = cdm,
  cohortSet = cohortSet,
  name = "cohort_table"
)

cohorts <- cohortSet %>%
  # Remove 'cohort' and 'json' columns
  select(-"cohort", -"json") %>%
  mutate(type = c("event", "event", "event", "event", "exit", "event", "event", "target")) %>%
  rename(
    cohortId = "cohort_definition_id",
    cohortName = "cohort_name",
  ) %>%
  select("cohortId", "cohortName", "type")

outputEnv <- computePathways(
  cohorts = cohorts,
  cohortTableName = "cohort_table",
  cdm = cdm
)

Andromeda::close(outputEnv)
DBI::dbDisconnect(con, shutdown = TRUE)
}

```

createSankeyDiagram *createSankeyDiagram*

Description

Create sankey diagram.

Usage

```

createSankeyDiagram(
  treatmentPathways,
  groupCombinations = FALSE,
  colors = NULL,
  ...
)

```

Arguments

treatmentPathways
 (data.frame())
 The contents of the treatmentPathways.csv-file as a data.frame().

```

groupCombinations
  (logical(1): FALSE)
  TRUE Group all combination treatments in category "Combination".
  FALSE Do not group combination treatments.
colors
  (character(n)) Vector of hex color codes.
...
  Paramaters for sankeyNetwork.

```

Value

(htmlwidget)

Examples

```

# Dummy data, typically read from treatmentPathways.csv
treatmentPathways <- data.frame(
  path = c("Acetaminophen", "Acetaminophen-Amoxicillin+Clavulanate",
           "Acetaminophen-Aspirin", "Amoxicillin+Clavulanate", "Aspirin"),
  freq = c(206, 6, 14, 48, 221),
  sex = rep("all", 5),
  age = rep("all", 5),
  index_year = rep("all", 5)
)

createSankeyDiagram(treatmentPathways)

```

createSankeyDiagram2 *createSankeyDiagram2*

Description

DEPRECATED Create sankey diagram.

Usage

```

createSankeyDiagram2(
  treatmentPathways,
  groupCombinations = FALSE,
  colors = NULL,
  ...
)

```

Arguments

```

treatmentPathways
  (data.frame())
  The contents of the treatmentPathways.csv-file as a data.frame().

```

```

groupCombinations
  (logical(1): FALSE)

  TRUE Group all combination treatments in category "Combination".
  FALSE Do not group combination treatments.

colors
  (character(n)) Vector of hex color codes.

...
  Paramaters for sankeyNetwork.

```

Value

```
(htmlwidget)
```

Examples

```

# Dummy data, typically read from treatmentPathways.csv
treatmentPathways <- data.frame(
  path = c("Acetaminophen", "Acetaminophen-Amoxicillin+Clavulanate",
           "Acetaminophen-Aspirin", "Amoxicillin+Clavulanate", "Aspirin"),
  freq = c(206, 6, 14, 48, 221),
  sex = rep("all", 5),
  age = rep("all", 5),
  index_year = rep("all", 5)
)

createSankeyDiagram(treatmentPathways)

```

```
createSunburstPlot     createSunburstPlot
```

Description

New sunburstPlot function

Usage

```
createSunburstPlot(treatmentPathways, groupCombinations = FALSE, ...)
```

Arguments

```

treatmentPathways
  (data.frame())
  The contents of the treatmentPathways.csv-file as a data.frame().

groupCombinations
  (logical(1): FALSE)

  TRUE Group all combination treatments in category "Combination".
  FALSE Do not group combination treatments.

...
  Paramaters for sunburst.

```

Value

(htmlwidget)

Examples

```
# Dummy data, typically read from treatmentPathways.csv
treatmentPathways <- data.frame(
  path = c("Acetaminophen", "Acetaminophen-Amoxicillin+Clavulanate",
           "Acetaminophen-Aspirin", "Amoxicillin+Clavulanate", "Aspirin"),
  freq = c(206, 6, 14, 48, 221),
  sex = rep("all", 5),
  age = rep("all", 5),
  index_year = rep("all", 5)
)

createSunburstPlot(treatmentPathways)
```

createSunburstPlot2 *createSunburstPlot2*

Description

DEPRECATED New sunburstPlot function

Usage

