

# Package ‘omopgenerics’

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**Title** Methods and Classes for the OMOP Common Data Model

**Version** 1.3.3

**Description** Provides definitions of core classes and methods used by analytic pipelines that query the OMOP (Observational Medical Outcomes Partnership) common data model.

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---

|                 |                                                                |
|-----------------|----------------------------------------------------------------|
| achillesColumns | <i>Required columns for each of the achilles result tables</i> |
|-----------------|----------------------------------------------------------------|

---

Description

Required columns for each of the achilles result tables

Usage

```
achillesColumns(table, version = "5.3", onlyRequired = lifecycle::deprecated())
```

Arguments

- |              |                                                                                                                          |
|--------------|--------------------------------------------------------------------------------------------------------------------------|
| table        | Table for which to see the required columns. One of "achilles_analysis", "achilles_results", or "achilles_results_dist". |
| version      | Version of the OMOP Common Data Model.                                                                                   |
| onlyRequired | deprecated.                                                                                                              |

Value

Character vector with the column names

Examples

```
library(omopgenerics)
achillesColumns("achilles_analysis")
achillesColumns("achilles_results")
achillesColumns("achilles_results_dist")
```

---

|                |                                                                          |
|----------------|--------------------------------------------------------------------------|
| achillesTables | <i>Names of the tables that contain the results of achilles analyses</i> |
|----------------|--------------------------------------------------------------------------|

---

**Description**

Names of the tables that contain the results of achilles analyses

**Usage**

```
achillesTables(version = "5.3")
```

**Arguments**

|         |                                        |
|---------|----------------------------------------|
| version | Version of the OMOP Common Data Model. |
|---------|----------------------------------------|

**Value**

Names of the tables that are contain the results from the achilles analyses

**Examples**

```
library(omopgenerics)
achillesTables()
```

---

|                   |                                                     |
|-------------------|-----------------------------------------------------|
| additionalColumns | <i>Identify variables in additional_name column</i> |
|-------------------|-----------------------------------------------------|

---

**Description**

Identifies and returns the unique values in additional\_name column.

**Usage**

```
additionalColumns(result)
```

**Arguments**

|        |           |
|--------|-----------|
| result | A tibble. |
|--------|-----------|

**Value**

Unique values of the additional name column.

**Examples**

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))

  x

  x |> additionalColumns()
}
```

---

|             |                                                                   |
|-------------|-------------------------------------------------------------------|
| addSettings | <i>Add settings columns to a &lt;summarised_result&gt; object</i> |
|-------------|-------------------------------------------------------------------|

---

**Description**

Add settings columns to a <summarised\_result> object

**Usage**

```
addSettings(result, settingsColumn = settingsColumns(result))
```

**Arguments**

|                |                                                                                                                                                  |
|----------------|--------------------------------------------------------------------------------------------------------------------------------------------------|
| result         | A <summarised_result> object.                                                                                                                    |
| settingsColumn | Settings to be added as columns, by default settingsColumns(result) will be added. If NULL or empty character vector, no settings will be added. |

**Value**

A <summarised\_result> object with the added setting columns.

**Examples**

```

{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))

  x

  x |> addSettings()
}

```

---

assertCharacter

---

*Assert that an object is a character and fulfill certain conditions.*


---

**Description**

Assert that an object is a character and fulfill certain conditions.

**Usage**

```

assertCharacter(
  x,
  length = NULL,
  na = FALSE,
  null = FALSE,
  unique = FALSE,
  named = FALSE,
  minNumCharacter = 0,
  call = parent.frame(),
  msg = NULL
)

```



**Arguments**

|                 |                                                           |
|-----------------|-----------------------------------------------------------|
| x               | Variable to check.                                        |
| length          | Required length. If NULL length is not checked.           |
| na              | Whether it can contain NA values.                         |
| null            | Whether it can be NULL.                                   |
| unique          | Whether it has to contain unique elements.                |
| named           | Whether it has to be named.                               |
| minNumCharacter | Minimum number of characters that all elements must have. |
| call            | Call argument that will be passed to cli error message.   |
| msg             | Custom error message.                                     |

---

|              |                                                            |
|--------------|------------------------------------------------------------|
| assertChoice | <i>Assert that an object is within a certain oprtions.</i> |
|--------------|------------------------------------------------------------|

---

**Description**

Assert that an object is within a certain oprtions.

**Usage**

