

Package ‘OmopSketch’

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Title Characterise Tables of an OMOP Common Data Model Instance

Version 0.4.0

Maintainer Cecilia Campanile <cecilia.campanile@ndorms.ox.ac.uk>

Description Summarises key information in data mapped to the Observational Medical Outcomes Partnership (OMOP) common data model. Assess suitability to perform specific epidemiological studies and explore the different domains to obtain feasibility counts and trends.

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Depends R (>= 4.1)

URL <https://OHDSI.github.io/OmopSketch/>

BugReports <https://github.com/OHDSI/OmopSketch/issues>

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Author Marta Alcalde-Herraiz [aut] (ORCID: <<https://orcid.org/0009-0002-4405-1814>>),
Kim Lopez-Guell [aut] (ORCID: <<https://orcid.org/0000-0002-8462-8668>>),
Elin Rowlands [aut] (ORCID: <<https://orcid.org/0009-0005-5166-0417>>),

Cecilia Campanile [aut, cre] (ORCID:
<<https://orcid.org/0009-0007-6629-4661>>),
Edward Burn [aut] (ORCID: <<https://orcid.org/0000-0002-9286-1128>>),
Martí Català [aut] (ORCID: <<https://orcid.org/0000-0003-3308-9905>>)

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databaseCharacteristics
<i>Summarise Database Characteristics for OMOP CDM</i>

Description

Summarise Database Characteristics for OMOP CDM

Usage

```
databaseCharacteristics(
  cdm,
  omopTableName = c("person", "observation_period", "visit_occurrence",
    "condition_occurrence", "drug_exposure", "procedure_occurrence", "device_exposure",
    "measurement", "observation", "death"),
  sex = FALSE,
  ageGroup = NULL,
  dateRange = NULL,
  interval = "overall",
  conceptIdCount = FALSE,
  ...
)
```

Arguments

<code>cdm</code>	A <code>cdm_reference</code> object representing the Common Data Model (CDM) reference.
<code>omopTableName</code>	A character vector specifying the OMOP tables from the CDM to include in the analysis. If "person" is present, it will only be used for missing value summarisation.
<code>sex</code>	Logical; whether to stratify results by sex (TRUE) or not (FALSE).
<code>ageGroup</code>	A list of age groups to stratify the results by. Each element represents a specific age range.
<code>dateRange</code>	A vector of two dates defining the desired study period. Only the <code>start_date</code> column of the OMOP table is checked to ensure it falls within this range. If <code>dateRange</code> is NULL, no restriction is applied.
<code>interval</code>	Time interval to stratify by. It can either be "years", "quarters", "months" or "overall".
<code>conceptIdCount</code>	Logical; whether to summarise concept ID counts (TRUE) or not (FALSE).
<code>...</code>	additional arguments passed to the <code>OmopSketch</code> functions that are used internally.

Value

A `summarised_result` object containing the results of the characterisation.

Examples

```
cdm <- mockOmopSketch(numberIndividuals = 100)

result <- databaseCharacteristics(cdm)

PatientProfiles::mockDisconnect(cdm)
```

mockOmopSketch	<i>Creates a mock database to test OmopSketch package.</i>
----------------	--

Description

Creates a mock database to test OmopSketch package.

Usage

```
mockOmopSketch(  
  con = NULL,  
  writeSchema = NULL,  
  numberIndividuals = 100,  
  seed = NULL  
)
```

Arguments

con	A DBI connection to create the cdm mock object. By default, the connection would be a 'duckdb' one.
writeSchema	Name of an schema of the DBI connection with writing permissions.
numberIndividuals	Number of individuals to create in the cdm reference object.
seed	An optional integer used to set the seed for random number generation, ensuring reproducibility of the generated data. If provided, this seed allows the function to produce consistent results each time it is run with the same inputs. If 'NULL', the seed is not set, which can lead to different outputs on each run.

Value

A mock cdm_reference object.

Examples

```
mockOmopSketch(numberIndividuals = 100)
```

plotConceptSetCounts *Plot the concept counts of a summariseConceptSetCounts output.*

Description

Plot the concept counts of a summariseConceptSetCounts output.

Usage

```
plotConceptSetCounts(result, facet = NULL, colour = NULL)
```

Arguments

result	A summarised_result object (output of summariseConceptSetCounts).
facet	Columns to face by. Formula format can be provided. See possible columns to face by with: visOmapResults::tidyColumns().
colour	Columns to colour by. See possible columns to colour by with: visOmapResults::tidyColumns().