```
createSunburstPlot2(treatmentPathways, groupCombinations = FALSE, ...)
```

Arguments

treatmentPathways
(data.frame())
The contents of the treatmentPathways.csv-file as a data.frame().

groupCombinations
(logical(1): FALSE)

TRUE Group all combination treatments in category "Combination".
FALSE Do not group combination treatments.

... Paramaters for [sunburst](#).

Value

(htmlwidget)

Examples

```
# Dummy data, typically read from treatmentPathways.csv
treatmentPathways <- data.frame(
  path = c("Acetaminophen", "Acetaminophen-Amoxicillin+Clavulanate",
           "Acetaminophen-Aspirin", "Amoxicillin+Clavulanate", "Aspirin"),
  freq = c(206, 6, 14, 48, 221),
  sex = rep("all", 5),
  age = rep("all", 5),
  index_year = rep("all", 5)
)

createSunburstPlot2(treatmentPathways)
```

```
executeTreatmentPatterns
```

```
executeTreatmentPatterns
```

Description

Compute treatment patterns according to the specified parameters within specified cohorts. For more customization, or investigation of patient level outcomes, you can run [computePathways](#) and [export](#) separately.

Usage

```
executeTreatmentPatterns(
  cohorts,
  cohortTableName,
  outputPath,
  cdm = NULL,
  connectionDetails = NULL,
  cdmSchema = NULL,
  resultSchema = NULL,
  tempEmulationSchema = NULL,
  minEraDuration = 0,
  eraCollapseSize = 30,
  combinationWindow = 30,
  minCellCount = 5
)
```

Arguments

cohorts (data.frame())
Data frame containing the following columns and data types:
cohortId numeric(1) Cohort ID's of the cohorts to be used in the cohort table.
cohortName character(1) Cohort names of the cohorts to be used in the cohort table.

type character(1) ["**target**", "**event**", "**exit**"] Cohort type, describing if the cohort is a target, event, or exit cohort

cohortTableName (character(1))
Cohort table name.

outputPath (character(1))

cdm (CDMConnector::cdm_from_con(): NULL)
Optional; Ignores connectionDetails, cdmSchema, and resultSchema.

connectionDetails (DatabaseConnector::createConnectionDetails(): NULL)
Optional; In congruence with cdmSchema and resultSchema. Ignores cdm.

cdmSchema (character(1): NULL)
Optional; In congruence with connectionDetails and resultSchema. Ignores cdm.

resultSchema (character(1): NULL)
Optional; In congruence with connectionDetails and cdmSchema. Ignores cdm.

tempEmulationSchema (character(1)) Schema to emulate temp tables.

minEraDuration (integer(1): 0)
Minimum time an event era should last to be included in analysis

eraCollapseSize (integer(1): 30)
Window of time between which two eras of the same event cohort are collapsed into one era

combinationWindow (integer(1): 30)
Window of time two event cohorts need to overlap to be considered a combination treatment

minCellCount (integer(1): 5)
Minimum count required per pathway. Censors data below x as <x. This minimum value will carry over to the sankey diagram and sunburst plot.

Value

(invisible(NULL))

Examples

```
library(TreatmentPatterns)
library(CDMConnector)
library(dplyr)
if (require("CirceR", character.only = TRUE, quietly = TRUE)) {
  withr::local_envvar(
    EUNOMIA_DATA_FOLDER = Sys.getenv("EUNOMIA_DATA_FOLDER", unset = tempfile())
  )
}
```

```

)

downloadEunomiaData(overwrite = TRUE)

con <- DBI::dbConnect(duckdb::duckdb(), dbdir = eunomia_dir())
cdm <- cdmFromCon(con, cdmSchema = "main", writeSchema = "main")

cohortSet <- readCohortSet(
  path = system.file(package = "TreatmentPatterns", "exampleCohorts")
)

cdm <- generateCohortSet(
  cdm = cdm,
  cohortSet = cohortSet,
  name = "cohort_table"
)

cohorts <- cohortSet %>%
  # Remove 'cohort' and 'json' columns
  select("-cohort", "-json") %>%
  mutate(type = c("event", "event", "event", "event", "exit", "event", "event", "target")) %>%
  rename(
    cohortId = "cohort_definition_id",
    cohortName = "cohort_name",
  ) %>%
  select("cohortId", "cohortName", "type")

executeTreatmentPatterns(
  cohorts = cohorts,
  cohortTableName = "cohort_table",
  cdm = cdm,
  outputPath = tempdir()
)