```
assertChoice(
  x,
  choices,
  length = NULL,
  na = FALSE,
  null = FALSE,
  unique = FALSE,
  named = FALSE,
  call = parent.frame(),
  msg = NULL
)
```

**Arguments**

|         |                                                         |
|---------|---------------------------------------------------------|
| x       | Variable to check.                                      |
| choices | Options that x is allowed to be.                        |
| length  | Required length. If NULL length is not checked.         |
| na      | Whether it can contain NA values.                       |
| null    | Whether it can be NULL.                                 |
| unique  | Whether it has to contain unique elements.              |
| named   | Whether it has to be named.                             |
| call    | Call argument that will be passed to cli error message. |
| msg     | Custom error message.                                   |

---

|             |                                                   |
|-------------|---------------------------------------------------|
| assertClass | <i>Assert that an object has a certain class.</i> |
|-------------|---------------------------------------------------|

---

**Description**

Assert that an object has a certain class.

**Usage**

```
assertClass(  
  x,  
  class,  
  length = NULL,  
  null = FALSE,  
  all = FALSE,  
  extra = TRUE,  
  call = parent.frame(),  
  msg = NULL  
)
```

**Arguments**

|        |                                                                      |
|--------|----------------------------------------------------------------------|
| x      | To check.                                                            |
| class  | Expected class or classes.                                           |
| length | Required length. If NULL length is not checked.                      |
| null   | Whether it can be NULL.                                              |
| all    | Whether it should have all the classes or only at least one of them. |
| extra  | Whether the object can have extra classes.                           |
| call   | Call argument that will be passed to cli.                            |
| msg    | Custom error message.                                                |

---

|            |                    |
|------------|--------------------|
| assertDate | <i>Assert Date</i> |
|------------|--------------------|

---

**Description**

Assert Date

**Usage**

```
assertDate(  
  x,  
  length = NULL,  
  na = FALSE,  
  null = FALSE,  
  unique = FALSE,  
  named = FALSE,  
  call = parent.frame(),  
  msg = NULL  
)
```

**Arguments**

|        |                                                         |
|--------|---------------------------------------------------------|
| x      | Expression to check.                                    |
| length | Required length.                                        |
| na     | Whether it can contain NA values.                       |
| null   | Whether it can be NULL.                                 |
| unique | Whether it has to contain unique elements.              |
| named  | Whether it has to be named.                             |
| call   | Call argument that will be passed to cli error message. |
| msg    | Custom error message.                                   |

**Value**

x

---

|            |                                         |
|------------|-----------------------------------------|
| assertList | <i>Assert that an object is a list.</i> |
|------------|-----------------------------------------|

---

**Description**

Assert that an object is a list.

**Usage**

```
assertList(  
  x,  
  length = NULL,  
  na = FALSE,  
  null = FALSE,  
  unique = FALSE,  
  named = FALSE,  
  class = NULL,  
  call = parent.frame(),  
  msg = NULL  
)
```

**Arguments**

|        |                                                         |
|--------|---------------------------------------------------------|
| x      | Variable to check.                                      |
| length | Required length. If NULL length is not checked.         |
| na     | Whether it can contain NA values.                       |
| null   | Whether it can be NULL.                                 |
| unique | Whether it has to contain unique elements.              |
| named  | Whether it has to be named.                             |
| class  | Class that the elements must have.                      |
| call   | Call argument that will be passed to cli error message. |
| msg    | Custom error message.                                   |

---

|               |                                            |
|---------------|--------------------------------------------|
| assertLogical | <i>Assert that an object is a logical.</i> |
|---------------|--------------------------------------------|

---

**Description**

Assert that an object is a logical.

**Usage**

```
assertLogical(
  x,
  length = NULL,
  na = FALSE,
  null = FALSE,
  unique = FALSE,
  named = FALSE,
  call = parent.frame(),
  msg = NULL
)
```

**Arguments**

|        |                                                         |
|--------|---------------------------------------------------------|
| x      | Variable to check.                                      |
| length | Required length. If NULL length is not checked.         |
| na     | Whether it can contain NA values.                       |
| null   | Whether it can be NULL.                                 |
| unique | Whether it has to contain unique elements.              |
| named  | Whether it has to be named.                             |
| call   | Call argument that will be passed to cli error message. |
| msg    | Custom error message.                                   |

---

|               |                                            |
|---------------|--------------------------------------------|
| assertNumeric | <i>Assert that an object is a numeric.</i> |
|---------------|--------------------------------------------|

---

## Description

Assert that an object is a numeric.

## Usage