Value

A ggplot2 object showing the concept counts.

Examples

```
library(dplyr)

cdm <- mockOmapSketch()

result <- cdm |>
  summariseConceptSetCounts(
    conceptSet = list(
      "Renal agenesis" = 194152,
      "Manic mood" = c(4226696, 4304866, 37110496, 40371897)
    )
  )

result |>
  filter(variable_name == "Number subjects") |>
  plotConceptSetCounts(facet = "codelist_name", colour = "standard_concept_name")

PatientProfiles::mockDisconnect(cdm)
```

plotInObservation	Create a ggplot2 plot from the output of summariseInObservation().
-------------------	--

Description

Create a ggplot2 plot from the output of summariseInObservation().

Usage

```
plotInObservation(result, facet = NULL, colour = NULL)
```

Arguments

result	A summarised_result object (output of summariseInObservation).
facet	Columns to face by. Formula format can be provided. See possible columns to face by with: visOmopResults::tidyColumns().
colour	Columns to colour by. See possible columns to colour by with: visOmopResults::tidyColumns().

Value

A ggplot showing the table counts

Examples

```
library(dplyr)

cdm <- mockOmopSketch()

result <- summariseInObservation(
  cdm$observation_period,
  output = c("person-days", "record"),
  ageGroup = list("<=40" = c(0, 40), ">40" = c(41, Inf)),
  sex = TRUE
)

result |>
  filter(variable_name == "Number person-days") |>
  plotInObservation(facet = "sex", colour = "age_group")

PatientProfiles::mockDisconnect(cdm)
```

plotObservationPeriod *Create a plot from the output of summariseObservationPeriod().*

Description

Create a plot from the output of summariseObservationPeriod().

Usage

```
plotObservationPeriod(  
  result,  
  variableName = "Number subjects",  
  plotType = "barplot",  
  facet = NULL,  
  colour = NULL  
)
```

Arguments

result	A summarised_result object.
variableName	The variable to plot it can be: "number subjects", "records per person", "duration" or "days to next observation period".
plotType	The plot type, it can be: "barplot", "boxplot" or "densityplot".
facet	Columns to colour by. See possible columns to colour by with: visOmopResults::tidyColumns().
colour	Columns to colour by. See possible columns to colour by with: visOmopResults::tidyColumns().

Value

A ggplot2 object.

Examples

```
cdm <- mockOmopSketch(numberIndividuals = 100)  
  
result <- summariseObservationPeriod(cdm$observation_period)  
  
result |>  
  plotObservationPeriod(  
    variableName = "Duration in days",  
    plotType = "boxplot"  
  )  
  
PatientProfiles::mockDisconnect(cdm)
```

plotRecordCount	Create a ggplot of the records' count trend.
-----------------	--

Description

Create a ggplot of the records' count trend.

Usage

```
plotRecordCount(result, facet = NULL, colour = NULL)
```

Arguments

result	Output from summariseRecordCount().
facet	Columns to face by. Formula format can be provided. See possible columns to face by with: visOmomResults::tidyColumns().
colour	Columns to colour by. See possible columns to colour by with: visOmomResults::tidyColumns().

Value

A ggplot showing the table counts

Examples

```
cdm <- mockOmomSketch()

summarisedResult <- summariseRecordCount(
  cdm = cdm,
  omomTableName = "condition_occurrence",
  ageGroup = list("<=20" = c(0, 20), ">20" = c(21, Inf)),
  sex = TRUE
)

plotRecordCount(summarisedResult, colour = "age_group", facet = sex ~ .)

PatientProfiles::mockDisconnect(cdm = cdm)
```

summariseClinicalRecords

Summarise an omom table from a cdm object. You will obtain information related to the number of records, number of subjects, whether the records are in observation, number of present domains and number of present concepts.

Description

Summarise an omop table from a cdm object. You will obtain information related to the number of records, number of subjects, whether the records are in observation, number of present domains and number of present concepts.