DBI::dbDisconnect(con, shutdown = TRUE)
}

```

 export

export

Description

Export andromeda generated by `computePathways` object to sharable csv-files and/or a zip archive.

Usage

```

export(
  andromeda,
  outputPath,

```

```

    ageWindow = 10,
    minCellCount = 5,
    censorType = "minCellCount",
    archiveName = NULL
  )

```

Arguments

andromeda	(Andromeda::andromeda()) Andromeda object.
outputPath	(character(1))
ageWindow	(integer(n): 10) Number of years to bin age groups into. It may also be a vector of integers. I.e. <code>c(0, 18, 150)</code> which will results in age group 0-18 which includes subjects < 19. And age group 18-150 which includes subjects > 18.
minCellCount	(integer(1): 5) Minimum count required per pathway. Censors data below <code>x</code> as <code><x</code> . This minimum value will carry over to the sankey diagram and sunburst plot.
censorType	(character(1)) "minCellCount" Censors pathways <code><minCellCount</code> to <code>minCellCount</code> . "remove" Censors pathways <code><minCellCount</code> by removing them completely. "mean" Censors pathways <code><minCellCount</code> to the mean of all frequencies below <code>minCellCount</code>
archiveName	(character(1): NULL) If not NULL adds the exported files to a ZIP-file with the specified archive name.

Value

(invisible(NULL))

Examples

```

library(TreatmentPatterns)
library(CDMConnector)
library(dplyr)

if (require("CirceR", character.only = TRUE, quietly = TRUE)) {
  withr::local_envvar(
    EUNOMIA_DATA_FOLDER = Sys.getenv("EUNOMIA_DATA_FOLDER", unset = tempfile())
  )

  downloadEunomiaData(overwrite = TRUE)

  con <- DBI::dbConnect(duckdb::duckdb(), dbdir = eunomia_dir())
  cdm <- cdmFromCon(con, cdmSchema = "main", writeSchema = "main")

```

```

cohortSet <- readCohortSet(
  path = system.file(package = "TreatmentPatterns", "exampleCohorts")
)

cdm <- generateCohortSet(
  cdm = cdm,
  cohortSet = cohortSet,
  name = "cohort_table"
)

cohorts <- cohortSet %>%
  # Remove 'cohort' and 'json' columns
  select(-"cohort", -"json") %>%
  mutate(type = c("event", "event", "event", "event", "exit", "event", "event", "target")) %>%
  rename(
    cohortId = "cohort_definition_id",
    cohortName = "cohort_name",
  ) %>%
  select("cohortId", "cohortName", "type")

outputEnv <- computePathways(
  cohorts = cohorts,
  cohortTableName = "cohort_table",
  cdm = cdm
)

export(
  andromeda = outputEnv,
  outputPath = tempdir()
)

Andromeda::close(outputEnv)
DBI::dbDisconnect(con, shutdown = TRUE)
}

```

InputHandler

InputHandler

Description

Class to handle input from the user. Supports direct paths or input fields through `setDataPath()`.

Super class

[TreatmentPatterns::Module](#) -> InputHandler

Active bindings

reactiveValues (reactiveValues)
reactiveValues class created by [reactiveValues](#).

Methods**Public methods:**

- [InputHandler\\$uiMenu\(\)](#)
- [InputHandler\\$uiBody\(\)](#)
- [InputHandler\\$server\(\)](#)
- [InputHandler\\$uiDatabaseSelector\(\)](#)
- [InputHandler\\$setDataPath\(\)](#)
- [InputHandler\\$clone\(\)](#)

Method [uiMenu\(\)](#): Method to include a [menuItem](#) to link to the body.

Usage:

```
InputHandler$uiMenu(label = "File upload", tag = "fileUpload")
```

Arguments:

label (character(1))
Label to show for the menuItem.
tag (character(1))
Tag to use internally in input.

Returns: (menuItem)

Method [uiBody\(\)](#): Method to include a [tabItem](#) to include the body.

Usage:

```
InputHandler$uiBody()
```

Returns: (tabItem)

Method [server\(\)](#): Method to handle the back-end.

Usage:

```
InputHandler$server(input, output, session)
```

Arguments:

input (input)
Input from the server function.
output (output)
Output from the server function.
session (session)
Session from the server function.

Returns: (NULL)

Method [uiDatabaseSelector\(\)](#): Method to include a [uiOutput](#) to select between multiple uploaded files.

Usage:

InputHandler\$uiDatabaseSelector()

Returns: (uiOutput)

Method setDataPath(): Method to dictate where the data is coming from, either from the input through the shiny application, or from a specified path. When one is provided, the other is ignored.

Usage:

InputHandler\$setDataPath(tag = "uploadField", input = NULL, path = NULL)

Arguments:

tag (character(1))

Tag to use internally in input.

input (input)

Input from the server function of the shiny app.

path (character(1))

Path to a zip-file containing TreatmentPatterns output files.

Returns: (invisible(self))

Method clone(): The objects of this class are cloneable with this method.

Usage:

InputHandler\$clone(deep = FALSE)

Arguments:

deep Whether to make a deep clone.

InteractivePlots

InteractivePlots

Description

Class to handle the interactive plots of TreatmentPatterns (Sunburst plot & Sankey diagram)

Super class

[TreatmentPatterns::Module](#) -> InteractivePlots

Methods

Public methods:

- [InteractivePlots\\$uiMenu\(\)](#)
- [InteractivePlots\\$uiBody\(\)](#)
- [InteractivePlots\\$server\(\)](#)
- [InteractivePlots\\$clone\(\)](#)

Method uiMenu(): Method to include a [menuItem](#) to link to the body.

Usage:

```
InteractivePlots$uiMenu(label = "Plots", tag = "plots")
```

Arguments:

```
label (character(1))  
  Label to show for the menuItem.  
tag (character(1))  
  Tag to use internally in input.
```

Returns: (menuItem)

Method `uiBody()`: Method to include a [tabItem](#) to include the body.

Usage:

```
InteractivePlots$uiBody()
```

Returns: (tabItem)

Method `server()`: Method to handle the back-end.

Usage:

```
InteractivePlots$server(input, output, session, inputHandler)
```

Arguments:

```
input (input)  
  Input from the server function.  
output (output)  
  Output from the server function.  
session (session)  
  Session from the server function.  
inputHandler (inputHandler)  
  InputHandler class.
```

Returns: (NULL)

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
InteractivePlots$clone(deep = FALSE)
```

Arguments:

```
deep Whether to make a deep clone.
```

launchResultsExplorer *launchResultsExplorer*

Description

Launches the ResultExplorer shinyApp.

Usage

```
launchResultsExplorer()
```

Value

```
(shinyApp)
```

Examples

```
if (interactive()) {
  launchResultsExplorer()
}
```

 Module

Module

Description

Module super class

Active bindings

namespace Namespace of the module.

Methods**Public methods:**

- [Module\\$new\(\)](#)
- [Module\\$validate\(\)](#)
- [Module\\$uiMenu\(\)](#)
- [Module\\$uiBody\(\)](#)
- [Module\\$server\(\)](#)
- [Module\\$clone\(\)](#)

Method new(): Initializer method

Usage:

```
Module$new(namespace)
```

Arguments:

```
namespace (character(1))
```

Returns: (invisible(self))

Method validate(): Validator method

Usage:

```
Module$validate()
```

Returns: (invisible(self))

Method `uiMenu()`: Method to include a [menuItem](#) to link to the body.

Usage:

```
Module$uiMenu(label, tag)
```

Arguments:

label (character(1))

Label to show for the menuItem.

tag (character(1))

Tag to use internally in input.

Returns: (menuItem)

Method `uiBody()`: Method to include a [tabItem](#) to include the body.

Usage:

```
Module$uiBody()
```

Returns: (tabItem)

Method `server()`: Method to handle the back-end.

Usage:

```
Module$server(input, output, session)
```

Arguments:

input (input)

Input from the server function.

output (output)

Output from the server function.

session (session)

Session from the server function.

Returns: (NULL)

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
Module$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

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