

Package ‘IncidencePrevalence’

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Title Estimate Incidence and Prevalence using the OMOP Common Data Model

Version 1.2.0

Description Calculate incidence and prevalence using data mapped to the Observational Medical Outcomes Partnership (OMOP) common data model. Incidence and prevalence can be estimated for the total population in a database or for a stratification cohort.

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asIncidenceResult	<i>A tidy implementation of the summarised_result object for incidence results.</i>
-------------------	---

Description

A tidy implementation of the summarised_result object for incidence results.

Usage

asIncidenceResult(result, metadata = FALSE)

Arguments

result	A summarised_result object created by the IncidencePrevalence package.
metadata	If TRUE additional metadata columns will be included in the result.

Value

A tibble with a tidy version of the summarised_result object.

Examples

```
cdm <- mockIncidencePrevalence()
inc <- estimateIncidence(cdm, "target", "outcome")
tidy_inc <- asIncidenceResult(inc)
```

asPrevalenceResult	<i>A tidy implementation of the summarised_result object for prevalence results.</i>
--------------------	--

Description

A tidy implementation of the summarised_result object for prevalence results.

Usage

```
asPrevalenceResult(result, metadata = FALSE)
```

Arguments

result	A summarised_result object created by the IncidencePrevalence package.
metadata	If TRUE additional metadata columns will be included in the result.

Value

A tibble with a tidy version of the summarised_result object.

Examples

```
cdm <- mockIncidencePrevalence()
prev <- estimatePointPrevalence(cdm, "target", "outcome")
tidy_prev <- asPrevalenceResult(prev)
```

availableIncidenceGrouping

Variables that can be used for faceting and colouring incidence plots

Description

Variables that can be used for faceting and colouring incidence plots

Usage

```
availableIncidenceGrouping(result, varying = FALSE)
```

Arguments

result	Incidence results
varying	If FALSE, only variables with non-unique values will be returned, otherwise all available variables will be returned

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2014-01-01"), as.Date("2018-01-01"))
)
inc <- estimateIncidence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome"
)
availableIncidenceGrouping(inc)
```

availablePrevalenceGrouping

Variables that can be used for faceting and colouring prevalence plots

Description

Variables that can be used for faceting and colouring prevalence plots

Usage

```
availablePrevalenceGrouping(result, varying = FALSE)
```

Arguments

result	Prevalence results
varying	If FALSE, only variables with non-unique values will be returned, otherwise all available variables will be returned

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2014-01-01"), as.Date("2018-01-01"))
)
prev <- estimatePointPrevalence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome"
)
availablePrevalenceGrouping(prev)
```

benchmarkIncidencePrevalence

Run benchmark of incidence and prevalence analyses

Description

Run benchmark of incidence and prevalence analyses

Usage

```
benchmarkIncidencePrevalence(cdm, analysisType = "all")
```

Arguments

cdm	A CDM reference object
analysisType	A string of the following: "all", "only incidence", "only prevalence"

Value

a tibble with time taken for different analyses

Examples

```
cdm <- mockIncidencePrevalence(
  sampleSize = 100,
  earliestObservationStartDate = as.Date("2010-01-01"),
  latestObservationStartDate = as.Date("2010-01-01"),
  minDaysToObservationEnd = 364,
  maxDaysToObservationEnd = 364,
  outPre = 0.1
)

timings <- benchmarkIncidencePrevalence(cdm)
```

estimateIncidence	<i>Collect population incidence estimates</i>
-------------------	---

Description

Collect population incidence estimates

Usage

```
estimateIncidence(
  cdm,
  denominatorTable,
  outcomeTable,
  censorTable = NULL,
  denominatorCohortId = NULL,
  outcomeCohortId = NULL,
  censorCohortId = NULL,
  interval = "years",
  completeDatabaseIntervals = TRUE,
  outcomeWashout = Inf,
  repeatedEvents = FALSE,
  strata = list(),
  includeOverallStrata = TRUE
)
```

Arguments

cdm	A CDM reference object
denominatorTable	A cohort table with a set of denominator cohorts (for example, created using the <code>generateDenominatorCohortSet()</code> function).
outcomeTable	A cohort table in the cdm reference containing a set of outcome cohorts.

