Package 'CohortSymmetry'

March 24, 2025

Title Sequence Symmetry Analysis Using the Observational Medical
Outcomes Partnership Common Data Model

Version 0.2.4

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Description Calculating crude sequence ratio, adjusted sequence ratio and
confidence intervals using data mapped to the Observational Medical
Outcomes Partnership Common Data Model.

License Apache License (>= 2)

Encoding UTF-8

RoxygenNote 7.3.2

Depends R (>= 4.1.0)

Suggests testthat (>= 3.1.5), DBI (>= 1.0.0), cli, odbc, RPostgres,
tidyselect, knitr, dbplyr (>= 2.5.0), omock (>= 0.3.1),
visOmopResults (>= 0.4.0), flextable, gt, ggplot2, duckdb,
rmarkdown

Imports CDMConnector (>= 1.7.0), dplyr, PatientProfiles (>= 1.0.0),
rlang, tibble, tidyr, stats, here, omopgenerics (>= 1.0.0),
DrugUtilisation (>= 0.7.0), CodelistGenerator (>= 3.1.0)

Config/testthat/edition 3

URL https://ohdsi.github.io/CohortSymmetry/

BugReports https://github.com/OHDSI/CohortSymmetry/issues

VignetteBuilder knitr

NeedsCompilation no

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Contents

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generateSequenceCohortSet

Intersecting the index and marker cohorts prior to calculating Sequence Symmetry Ratios

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Description

Join two tables in the CDM (one for index and the other for marker cohorts) into a new table in the cdm taking into account the maximum time interval between events. Index and marker cohorts should be instantiated in advance by the user.

Usage

```
generateSequenceCohortSet(
  cdm,
  indexTable,
  markerTable,
  name,
  indexId = NULL,
  markerId = NULL,
  cohortDateRange = as.Date(c(NA, NA)),
  daysPriorObservation = 0,
  washoutWindow = 0,
  indexMarkerGap = Inf,
  combinationWindow = c(0, 365),
  movingAverageRestriction = 548
)
```

Arguments

cdm	A CDM reference.
indexTable	A table in the CDM that the index cohorts should come from.
markerTable	A table in the CDM that the marker cohorts should come from.
name	The name within the cdm that the output is called. Default is joined_cohorts.
indexId	Cohort definition IDs in indexTable to be considered for the analysis. Change to NULL if all indices are wished to be included.
markerId	Cohort definition IDs in markerTable to be considered for the analysis. Change to NULL if all markers are wished to be included.
cohortDateRange	
	Two dates indicating study period and the sequences that the user wants to restrict to.
daysPriorObservation	
	The minimum amount of prior observation required on both the index and marker cohorts per person.
washoutWindow	A washout window to be applied on both the index cohort event and marker cohort.
indexMarkerGap	The maximum allowable gap between the end of the first episode and the start of the second episode in a sequence/combination.
combinationWindow	
	A constrain to be placed on the gap between two initiations. Default c(0,365), meaning the gap should be larger than 0 but less than or equal to 365.
movingAverageRestriction	
	The moving window when calculating nSR, default is 548.

Value

A table within the cdm reference.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm <- generateSequenceCohortSet(
  cdm = cdm,
  name = "joined_cohorts",
  indexTable = "cohort_1",
  markerTable = "cohort_2"
)
 cdm$joined_cohorts
 CDMConnector::cdmDisconnect(cdm = cdm)
```

---

mockCohortSymmetry   *Creates mock cdm object for testing*

Description

Creates a mock cdm with two default synthetic cohorts, one is the index cohort and the other one is the marker cohort. However the users could specify them should they wish.

Usage

```
mockCohortSymmetry(
  seed = 1,
  indexCohort = NULL,
  markerCohort = NULL,
  con = NULL,
  schema = "main"
)
```

Arguments

seed	The seed to be inputted.
indexCohort	The tibble of your index cohort. Default is NULL, which means the default indexCohort is being used.
markerCohort	The tibble of your marker cohort. Default is NULL, which means the default markerCohort is being used.
con	Connection detail.
schema	Name of your write schema.

Value

A mock cdm object contains your index and marker cohort

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm
CDMConnector::cdmDisconnect(cdm = cdm)
```

---

plotSequenceRatios *A plot for the sequence ratios.*

Description

It provides a ggplot of the sequence ratios of index and marker cohorts.

Usage

```
plotSequenceRatios(
  result,
  onlyASR = FALSE,
  plotTitle = NULL,
  labs = c("SR", "Drug Pairs"),
  colours = c("red", "blue"),
  facet = NULL
)
```

Arguments

result	Table output from summariseSequenceRatios.
onlyASR	If set to be TRUE then only adjusted SR will be plotted. Otherwise if it is set to be FALSE then both adjusted and crude SR will be plotted.
plotTitle	Title of the plot, if NULL no title will be included in the plot.
labs	Axis labels for the plot.
colours	Colours for sequence ratio.
facet	The variable to facet by.