Usage

```
summariseClinicalRecords(
  cdm,
  omopTableName,
  recordsPerPerson = c("mean", "sd", "median", "q25", "q75", "min", "max"),
  inObservation = TRUE,
  standardConcept = TRUE,
  sourceVocabulary = TRUE,
  domainId = TRUE,
  typeConcept = TRUE,
  sex = FALSE,
  ageGroup = NULL,
  dateRange = NULL
)
```

Arguments

cdm	A cdm_reference object.
omopTableName	A character vector of the names of the tables to summarise in the cdm object.
recordsPerPerson	Generates summary statistics for the number of records per person. Set to NULL if no summary statistics are required.
inObservation	Boolean variable. Whether to include the percentage of records in observation.
standardConcept	Boolean variable. Whether to summarise standard concept information.
sourceVocabulary	Boolean variable. Whether to summarise source vocabulary information.
domainId	Boolean variable. Whether to summarise domain id of standard concept id information.
typeConcept	Boolean variable. Whether to summarise type concept id field information.
sex	Boolean variable. Whether to stratify by sex (TRUE) or not (FALSE).
ageGroup	A list of age groups to stratify results by.
dateRange	A vector of two dates defining the desired study period. Only the start_date column of the OMOP table is checked to ensure it falls within this range. If dateRange is NULL, no restriction is applied.

Value

A summarised_result object.

Examples

```

cdm <- mockOmopSketch()

summarisedResult <- summariseClinicalRecords(
  cdm = cdm,
  omopTableName = "condition_occurrence",
  recordsPerPerson = c("mean", "sd"),
  inObservation = TRUE,
  standardConcept = TRUE,
  sourceVocabulary = TRUE,
  domainId = TRUE,
  typeConcept = TRUE
)

summarisedResult

PatientProfiles::mockDisconnect(cdm = cdm)

```

summariseConceptCounts

Summarise concept counts in patient-level data. Only concepts recorded during observation period are counted.

Description

[Deprecated]

Usage

```

summariseConceptCounts(
  cdm,
  conceptId,
  countBy = c("record", "person"),
  concept = TRUE,
  interval = "overall",
  sex = FALSE,
  ageGroup = NULL,
  dateRange = NULL
)

```

Arguments

cdm	A cdm object
conceptId	List of concept IDs to summarise.
countBy	Either "record" for record-level counts or "person" for person-level counts
concept	TRUE or FALSE. If TRUE code use will be summarised by concept.

interval	Time interval to stratify by. It can either be "years", "quarters", "months" or "overall".
sex	TRUE or FALSE. If TRUE code use will be summarised by sex.
ageGroup	A list of ageGroup vectors of length two. Code use will be thus summarised by age groups.
dateRange	A vector of two dates defining the desired study period. Only the start_date column of the OMOP table is checked to ensure it falls within this range. If dateRange is NULL, no restriction is applied.

Value

A summarised_result object with results overall and, if specified, by strata.

summariseConceptIdCounts

Summarise concept use in patient-level data. Only concepts recorded during observation period are counted.

Description

Summarise concept use in patient-level data. Only concepts recorded during observation period are counted.

Usage

```
summariseConceptIdCounts(
  cdm,
  omopTableName,
  countBy = "record",
  year = lifecycle::deprecated(),
  interval = "overall",
  sex = FALSE,
  ageGroup = NULL,
  sample = NULL,
  dateRange = NULL
)
```

Arguments

cdm	A cdm object
omopTableName	A character vector of the names of the tables to summarise in the cdm object.
countBy	Either "record" for record-level counts or "person" for person-level counts
year	deprecated
interval	Time interval to stratify by. It can either be "years", "quarters", "months" or "overall".

sex	TRUE or FALSE. If TRUE code use will be summarised by sex.
ageGroup	A list of ageGroup vectors of length two. Code use will be thus summarised by age groups.
sample	An integer to sample the tables to only that number of records. If NULL no sample is done.
dateRange	A vector of two dates defining the desired study period. Only the start_date column of the OMOP table is checked to ensure it falls within this range. If dateRange is NULL, no restriction is applied.

Value

A summarised_result object with results overall and, if specified, by strata.

Examples

```
library(OmopSketch)
library(CDMConnector)
library(duckdb)

requireEunomia()
con <- dbConnect(duckdb(), eunomiaDir())
cdm <- cdmFromCon(con = con, cdmSchema = "main", writeSchema = "main")

summariseConceptIdCounts(cdm, "condition_occurrence")
```

summariseConceptSetCounts

Summarise concept counts in patient-level data. Only concepts recorded during observation period are counted.

Description

Summarise concept counts in patient-level data. Only concepts recorded during observation period are counted.