censorTable	A cohort table in the cdm reference containing a cohort to be used for censoring. Individuals will stop contributing time at risk from the date of their first record in the censor cohort. If they appear in the censor cohort before entering the denominator cohort they will be excluded. The censor cohort can only contain one record per individual.
denominatorCohortId	The cohort definition ids or the cohort names of the denominator cohorts of interest. If NULL all cohorts will be considered in the analysis.
outcomeCohortId	The cohort definition ids or the cohort names of the outcome cohorts of interest. If NULL all cohorts will be considered in the analysis.
censorCohortId	The cohort definition id or the cohort name of the cohort to be used for censoring. Must be specified if there are multiple cohorts in the censor table.
interval	Time intervals over which incidence is estimated. Can be "weeks", "months", "quarters", "years", or "overall". ISO weeks will be used for weeks. Calendar months, quarters, or years can be used, or an overall estimate for the entire time period observed (from earliest cohort start to last cohort end) can also be estimated. If more than one option is chosen then results will be estimated for each chosen interval.
completeDatabaseIntervals	TRUE/ FALSE. Where TRUE, incidence will only be estimated for those intervals where the denominator cohort captures all the interval.
outcomeWashout	The number of days used for a 'washout' period between the end of one outcome and an individual starting to contribute time at risk. If Inf, no time can be contributed after an event has occurred.
repeatedEvents	TRUE/ FALSE. If TRUE, an individual will be able to contribute multiple events during the study period (time while they are present in an outcome cohort and any subsequent washout will be excluded). If FALSE, an individual will only contribute time up to their first event.
strata	Variables added to the denominator cohort table for which to stratify estimates.
includeOverallStrata	Whether to include an overall result as well as strata specific results (when strata has been specified).

Value

Incidence estimates

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))
)
inc <- estimateIncidence(
  cdm = cdm,
```

```

    denominatorTable = "denominator",
    outcomeTable = "outcome"
)

```

estimatePeriodPrevalence

Estimate period prevalence

Description

Estimate period prevalence

Usage

```

estimatePeriodPrevalence(
  cdm,
  denominatorTable,
  outcomeTable,
  denominatorCohortId = NULL,
  outcomeCohortId = NULL,
  interval = "years",
  completeDatabaseIntervals = TRUE,
  fullContribution = FALSE,
  strata = list(),
  includeOverallStrata = TRUE
)

```

Arguments

cdm	A CDM reference object
denominatorTable	A cohort table with a set of denominator cohorts (for example, created using the generateDenominatorCohortSet() function).
outcomeTable	A cohort table in the cdm reference containing a set of outcome cohorts.
denominatorCohortId	The cohort definition ids or the cohort names of the denominator cohorts of interest. If NULL all cohorts will be considered in the analysis.
outcomeCohortId	The cohort definition ids or the cohort names of the outcome cohorts of interest. If NULL all cohorts will be considered in the analysis.
interval	Time intervals over which period prevalence is estimated. This can be "weeks", "months", "quarters", "years", or "overall". ISO weeks will be used for weeks. Calendar months, quarters, or years can be used as the period. If more than one option is chosen then results will be estimated for each chosen interval.

completeDatabaseIntervals TRUE/ FALSE. Where TRUE, prevalence will only be estimated for those intervals where the database captures all the interval (based on the earliest and latest observation period start dates, respectively).

fullContribution TRUE/ FALSE. Where TRUE, individuals will only be included if they in the database for the entire interval of interest. If FALSE they are only required to present for one day of the interval in order to contribute.

strata Variables added to the denominator cohort table for which to stratify estimates.

includeOverallStrata Whether to include an overall result as well as strata specific results (when strata has been specified).

Value

Period prevalence estimates

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))
)
estimatePeriodPrevalence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome",
  interval = "months"
)
```

estimatePointPrevalence

Estimate point prevalence

Description

Estimate point prevalence

Usage

```
estimatePointPrevalence(
  cdm,
  denominatorTable,
  outcomeTable,
  denominatorCohortId = NULL,
  outcomeCohortId = NULL,
```

```

    interval = "years",
    timePoint = "start",
    strata = list(),
    includeOverallStrata = TRUE
  )

```

Arguments

<code>cdm</code>	A CDM reference object
<code>denominatorTable</code>	A cohort table with a set of denominator cohorts (for example, created using the <code>generateDenominatorCohortSet()</code> function).
<code>outcomeTable</code>	A cohort table in the <code>cdm</code> reference containing a set of outcome cohorts.
<code>denominatorCohortId</code>	The cohort definition ids or the cohort names of the denominator cohorts of interest. If NULL all cohorts will be considered in the analysis.
<code>outcomeCohortId</code>	The cohort definition ids or the cohort names of the outcome cohorts of interest. If NULL all cohorts will be considered in the analysis.
<code>interval</code>	Time intervals over which period prevalence is estimated. Can be "weeks", "months", "quarters", or "years". ISO weeks will be used for weeks. Calendar months, quarters, or years can be used as the period. If more than one option is chosen then results will be estimated for each chosen interval.
<code>timePoint</code>	where to compute the point prevalence
<code>strata</code>	Variables added to the denominator cohort table for which to stratify estimates.
<code>includeOverallStrata</code>	Whether to include an overall result as well as strata specific results (when strata has been specified).

