Package 'CohortSymmetry'

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

Version 0.4.0

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Description Calculates crude sequence ratios, adjusted sequence ratios and confidence intervals using data mapped to the Observational Medical Outcomes Partnership Common Data Model. The methodology for sequence symmetry analysis is described by Pratt et al. (2015) <doi:10.1002/pds.3780> and Hendrix et al. (2024) <doi:10.1186/s12874-023-02108-y>.

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

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`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)
```

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.

Value

A mock cdm object contains your index and marker cohort

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
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,
  style = "default",
  labs = c("Sequence Ratio", "Index Marker Pair"),
  colours = NULL,
  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.
`style`	Style used for the plot. Passed to `visOmopResults::themeVisOmop()`.
`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$joined_cohort <- sequenceCohort(cdm = cdm,
                                    indexCohortTable = "cohort_1",
                                    markerCohortTable = "cohort_2",
                                    name = "joined_cohort")
sequence_ratio <- summariseSequenceRatios(cohort = cdm$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 (days)", "Individuals (N)"),
  xlim = c(-365, 365),
  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$joined_cohort <- sequenceCohort(cdm = cdm,
                                    indexCohortTable = "cohort_1",
                                    markerCohortTable = "cohort_2",
                                    name = "joined_cohort")
temporal_symmetry <- summariseTemporalSymmetry(cohort = cdm$joined_cohort)
plotTemporalSymmetry(result = temporal_symmetry)
CDMConnector::cdmDisconnect(cdm = cdm)
```

---

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

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

```
sequenceCohort(
  cdm,
  indexCohortTable,
  markerCohortTable,
  name,
  indexCohortId = NULL,
  markerCohortId = NULL,
  cohortDateRange = as.Date(c(NA, NA)),
  sequencePriorObservation = 365,
  indexMarkerWashout = 365,
  indexMarkerGap = Inf,
  combinationWindow = c(0, 365)
)
```

Arguments

cdm	A CDM reference.
indexCohortTable	A table in the CDM that the index cohorts should come from.
markerCohortTable	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.

`indexCohortId` Cohort definition IDs in indexCohortTable to be considered for the analysis. Change to NULL if all indices are wished to be included.

`markerCohortId` Cohort definition IDs in markerCohortTable 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.

`sequencePriorObservation`
The minimum amount of prior observation required on the index marker sequence. Default is 365 days.

`indexMarkerWashout`
A washout window to be applied on both the index cohort and marker cohort. Default is 365 days.

`indexMarkerGap` The maximum allowable gap between the end of the first episode and the start of the second episode in a sequence/combination. Default is Inf.

`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.

Value

A table within the cdm reference.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm$joined_cohorts <- sequenceCohort(
  cdm = cdm,
  name = "joined_cohorts",
  indexCohortTable = "cohort_1",
  markerCohortTable = "cohort_2"
)
 cdm$joined_cohorts
```

---

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$joined_cohorts <- sequenceCohort(cdm = cdm,
                                     name = "joined_cohorts",
                                     indexCohortTable = "cohort_1",
                                     markerCohortTable = "cohort_2")
pssa_result <- summariseSequenceRatios(cohort = cdm$joined_cohorts)
pssa_result
```

---

summariseTemporalSymmetry

Summarise temporal symmetry

Description

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

Usage

```
summariseTemporalSymmetry(cohort, cohortId = NULL, days = 30)
```

Arguments

cohort	A cohort table in the cdm.
cohortId	The Ids in the cohort that are to be included in the analyses.
days	Numerical timescale for the x axis of the plot in days (Default is 30 days, if users want years put 365, days put 1).

Value

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

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm$joined_cohorts <- sequenceCohort(cdm = cdm,
                                     name = "joined_cohorts",
                                     indexCohortTable = "cohort_1",
                                     markerCohortTable = "cohort_2")
temporal_symmetry <- summariseTemporalSymmetry(cohort = cdm$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",
  style = "default",
  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.
style	Style used for the table.
hide	Columns to drop from the output table.

Value

A formatted version of the sequence_symmetry object.

Examples

```
library(CohortSymmetry)
cdm <- mockCohortSymmetry()
cdm$joined_cohort <- sequenceCohort(cdm = cdm,
                                    indexCohortTable = "cohort_1",
                                    markerCohortTable = "cohort_2",
                                    name = "joined_cohort")
res <- summariseSequenceRatios(cohort = cdm$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",
  style = "default",
  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.
style	Style used for the table.
hide	Columns to drop from the output table.

Value

A formatted version of the temporal_symmetry object.

Examples

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

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