

Package ‘CohortPathways’

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Type Package

Title Cohort Pathways to create pathways for Target and Event cohorts

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Description An R package that creates new cohort(s) from previously instantiated cohorts.

Depends DatabaseConnector (>= 5.0.0),
R (>= 4.1.0)

Imports checkmate,
dplyr,
lifecycle,
ParallelLogger,
SqlRender,
sunburstR

Suggests remotes,
rmarkdown,
knitr,
testthat,
withr

Remotes ohdsi/ParallelLogger

License Apache License

RoxygenNote 7.2.2

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

Encoding UTF-8

Language en-US

URL <https://ohdsi.github.io/CohortPathways/>, <https://github.com/OHDSI/CohortPathways>

BugReports <https://github.com/OHDSI/CohortPathways/issues>

R topics documented:

| | |
|---------------------------------|---|
| executeCohortPathways | 2 |
| plotCohortPathways | 3 |

Index**5**

executeCohortPathways *Execute cohort pathway analysis.*

Description

Runs the cohort pathways on all instantiated combinations of target and event cohorts. Assumes the cohorts have already been instantiated.

Usage

```
executeCohortPathways(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema,
  cohortTableName = "cohort",
  targetDatabaseSchema = NULL,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),
  targetCohortIds,
  eventCohortIds,
  cohortDefinitionSet,
  exportFolder,
  minCellCount = 5,
  allowRepeats = FALSE,
  maxDepth = 5,
  collapseWindow = 30,
  overwrite = TRUE
)
```

Arguments

- | | |
|----------------------|--|
| connectionDetails | An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package. Can be left NULL if connection is provided. |
| connection | An object of type connection as created using the connect function in the DatabaseConnector package. Can be left NULL if connectionDetails is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes. |
| cohortDatabaseSchema | Schema name where your cohort tables reside. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'. |
| tempEmulationSchema | Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created. |
| targetCohortIds | A vector of one or more Cohort Ids corresponding to target cohort (s). |
| eventCohortIds | A vector of one or more Cohort Ids corresponding to event cohort (s). |

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| cohortDefinitionSet | A data frame object with minimum two columns, cohortId and cohortName. It should have all the cohortId's in targetCohortId and eventCohortId. This is the source of cohort names. |
| exportFolder | The folder where the output will be exported to. If this folder does not exist it will be created. |
| minCellCount | (Default = 5) The minimum cell count for fields contains person counts or fractions. |
| allowRepeats | (Default = FALSE) Allow cohort events/combo to appear multiple times in the same pathway. |
| maxDepth | (Default = 5) Maximum number of steps in a given pathway to be included in the sunburst plot. |
| collapseWindow | (Default = 30) Any dates found within the specified collapse days will be reassigned the earliest date. Collapsing dates reduces pathway variation, leading to a reduction in 'noise' in the result. |
| overwrite | (Default = TRUE) Do you want to overwrite results? |
| targetDatabaseSchema | (Optional) Schema name where output pathway tables would reside. This is also known as as resultsDatabaseSchema. If not specified, scratch schema will be used. The output may not persist in the database after disconnection. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'. |
| cohortTable | The name of the cohort table. |

Examples

```
## Not run:
connectionDetails <- createConnectionDetails(
  dbms = "postgresql",
  server = "ohdsi.com",
  port = 5432,
  user = "me",
  password = "secure"
)

executeCohortPathways(
  connectionDetails = connectionDetails,
  cohorts = cohorts,
  exportFolder = "export",
  cohortDatabaseSchema = "results"
)

## End(Not run)
```

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| plotCohortPathways | <i>Plot cohort pathway.</i> |
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Description

Uses the output of executeCohortPathways and using sunburstD3 produces sunburst plots

Usage

```
plotCohortPathways(
  resultsFolder,
  exportFolder,
  pathwayAnalysisGenerationId = NULL,
  targetCohortId = NULL,
  height = 400,
  width = "100%"
)
```

Arguments

| | |
|--|--|
| <code>resultsFolder</code> | The folder where the output from <code>executeCohortPathways</code> is located. If provided, then the function will look for <code>pathwayAnalysisCodes.csv</code> and <code>pathwayAnalysisPaths.csv</code> . Ignored if <code>pathwayAnalysisCodes</code> or <code>pathwayAnalysisPaths</code> are provided. |
| <code>exportFolder</code> | The folder where the output will be exported to. If this folder does not exist it will be created. |
| <code>pathwayAnalysisGenerationId</code> | (Optional) Generation id of pathway. This uniquely identifies every generation execution. |
| <code>targetCohortId</code> | (Optional) The cohort id of the target cohort. |
| <code>height</code> | (Optional) height and width of sunburst htmlwidget containing div specified in any valid CSS size unit. |
| <code>width</code> | (Optional) height and width of sunburst htmlwidget containing div specified in any valid CSS size unit. |

Examples

```
## Not run:

executeCohortPathways(
  resultsFolder = "results",
  pathwayAnalysisGenerationId = 1234,
  targetCohortId = 1
)

## End(Not run)
```

Index

connect, [2](#)
createConnectionDetails, [2](#)
executeCohortPathways, [2](#)
plotCohortPathways, [3](#)