Value

Point prevalence estimates

Examples

```

cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))
)
estimatePointPrevalence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome",
  interval = "months"
)

```

generateDenominatorCohortSet

Identify a set of denominator populations

Description

generateDenominatorCohortSet() creates a set of cohorts that can be used for the denominator population in analyses of incidence, using estimateIncidence(), or prevalence, using estimatePointPrevalence() or estimatePeriodPrevalence().

Usage

```
generateDenominatorCohortSet(
  cdm,
  name,
  cohortDateRange = as.Date(c(NA, NA)),
  ageGroup = list(c(0, 150)),
  sex = "Both",
  daysPriorObservation = 0,
  requirementInteractions = TRUE
)
```

Arguments

cdm	A CDM reference object
name	Name of the cohort table to be created. Note if a table already exists with this name in the database (give the prefix being used for the cdm reference) it will be overwritten.
cohortDateRange	Two dates. The first indicating the earliest cohort start date and the second indicating the latest possible cohort end date. If NULL or the first date is set as missing, the earliest observation_start_date in the observation_period table will be used for the former. If NULL or the second date is set as missing, the latest observation_end_date in the observation_period table will be used for the latter.
ageGroup	A list of age groups for which cohorts will be generated. A value of list(c(0, 17), c(18, 30)) would, for example, lead to the creation of cohorts for those aged from 0 to 17, and from 18 to 30. In this example an individual turning 18 during the time period would appear in both cohorts (leaving the first cohort the day before their 18th birthday and entering the second from the day of their 18th birthday).
sex	Sex of the cohorts. This can be one or more of: "Male", "Female", or "Both".
daysPriorObservation	The number of days of prior observation observed in the database required for an individual to start contributing time in a cohort.

requirementInteractions

If TRUE, cohorts will be created for all combinations of ageGroup, sex, and daysPriorObservation. If FALSE, only the first value specified for the other factors will be used. Consequently, order of values matters when requirementInteractions is FALSE.

Value

A cdm reference

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm,
  name = "denominator",
  cohortDateRange = as.Date(c("2008-01-01", "2020-01-01"))
)
cdm
```

generateTargetDenominatorCohortSet

Identify a set of denominator populations using a target cohort

Description

generateTargetDenominatorCohortSet() creates a set of cohorts that can be used for the denominator population in analyses of incidence, using estimateIncidence(), or prevalence, using estimatePointPrevalence() or estimatePeriodPrevalence().

Usage

```
generateTargetDenominatorCohortSet(
  cdm,
  name,
  targetCohortTable,
  targetCohortId = NULL,
  cohortDateRange = as.Date(c(NA, NA)),
  timeAtRisk = c(0, Inf),
  ageGroup = list(c(0, 150)),
  sex = "Both",
  daysPriorObservation = 0,
  requirementsAtEntry = TRUE,
  requirementInteractions = TRUE
)
```

Arguments

cdm	A CDM reference object
name	Name of the cohort table to be created.
targetCohortTable	A cohort table in the cdm reference to use to limit cohort entry and exit (with individuals only contributing to a cohort when they are contributing to the cohort in the target table).
targetCohortId	The cohort definition ids or the cohort names of the cohorts of interest for the target table. If NULL all cohorts will be considered in the analysis.
cohortDateRange	Two dates. The first indicating the earliest cohort start date and the second indicating the latest possible cohort end date. If NULL or the first date is set as missing, the earliest observation_start_date in the observation_period table will be used for the former. If NULL or the second date is set as missing, the latest observation_end_date in the observation_period table will be used for the latter.
timeAtRisk	Lower and upper bound for the time at risk window to apply relative to the target cohort entry. A value of <code>list(c(0, 30), c(31, 60))</code> would, for example, create one set of denominator cohorts with time up to the 30 days following target cohort entry and another set with time from 31 days following entry to 60 days. If time at risk start is after target cohort exit and/ or observation period end then no time will be contributed. If time at risk end is after cohort exit and/ or observation period, then only time up to these will be contributed.
ageGroup	A list of age groups for which cohorts will be generated. A value of <code>list(c(0, 17), c(18, 30))</code> would, for example, lead to the creation of cohorts for those aged from 0 to 17, and from 18 to 30.
sex	Sex of the cohorts. This can be one or more of: "Male", "Female", or "Both".
daysPriorObservation	The number of days of prior observation observed in the database required for an individual to start contributing time in a cohort.
requirementsAtEntry	If TRUE, individuals must satisfy requirements for inclusion on their cohort start date for the target cohort. If FALSE, individuals will be included once they satisfy all requirements.
requirementInteractions	If TRUE, cohorts will be created for all combinations of ageGroup, sex, and daysPriorObservation. If FALSE, only the first value specified for the other factors will be used. Consequently, order of values matters when requirementInteractions is FALSE.

Value

A cdm reference

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
```

```

cdm <- generateTargetDenominatorCohortSet(
  cdm = cdm,
  name = "denominator",
  targetCohortTable = "target",
  cohortDateRange = as.Date(c("2008-01-01", "2020-01-01"))
)
cdm