Usage

```
summariseConceptSetCounts(
  cdm,
  conceptSet,
  countBy = c("record", "person"),
  concept = TRUE,
  interval = "overall",
  sex = FALSE,
  ageGroup = NULL,
  dateRange = NULL
)
```

Arguments

cdm	A cdm object
conceptSet	List of concept IDs to summarise.
countBy	Either "record" for record-level counts or "person" for person-level counts
concept	TRUE or FALSE. If TRUE code use will be summarised by concept.
interval	Time interval to stratify by. It can either be "years", "quarters", "months" or "overall".
sex	TRUE or FALSE. If TRUE code use will be summarised by sex.
ageGroup	A list of ageGroup vectors of length two. Code use will be thus summarised by age groups.
dateRange	A vector of two dates defining the desired study period. Only the start_date column of the OMOP table is checked to ensure it falls within this range. If dateRange is NULL, no restriction is applied.

Value

A summarised_result object with results overall and, if specified, by strata.

Examples

```
library(OmopSketch)

cdm <- mockOmopSketch()

cs <- list(sumatriptan = c(35604883, 35604879, 35604880, 35604884))

results <- summariseConceptSetCounts(cdm, conceptSet = cs)

results

PatientProfiles::mockDisconnect(cdm)
```

summariseInObservation

Summarise the number of people in observation during a specific interval of time.

Description

Summarise the number of people in observation during a specific interval of time.

Usage

```
summariseInObservation(
  observationPeriod,
  interval = "overall",
  output = "record",
  ageGroup = NULL,
  sex = FALSE,
  dateRange = NULL
)
```

Arguments

observationPeriod	An observation_period omop table. It must be part of a cdm_reference object.
interval	Time interval to stratify by. It can either be "years", "quarters", "months" or "overall".
output	Output format. It can be either the number of records ("record") that are in observation in the specific interval of time, the number of person-days ("person-days"), the number of subjects ("person"), the number of females ("sex") or the median age of population in observation ("age").
ageGroup	A list of age groups to stratify results by.
sex	Boolean variable. Whether to stratify by sex (TRUE) or not (FALSE). For output = "sex" this stratification is not applied.
dateRange	A vector of two dates defining the desired study period. Only the start_date column of the OMOP table is checked to ensure it falls within this range. If dateRange is NULL, no restriction is applied.

Value

A summarised_result object.

Examples

```
library(dplyr, warn.conflicts = FALSE)

cdm <- mockOmopSketch()

result <- summariseInObservation(
  cdm$observation_period,
  interval = "months",
  output = c("person-days", "record"),
  ageGroup = list("<=60" = c(0, 60), ">60" = c(61, Inf)),
  sex = TRUE
)

result |>
  glimpse()
```

```
PatientProfiles::mockDisconnect(cdm)
```

```
summariseMissingData    Summarise missing data in omop tables
```

Description

Summarise missing data in omop tables

Usage

```
summariseMissingData(
  cdm,
  omopTableName,
  col = NULL,
  sex = FALSE,
  year = lifecycle::deprecated(),
  interval = "overall",
  ageGroup = NULL,
  sample = 1e+06,
  dateRange = NULL
)
```

Arguments

<code>cdm</code>	A cdm object
<code>omopTableName</code>	A character vector of the names of the tables to summarise in the cdm object.
<code>col</code>	A character vector of column names to check for missing values. If NULL, all columns in the specified tables are checked. Default is NULL.
<code>sex</code>	TRUE or FALSE. If TRUE code use will be summarised by sex.
<code>year</code>	deprecated
<code>interval</code>	Time interval to stratify by. It can either be "years", "quarters", "months" or "overall".
<code>ageGroup</code>	A list of ageGroup vectors of length two. Code use will be thus summarised by age groups.
<code>sample</code>	An integer to sample the table to only that number of records. If NULL no sample is done.
<code>dateRange</code>	A vector of two dates defining the desired study period. Only the <code>start_date</code> column of the OMOP table is checked to ensure it falls within this range. If <code>dateRange</code> is NULL, no restriction is applied.

Value

A summarised_result object with results overall and, if specified, by strata.

Examples

```
cdm <- mockOmopSketch(numberIndividuals = 100)

result <- summariseMissingData (cdm = cdm,
omopTableName = c("condition_occurrence", "visit_occurrence"))

PatientProfiles::mockDisconnect(cdm)
```

summariseObservationPeriod

Summarise the observation period table getting some overall statistics in a summarised_result object.

Description

Summarise the observation period table getting some overall statistics in a summarised_result object.

