

# Package ‘CohortPathways’

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**Type** Package

**Title** Create Pathways From Target to Event Cohorts

**Version** 0.0.1

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**Description** This software tool is designed to compute the temporal relationship defined as pathways between any two instantiated cohorts. The cohorts are input as Target and event cohorts.

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

**Imports** checkmate,  
dplyr,  
lifecycle,  
readr,  
rlang,  
SqlRender,  
tidyr

**Suggests** remotes,  
rmarkdown,  
knitr,  
testthat,  
withr

**License** Apache License

**RoxygenNote** 7.2.3

**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

**Index** . . . . . 4

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executeCohortPathways *Execute cohort pathway analysis.*

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## 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 <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.   |
| connection           | An object of type connection as created using the <a href="#">connect</a> 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'.  |
| cohortTableName      | The name of the cohort table.   |
| 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'. |

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).
cohortDefinitionSet	A data frame object with minimum two columns, cohortId and 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?

### Value

Nothing is returned

### 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)
```

# Index

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