

# Package ‘IncidencePrevalence’

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**Title** Estimate Incidence and Prevalence using the OMOP Common Data Model

**Version** 1.1.0

**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     *A tidy implementation of the summarised\_result object for prevalence results.*

---

**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,
  denominatorCohortId = NULL,
  outcomeCohortId = 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.
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 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"
)

```

**Description**

Estimate period prevalence

**Usage**

```
estimatePeriodPrevalence(
  cdm,
  denominatorTable,
  outcomeTable,
  denominatorCohortId = NULL,
  outcomeCohortId = NULL,
  interval = "years",
  completeDatabaseIntervals = TRUE,
  fullContribution = FALSE,
  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 <code>NULL</code> 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 <code>NULL</code> all cohorts will be considered in the analysis.
<code>interval</code>	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.
<code>completeDatabaseIntervals</code>	<code>TRUE/ FALSE</code> . Where <code>TRUE</code> , 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).
<code>fullContribution</code>	<code>TRUE/ FALSE</code> . Where <code>TRUE</code> , individuals will only be included if they in the database for the entire interval of interest. If <code>FALSE</code> they are only required to present for one day of the interval in order to contribute.
<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**

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**

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. 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.
timePoint	where to compute the point prevalence
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**

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 <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. 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

<code>cdm</code>	A CDM reference object
<code>name</code>	Name of the cohort table to be created.
<code>targetCohortTable</code>	A cohort table in the <code>cdm</code> 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).
<code>targetCohortId</code>	The cohort definition ids or the cohort names of the cohorts of interest for the target table. If <code>NULL</code> all cohorts will be considered in the analysis.
<code>cohortDateRange</code>	Two dates. The first indicating the earliest cohort start date and the second indicating the latest possible cohort end date. If <code>NULL</code> or the first date is set as missing, the earliest <code>observation_start_date</code> in the <code>observation_period</code> table will be used for the former. If <code>NULL</code> or the second date is set as missing, the latest <code>observation_end_date</code> in the <code>observation_period</code> 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,
  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

`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

*Plot incidence results*

---

**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 faceting 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 faceting 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      *Plot prevalence results*

---

### 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 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 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 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"))
)
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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