Usage

```
summariseObservationPeriod(
  observationPeriod,
  estimates = c("mean", "sd", "min", "q05", "q25", "median", "q75", "q95", "max",
    "density"),
  byOrdinal = TRUE,
  ageGroup = NULL,
  sex = FALSE,
  dateRange = NULL
)
```

Arguments

observationPeriod	observation_period omop table.
estimates	Estimates to summarise the variables of interest (records per person, duration in days and days to next observation period).
byOrdinal	Boolean variable. Whether to stratify by the ordinal observation period (e.g., 1st, 2nd, etc.) (TRUE) or simply analyze overall data (FALSE)
ageGroup	A list of age groups to stratify results by.
sex	Boolean variable. Whether to stratify by sex (TRUE) or not (FALSE).
dateRange	A vector of two dates defining the desired study period. Only the start_date column of the OMOP table is checked to ensure it falls within this range. If dateRange is NULL, no restriction is applied.

Value

A summarised_result object with the summarised data.

Examples

```
library(dplyr, warn.conflicts = FALSE)

cdm <- mockOmopSketch(numberIndividuals = 100)

result <- summariseObservationPeriod(cdm$observation_period)

result |>
  glimpse()

PatientProfiles::mockDisconnect(cdm)
```

summariseOmopSnapshot	<i>Summarise a cdm_reference object creating a snapshot with the meta-data of the cdm_reference object.</i>
-----------------------	---

Description

Summarise a cdm_reference object creating a snapshot with the metadata of the cdm_reference object.

Usage

```
summariseOmopSnapshot(cdm)
```

Arguments

cdm A cdm_reference object.

Value

A summarised_result object.

Examples

```
cdm <- mockOmopSketch(numberIndividuals = 10)

summariseOmopSnapshot(cdm)
```

summariseRecordCount	<i>Summarise record counts of an omop_table using a specific time interval. Only records that fall within the observation period are considered.</i>
----------------------	--

Description

Summarise record counts of an omop_table using a specific time interval. Only records that fall within the observation period are considered.

Usage

```
summariseRecordCount(
  cdm,
  omopTableName,
  interval = "overall",
  ageGroup = NULL,
  sex = FALSE,
  sample = NULL,
  dateRange = NULL
)
```

Arguments

cdm	A cdm_reference object.
omopTableName	A character vector of omop tables from the cdm.
interval	Time interval to stratify by. It can either be "years", "quarters", "months" or "overall".
ageGroup	A list of age groups to stratify results by.
sex	Whether to stratify by sex (TRUE) or not (FALSE).
sample	An integer to sample the tables to only that number of records. If NULL no sample is done.
dateRange	A vector of two dates defining the desired study period. Only the start_date column of the OMOP table is checked to ensure it falls within this range. If dateRange is NULL, no restriction is applied.

Value

A summarised_result object.

Examples

```
library(dplyr, warn.conflicts = FALSE)

cdm <- mockOmopSketch()
```

```

summarisedResult <- summariseRecordCount(
  cdm = cdm,
  omopTableName = c("condition_occurrence", "drug_exposure"),
  interval = "years",
  ageGroup = list("<=20" = c(0, 20), ">20" = c(21, Inf)),
  sex = TRUE
)

summarisedResult |>
  glimpse()

PatientProfiles::mockDisconnect(cdm = cdm)

```

tableClinicalRecords *Create a visual table from a summariseClinicalRecord() output.*

Description

Create a visual table from a summariseClinicalRecord() output.

Usage

```
tableClinicalRecords(result, type = "gt")
```

Arguments

result	Output from summariseClinicalRecords().
type	Type of formatting output table, either "gt" or "flextable".

Value

A gt or flextable object with the summarised data.

Examples

```

cdm <- mockOmopSketch()

summarisedResult <- summariseClinicalRecords(
  cdm = cdm,
  omopTableName = c("condition_occurrence", "drug_exposure"),
  recordsPerPerson = c("mean", "sd"),
  inObservation = TRUE,
  standardConcept = TRUE,
  sourceVocabulary = TRUE,
  domainId = TRUE,
  typeConcept = TRUE
)

```

```

summarisedResult |>
  suppress(minCellCount = 5) |>
  tableClinicalRecords()

PatientProfiles::mockDisconnect(cdm)

```

`tableConceptIdCounts` *Create a visual table from a summariseConceptIdCounts() result.*

Description

Create a visual table from a summariseConceptIdCounts() result.