```
assertNumeric(  
  x,  
  integerish = FALSE,  
  min = -Inf,  
  max = Inf,  
  length = NULL,  
  na = FALSE,  
  null = FALSE,  
  unique = FALSE,  
  named = FALSE,  
  call = parent.frame(),  
  msg = NULL  
)
```

## Arguments

|            |                                                         |
|------------|---------------------------------------------------------|
| x          | Variable to check.                                      |
| integerish | Whether it has to be an integer                         |
| min        | Minimum value that the object can be.                   |
| max        | Maximum value that the object can be.                   |
| length     | Required length. If NULL length is not checked.         |
| na         | Whether it can contain NA values.                       |
| null       | Whether it can be NULL.                                 |
| unique     | Whether it has to contain unique elements.              |
| named      | Whether it has to be named.                             |
| call       | Call argument that will be passed to cli error message. |
| msg        | Custom error message.                                   |

---

|             |                                          |
|-------------|------------------------------------------|
| assertTable | <i>Assert that an object is a table.</i> |
|-------------|------------------------------------------|

---

## Description

Assert that an object is a table.

## Usage

```
assertTable(  
  x,  
  class = NULL,  
  numberColumns = NULL,  
  numberRows = NULL,  
  columns = character(),  
  allowExtraColumns = TRUE,  
  null = FALSE,  
  unique = FALSE,  
  call = parent.frame(),  
  msg = NULL  
)
```

## Arguments

|                   |                                                                       |
|-------------------|-----------------------------------------------------------------------|
| x                 | Variable to check.                                                    |
| class             | A class that the table must have: "tbl", "data.frame", "tbl_sql", ... |
| numberColumns     | Number of columns that it has to contain.                             |
| numberRows        | Number of rows that it has to contain.                                |
| columns           | Name of the columns required.                                         |
| allowExtraColumns | Whether extra columns are allowed.                                    |
| null              | Whether it can be NULL.                                               |
| unique            | Whether it has to contain unique rows.                                |
| call              | Call argument that will be passed to cli error message.               |
| msg               | Custom error message.                                                 |

---

|            |                                           |
|------------|-------------------------------------------|
| assertTrue | <i>Assert that an expression is TRUE.</i> |
|------------|-------------------------------------------|

---

**Description**

Assert that an expression is TRUE.

**Usage**

```
assertTrue(x, null = FALSE, call = parent.frame(), msg = NULL)
```

**Arguments**

|      |                                                         |
|------|---------------------------------------------------------|
| x    | Expression to check.                                    |
| null | Whether it can be NULL.                                 |
| call | Call argument that will be passed to cli error message. |
| msg  | Custom error message.                                   |

---

|           |                                      |
|-----------|--------------------------------------|
| attrition | <i>Get attrition from an object.</i> |
|-----------|--------------------------------------|

---

**Description**

Get attrition from an object.

**Usage**

```
attrition(x)
```

**Arguments**

|   |                                                  |
|---|--------------------------------------------------|
| x | An object for which to get an attrition summary. |
|---|--------------------------------------------------|

**Value**

A table with the attrition.

---

`attrition.cohort_table`*Get cohort attrition from a cohort\_table object.*

---

**Description**

Get cohort attrition from a cohort\_table object.

**Usage**

```
## S3 method for class 'cohort_table'  
attrition(x)
```

**Arguments**

x                    A cohort\_table

**Value**

A table with the attrition.

**Examples**

```
library(omopgenerics)  
library(dplyr, warn.conflicts = FALSE)  
  
person <- tibble(  
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,  
  race_concept_id = 0, ethnicity_concept_id = 0  
)  
observation_period <- tibble(  
  observation_period_id = 1, person_id = 1,  
  observation_period_start_date = as.Date("2000-01-01"),  
  observation_period_end_date = as.Date("2023-12-31"),  
  period_type_concept_id = 0  
)  
cohort <- tibble(  
  cohort_definition_id = c(1, 1, 1, 2),  
  subject_id = 1,  
  cohort_start_date = as.Date(c("2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01")),  
  cohort_end_date = as.Date(c("2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01")),  
)  
cdm <- cdmFromTables(  
  tables = list("person" = person, "observation_period" = observation_period),  
  cdmName = "my_example_cdm",  
  cohortTables = list("cohort1" = cohort)  
)  
  
attrition(cdm$cohort1)
```



---

|      |                                                    |
|------|----------------------------------------------------|
| bind | <i>Bind two or more objects of the same class.</i> |
|------|----------------------------------------------------|

---

**Description**

Bind two or more objects of the same class.

**Usage**

```
bind(...)
```

**Arguments**

|     |                  |
|-----|------------------|
| ... | Objects to bind. |
|-----|------------------|

**Value**

New object.

---

|                   |                                       |
|-------------------|---------------------------------------|
| bind.cohort_table | <i>Bind two or more cohort tables</i> |
|-------------------|---------------------------------------|

---

**Description**

Bind two or more cohort tables

**Usage**