Value

A plot for the sequence ratios of index and marker cohorts.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm <- generateSequenceCohortSet(cdm = cdm,
                                 indexTable = "cohort_1",
                                 markerTable = "cohort_2",
                                 name = "joined_cohort")
sequence_ratio <- summariseSequenceRatios(cohort = cdm$joined_cohort)
plotSequenceRatios(result = sequence_ratio)
CDMConnector::cdmDisconnect(cdm = cdm)
```

---

plotTemporalSymmetry   *A plot for the temporal symmetry of cohorts.*

Description

It provides a ggplot of the temporal symmetry of two or more cohorts.

Usage

```
plotTemporalSymmetry(
  result,
  plotTitle = NULL,
  labs = c("Time (months)", "Individuals (N)"),
  xlim = c(-12, 12),
  colours = c("blue", "red"),
  scales = "free"
)
```

Arguments

result	Table output from summariseTemporalSymmetry.
plotTitle	Title of the plot, if NULL no title will be plotted.
labs	Axis labels for the plot.
xlim	Limits for the x axis of the plot.
colours	Colours for both parts of the plot, pre- and post- time 0.
scales	Whether to set free y scales for the facet wrap when there are multiple plots (i.e. each plot has its own scaled y axis) or set them equal for all. Only accepts "free" for the former and "fixed" for the latter.

Value

A plot for the temporal symmetry of cohorts.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm <- generateSequenceCohortSet(cdm = cdm,
                                 indexTable = "cohort_1",
                                 markerTable = "cohort_2",
                                 name = "joined_cohort")
temporal_symmetry <- summariseTemporalSymmetry(cohort = cdm$joined_cohort)
plotTemporalSymmetry(result = temporal_symmetry)
CDMConnector::cdmDisconnect(cdm = cdm)
```

---

summariseSequenceRatios

Sequence ratio calculations

Description

Using generateSequenceCohortSet to obtain sequence ratios for the desired outcomes.

Usage

```
summariseSequenceRatios(cohort, cohortId = NULL, confidenceInterval = 95)
```

Arguments

cohort   A cohort table in the cdm.

cohortId   The Ids in the cohort that are to be included in the analyses.

confidenceInterval

                  Default is 95, indicating the central 95% confidence interval.

Value

A local table with all the analyses.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm <- generateSequenceCohortSet(cdm = cdm,
                                 name = "joined_cohorts",
                                 indexTable = "cohort_1",
                                 markerTable = "cohort_2")
pssa_result <- summariseSequenceRatios(cohort = cdm$joined_cohorts)
pssa_result
CDMConnector::cdmDisconnect(cdm)
```

---

summariseTemporalSymmetry

Summarise temporal symmetry

Description

Using generateSequenceCohortSet to obtain temporal symmetry (aggregated counts) of two cohorts.

Usage

```
summariseTemporalSymmetry(cohort, cohortId = NULL, timescale = "month")
```

Arguments

cohort   A cohort table in the cdm.

cohortId   The Ids in the cohort that are to be included in the analyses.

timescale   Timescale for the x axis of the plot (month, day, year).

Value

An aggregated table with difference in time (marker - index) and the relevant counts.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm <- generateSequenceCohortSet(cdm = cdm,
                                 name = "joined_cohorts",
                                 indexTable = "cohort_1",
                                 markerTable = "cohort_2")
temporal_symmetry <- summariseTemporalSymmetry(cohort = cdm$joined_cohorts)
CDMConnector::cdmDisconnect(cdm)
```

---

tableSequenceRatios   *A formatted visualization of sequence_symmetry objects.*

Description

It provides a formatted table with the contents of the summariseSequenceRatios output.

Usage

```
tableSequenceRatios(
  result,
  header = "marker_cohort_name",
  groupColumn = "cdm_name",
  type = "gt",
  hide = "variable_level"
)
```

Arguments

`result`	A sequence_symmetry object.
`header`	A vector specifying the elements to include in the header. See visOmopResults package for more information on how to use this parameter.
`groupColumn`	Columns to use as group labels. See visOmopResults package for more information on how to use this parameter.
`type`	The desired format of the output table.
`hide`	Columns to drop from the output table.

Value

A formatted version of the sequence_symmetry object.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm <- generateSequenceCohortSet(cdm = cdm,
                                 indexTable = "cohort_1",
                                 markerTable = "cohort_2",
                                 name = "joined_cohort")
res <- summariseSequenceRatios(cohort = cdm$joined_cohort)
gtResult <- tableSequenceRatios(res)
CDMConnector::cdmDisconnect(cdm = cdm)
```

---

tableTemporalSymmetry   *A formatted visualization of temporal_symmetry objects.*

Description

It provides a formatted table with the contents of the summariseTemporalSymmetry output.

Usage

```
tableTemporalSymmetry(
  result,
  header = "variable_level",
  groupColumn = c("cdm_name", "index_name"),
  type = "gt",
  hide = "variable_name"
)
```

Arguments

`result`	A temporal_symmetry object.
`header`	A vector specifying the elements to include in the header. See visOmopResults package for more information on how to use this parameter.
`groupColumn`	Columns to use as group labels. See visOmopResults package for more information on how to use this parameter.
`type`	The desired format of the output table.
`hide`	Columns to drop from the output table.

Value

A formatted version of the temporal_symmetry object.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm <- generateSequenceCohortSet(cdm = cdm,
                                 indexTable = "cohort_1",
                                 markerTable = "cohort_2",
                                 name = "joined_cohort")
res <- summariseTemporalSymmetry(cohort = cdm$joined_cohort)
gtResult <- tableTemporalSymmetry(result = res)
CDMConnector::cdmDisconnect(cdm = cdm)
```

Index