```

IncidencePrevalenceBenchmarkResults

Benchmarking results

Description

Benchmarking results

Usage

```
IncidencePrevalenceBenchmarkResults
```

Format

A list of results from benchmarking

```
mockIncidencePrevalence
```

Generate example subset of the OMOP CDM for estimating incidence and prevalence

Description

Generate example subset of the OMOP CDM for estimating incidence and prevalence

Usage

```

mockIncidencePrevalence(
  personTable = NULL,
  observationPeriodTable = NULL,
  targetCohortTable = NULL,
  outcomeTable = NULL,
  censorTable = NULL,
  sampleSize = 1,
  outPre = 1,
  seed = 444,
  earliestDateOfBirth = NULL,

```

```

    latestDateOfBirth = NULL,
    earliestObservationStartDate = as.Date("1900-01-01"),
    latestObservationStartDate = as.Date("2010-01-01"),
    minDaysToObservationEnd = 1,
    maxDaysToObservationEnd = 4380,
    minOutcomeDays = 1,
    maxOutcomeDays = 10,
    maxOutcomes = 1
  )

```

Arguments

personTable	A tibble in the format of the person table.
observationPeriodTable	A tibble in the format of the observation period table.
targetCohortTable	A tibble in the format of a cohort table which can be used for stratification
outcomeTable	A tibble in the format of a cohort table which can be used for outcomes
censorTable	A tibble in the format of a cohort table which can be used for censoring
sampleSize	The number of unique patients.
outPre	The fraction of patients with an event.
seed	The seed for simulating the data set. Use the same seed to get same data set.
earliestDateOfBirth	The earliest date of birth of a patient in person table.
latestDateOfBirth	The latest date of birth of a patient in person table.
earliestObservationStartDate	The earliest observation start date for patient format.
latestObservationStartDate	The latest observation start date for patient format.
minDaysToObservationEnd	The minimum number of days of the observational integer.
maxDaysToObservationEnd	The maximum number of days of the observation period integer.
minOutcomeDays	The minimum number of days of the outcome period default set to 1.
maxOutcomeDays	The maximum number of days of the outcome period default set to 10.
maxOutcomes	The maximum possible number of outcomes per person can have default set to 1.

Value

A cdm reference to a duckdb database with mock data.

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 100)
cdm
```

optionsTableIncidence *Additional arguments for the functions tableIncidence.*

Description

It provides a list of allowed inputs for .option argument in tableIncidence, and their given default values.

Usage

```
optionsTableIncidence()
```

Value

The default .options named list.

Examples

```
{
  optionsTableIncidence()
}
```

optionsTablePrevalence
Additional arguments for the functions tablePrevalence.

Description

It provides a list of allowed inputs for .option argument in tablePrevalence, and their given default values.

Usage

```
optionsTablePrevalence()
```

Value

The default .options named list.

Examples

```
{
  optionsTablePrevalence()
}
```

plotIncidence	<i>Plot incidence results</i>
---------------	-------------------------------

Description

Plot incidence results

Usage