Usage

```
tableConceptIdCounts(result, display = "overall", type = "reactable")
```

Arguments

<code>result</code>	A summarised_result object.
<code>display</code>	A character string indicating which subset of the data to display. Options are: • "overall": Show all source and standard concepts. • "standard": Show only standard concepts. • "source": Show only source codes. • "missing standard": Show only source codes that are missing a mapped standard concept.
<code>type</code>	Type of formatting output table, either "reactable" or "datatable".

Value

A gt or flextable object with the summarised data.

Examples

```

library(OmopSketch)
library(CDMConnector)
library(duckdb)

requireEunomia()
con <- dbConnect(duckdb(), eunomiaDir())
cdm <- cdmFromCon(con = con, cdmSchema = "main", writeSchema = "main")

result <- summariseConceptIdCounts(cdm, "condition_occurrence")
result |> tableConceptIdCounts()

```

tableInObservation	Create a visual table from a summariseInObservation() result.
--------------------	---

Description

Create a visual table from a summariseInObservation() result.

Usage

```
tableInObservation(result, type = "gt")
```

Arguments

result	A summarised_result object.
type	Type of formatting output table, either "gt", "reactable" or "datatable".

Value

A gt or flextable object with the summarised data.

Examples

```
library(dplyr, warn.conflicts = FALSE)

cdm <- mockOmopSketch()

result <- summariseInObservation(
  cdm$observation_period,
  interval = "months",
  output = c("person-days", "record"),
  ageGroup = list("<=60" = c(0, 60), ">60" = c(61, Inf)),
  sex = TRUE
)

result |>
  tableInObservation()

PatientProfiles::mockDisconnect(cdm)
```

tableMissingData	Create a visual table from a summariseMissingData() result.
------------------	---

Description

Create a visual table from a summariseMissingData() result.

Usage

```
tableMissingData(result, type = "gt")
```

Arguments

result	A summarised_result object.
type	Type of formatting output table, either "gt" or "flextable".

Value

A gt or flextable object with the summarised data.

Examples

```
cdm <- mockOmopSketch(numberIndividuals = 100)

result <- summariseMissingData(cdm = cdm,
  omopTableName = c("condition_occurrence", "visit_occurrence"))

result |> tableMissingData()

PatientProfiles::mockDisconnect(cdm)
```

tableObservationPeriod	Create a visual table from a summariseObservationPeriod() result.
------------------------	---

Description

Create a visual table from a summariseObservationPeriod() result.

Usage

```
tableObservationPeriod(result, type = "gt")
```

Arguments

`result` A summarised_result object.
`type` Type of formatting output table, either "gt" or "flextable".

Value

A gt or flextable object with the summarised data.

Examples

```
cdm <- mockOmopSketch(numberIndividuals = 100)

result <- summariseObservationPeriod(cdm$observation_period)

tableObservationPeriod(result)

PatientProfiles::mockDisconnect(cdm)
```

tableOmopSnapshot	Create a visual table from a summarise_omop_snapshot result.
-------------------	--

Description

Create a visual table from a summarise_omop_snapshot result.

Usage

```
tableOmopSnapshot(result, type = "gt")
```

Arguments

`result` Output from summariseOmopSnapshot().
`type` Type of formatting output table, either "gt" or "flextable".

Value

A gt or flextable object with the summarised data.

Examples

```
cdm <- mockOmopSketch(numberIndividuals = 10)

result <- summariseOmopSnapshot(cdm)

result |>
  tableOmopSnapshot()

PatientProfiles::mockDisconnect(cdm)
```

tableRecordCount	Create a visual table from a summariseRecordCount() result.
------------------	---

Description

Create a visual table from a summariseRecordCount() result.

Usage

```
tableRecordCount(result, type = "gt")
```

Arguments

result	A summarised_result object.
type	Type of formatting output table, either "gt", "reactable" or "datatable".

Value

A gt or flextable object with the summarised data.

Examples

```
library(dplyr, warn.conflicts = FALSE)

cdm <- mockOmopSketch()

summarisedResult <- summariseRecordCount(
  cdm = cdm,
  omopTableName = c("condition_occurrence", "drug_exposure"),
  interval = "years",
  ageGroup = list("<=20" = c(0, 20), ">20" = c(21, Inf)),
  sex = TRUE
)

summarisedResult |>
  tableRecordCount()

PatientProfiles::mockDisconnect(cdm = cdm)
```

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