```
plotIncidence(
  result,
  x = "incidence_start_date",
  y = "incidence_100000_pys",
  line = FALSE,
  point = TRUE,
  ribbon = FALSE,
  ymin = "incidence_100000_pys_95CI_lower",
  ymax = "incidence_100000_pys_95CI_upper",
  facet = NULL,
  colour = NULL
)
```

Arguments

result	Incidence results
x	Variable to plot on x axis
y	Variable to plot on y axis.
line	Whether to plot a line using geom_line
point	Whether to plot points using geom_point
ribbon	Whether to plot a ribbon using geom_ribbon
ymin	Lower limit of error bars, if provided is plot using geom_errorbar
ymax	Upper limit of error bars, if provided is plot using geom_errorbar
facet	Variables to use for facets. To see available variables for facetting use the function availableIncidenceGrouping().
colour	Variables to use for colours. To see available variables for colouring use the function availableIncidenceGrouping().

Value

A ggplot with the incidence results plotted

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))
)
inc <- estimateIncidence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome"
)
plotIncidence(inc)
```

plotIncidencePopulation

Bar plot of denominator counts, outcome counts, and person-time from incidence results

Description

Bar plot of denominator counts, outcome counts, and person-time from incidence results

Usage

```
plotIncidencePopulation(
  result,
  x = "incidence_start_date",
  y = "denominator_count",
  facet = NULL,
  colour = NULL
)
```

Arguments

result	Incidence results
x	Variable to plot on x axis
y	Variable to plot on y axis.
facet	Variables to use for facets. To see available variables for facetting use the functions availableIncidenceGrouping().
colour	Variables to use for colours. To see available variables for colouring use the function availableIncidenceGrouping().

Value

A ggplot object

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2014-01-01"), as.Date("2018-01-01"))
)
inc <- estimateIncidence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome"
)
plotIncidencePopulation(inc)
```

plotPrevalence	<i>Plot prevalence results</i>
----------------	--------------------------------

Description

Plot prevalence results

Usage

```
plotPrevalence(
  result,
  x = "prevalence_start_date",
  y = "prevalence",
  line = FALSE,
  point = TRUE,
  ribbon = FALSE,
  ymin = "prevalence_95CI_lower",
  ymax = "prevalence_95CI_upper",
  facet = NULL,
  colour = NULL
)
```

Arguments

result	Prevalence results
x	Variable to plot on x axis
y	Variable to plot on y axis.
line	Whether to plot a line using <code>geom_line</code>

point	Whether to plot points using geom_point
ribbon	Whether to plot a ribbon using geom_ribbon
ymin	Lower limit of error bars, if provided is plot using geom_errorbar
ymax	Upper limit of error bars, if provided is plot using geom_errorbar
facet	Variables to use for facets. To see available variables for facetting use the function availablePrevalenceGrouping().
colour	Variables to use for colours. To see available variables for colouring use the function availablePrevalenceGrouping().

Value

A ggplot with the prevalence results plotted

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2014-01-01"), as.Date("2018-01-01"))
)
prev <- estimatePointPrevalence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome"
)
plotPrevalence(prev)
```

plotPrevalencePopulation

Bar plot of denominator and outcome counts from prevalence results

Description

Bar plot of denominator and outcome counts from prevalence results

Usage

```
plotPrevalencePopulation(
  result,
  x = "prevalence_start_date",
  y = "denominator_count",
  facet = NULL,
  colour = NULL
)
```

Arguments

result	Prevalence results
x	Variable to plot on x axis
y	Variable to plot on y axis.
facet	Variables to use for facets. To see available variables for facetting use the functions availablePrevalenceGrouping().
colour	Variables to use for colours. To see available variables for colouring use the function availablePrevalenceGrouping().

Value

A ggplot object

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2014-01-01"), as.Date("2018-01-01"))
)
prev <- estimatePointPrevalence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome"
)
plotPrevalencePopulation(prev)
```

tableIncidence	<i>Table of incidence results</i>
----------------	-----------------------------------

Description

Table of incidence results

Usage

```
tableIncidence(
  result,
  type = "gt",
  header = c("estimate_name"),
  groupColumn = c("cdm_name", "outcome_cohort_name"),
  settingsColumn = c("denominator_age_group", "denominator_sex"),
  hide = c("denominator_cohort_name", "analysis_interval"),
  .options = list()
)
```

Arguments

result	Incidence results
type	Type of table. Can be "gt", "flextable", or "tibble"
header	A vector specifying the elements to include in the header. The order of elements matters, with the first being the topmost header. The header vector can contain one of the following variables: "cdm_name", "denominator_cohort_name", "outcome_cohort_name", "incidence_start_date", "incidence_end_date", "estimate_name", variables in the strata_name column, and any of the settings columns specified in settingsColumn argument. The header can also include other names to use as overall header labels
groupColumn	Variables to use as group labels. Allowed columns are the same as in header
settingsColumn	Variables from the settings attribute to display in the table
hide	Table columns to exclude, options are the ones described in header
.options	Table options to apply

Value

Table of results

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))
)
inc <- estimateIncidence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome"
)
tableIncidence(inc)
```

tableIncidenceAttrition

Table of incidence attrition results

Description

Table of incidence attrition results

Usage

```
tableIncidenceAttrition(  
  result,  
  type = "gt",  
  header = "variable_name",  
  groupColumn = c("cdm_name", "outcome_cohort_name"),  
  settingsColumn = NULL,  
  hide = c("denominator_cohort_name", "estimate_name", "reason_id", "variable_level")  
)
```

Arguments

- result A summarised_result object. Output of summariseCohortAttrition().
- type Type of table. Check supported types with visOmoResults::tableType().
- header Columns to use as header. See options with colnames(omopgenerics::splitAll(result)).
Variables in settingsColumn are also allowed
- groupColumn Variables to use as group labels. Allowed columns are the same as in header
- settingsColumn Variables from the settings attribute to display in the table
- hide Table columns to exclude, options are the ones described in header

Value

A visual table.

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)  
cdm <- generateDenominatorCohortSet(  
  cdm = cdm, name = "denominator",  
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))  
)  
inc <- estimateIncidence(  
  cdm = cdm,  
  denominatorTable = "denominator",  
  outcomeTable = "outcome"  
)  
tableIncidenceAttrition(inc)
```

tablePrevalence	<i>Table of prevalence results</i>
-----------------	------------------------------------

Description

Table of prevalence results

Usage

```
tablePrevalence(
  result,
  type = "gt",
  header = c("estimate_name"),
  groupColumn = c("cdm_name", "outcome_cohort_name"),
  settingsColumn = c("denominator_age_group", "denominator_sex"),
  hide = c("denominator_cohort_name", "analysis_interval"),
  .options = list()
)
```

Arguments

result	Prevalence results
type	Type of table. Can be "gt", "flextable", or "tibble"
header	A vector specifying the elements to include in the header. The order of elements matters, with the first being the topmost header. The header vector can contain one of the following variables: "cdm_name", "denominator_cohort_name", "outcome_cohort_name", "prevalence_start_date", "prevalence_end_date", "estimate_name", variables in the strata_name column, and any of the settings columns specified in settingsColumn argument. The header can also include other names to use as overall header labels
groupColumn	Variables to use as group labels. Allowed columns are the same as in header
settingsColumn	Variables from the settings attribute to display in the table
hide	Table columns to exclude, options are the ones described in header
.options	Table options to apply

Value

Table of prevalence results

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm,
  name = "denominator",
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))
)
prev <- estimatePointPrevalence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome",
  interval = "months"
)
tablePrevalence(prev)
```

tablePrevalenceAttrition

Table of prevalence attrition results

Description

Table of prevalence attrition results

Usage

```
tablePrevalenceAttrition(
  result,
  type = "gt",
  header = "variable_name",
  groupColumn = c("cdm_name", "outcome_cohort_name"),
  settingsColumn = NULL,
  hide = c("denominator_cohort_name", "estimate_name", "reason_id", "variable_level")
)
```

Arguments

result	A summarised_result object. Output of summariseCohortAttrition().
type	Type of table. Check supported types with visOmopResults::tableType().
header	Columns to use as header. See options with colnames(omopgenerics::splitAll(result)). Variables in settingsColumn are also allowed
groupColumn	Variables to use as group labels. Allowed columns are the same as in header
settingsColumn	Variables from the settings attribute to display in the table
hide	Table columns to exclude, options are the ones described in header

Value

A visual table.

Examples

```
cdm <- mockIncidencePrevalence(sampleSize = 1000)
cdm <- generateDenominatorCohortSet(
  cdm = cdm, name = "denominator",
  cohortDateRange = c(as.Date("2008-01-01"), as.Date("2018-01-01"))
)
prev <- estimatePointPrevalence(
  cdm = cdm,
  denominatorTable = "denominator",
  outcomeTable = "outcome",
  interval = "months"
)
tablePrevalenceAttrition(prev)
```

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