```
## S3 method for class 'cohort_table'
bind(..., name)
```

**Arguments**

|      |                                                                      |
|------|----------------------------------------------------------------------|
| ...  | Generated cohort set objects to bind. At least two must be provided. |
| name | Name of the new generated cohort set.                                |

**Value**

The cdm object with a new generated cohort set containing all of the cohorts passed.

**Examples**

```

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

cohort1 <- tibble(
  cohort_definition_id = 1,
  subject_id = 1:3,
  cohort_start_date = as.Date("2010-01-01"),
  cohort_end_date = as.Date("2010-01-05")
)
cohort2 <- tibble(
  cohort_definition_id = c(2, 2, 3, 3, 3),
  subject_id = c(1, 2, 3, 1, 2),
  cohort_start_date = as.Date("2010-01-01"),
  cohort_end_date = as.Date("2010-01-05")
)
cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock",
  cohortTables = list("cohort1" = cohort1, "cohort2" = cohort2)
)

cdm <- bind(cdm$cohort1, cdm$cohort2, name = "cohort3")
settings(cdm$cohort3)
cdm$cohort3

```

---

`bind.summarised_result`

*Bind two or summarised\_result objects*

---

**Description**

Bind two or summarised\_result objects

**Usage**

```

## S3 method for class 'summarised_result'
bind(...)

```

**Arguments**

... summarised\_result objects

**Value**

A summarised\_result object the merged objects.

**Examples**

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock",
  cohortTables = list("cohort1" = tibble(
    cohort_definition_id = 1,
    subject_id = 1:3,
    cohort_start_date = as.Date("2010-01-01"),
    cohort_end_date = as.Date("2010-01-05")
  ))
)

result1 <- summary(cdm)
result2 <- summary(cdm$cohort1)

mergedResult <- bind(result1, result2)
mergedResult
```

---

cdmClasses

---

*Separate the cdm tables in classes*


---

**Description**

Separate the cdm tables in classes

Usage

```
cdmClasses(cdm)
```

Arguments

cdm                    A cdm\_reference object.

Value

A list of table names, the name of the list indicates the class.

---

|               |                                      |
|---------------|--------------------------------------|
| cdmDisconnect | <i>Disconnect from a cdm object.</i> |
|---------------|--------------------------------------|

---

Description

Disconnect from a cdm object.

Usage

```
cdmDisconnect(cdm, ...)
```

Arguments

cdm                    A cdm reference or the source of a cdm reference.  
...                    Used for consistency.

Value

```
TRUE if process wass successful. library(omopgenerics) library(dplyr, warn.conflicts = FALSE)

person <- tibble( person_id = 1, gender_concept_id = 0, year_of_birth = 1990, race_concept_id
= 0, ethnicity_concept_id = 0 ) observation_period <- tibble( observation_period_id = 1, per-
son_id = 1, observation_period_start_date = as.Date("2000-01-01"), observation_period_end_date
= as.Date("2023-12-31"), period_type_concept_id = 0 ) cdm <- cdmFromTables( tables = list("person"
= person, "observation_period" = observation_period), cdmName = "mock" )

cdmDisconnect(cdm)
```

---

cdmFromTables*Create a cdm object from local tables*

---

**Description**

Create a cdm object from local tables

**Usage**

```
cdmFromTables(tables, cdmName, cohortTables = list(), cdmVersion = NULL)
```

**Arguments**

|              |                                                                                                     |
|--------------|-----------------------------------------------------------------------------------------------------|
| tables       | List of tables to be part of the cdm object.                                                        |
| cdmName      | Name of the cdm object.                                                                             |
| cohortTables | List of tables that contains cohort, cohort_set and cohort_attrition can be provided as attributes. |
| cdmVersion   | Version of the cdm_reference                                                                        |

**Value**

A cdm\_reference object.

**Examples**

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test"
)
```

---

`cdmName`*Get the name of a cdm\_reference associated object*

---

**Description**

Get the name of a cdm\_reference associated object

**Usage**

```
cdmName(x)
```

**Arguments**

`x`                      A cdm\_reference or cdm\_table object.

**Value**

Name of the cdm\_reference.

**Examples**

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdmName(cdm)

cdmName(cdm$person)
```

---

|              |                                              |
|--------------|----------------------------------------------|
| cdmReference | <i>Get the cdm_reference of a cdm_table.</i> |
|--------------|----------------------------------------------|

---

## Description

Get the cdm\_reference of a cdm\_table.

## Usage

```
cdmReference(table)
```

## Arguments

|       |              |
|-------|--------------|
| table | A cdm_table. |
|-------|--------------|

## Value

A cdm\_reference.

## Examples

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdmReference(cdm$person)
```

---

|           |                                                       |
|-----------|-------------------------------------------------------|
| cdmSelect | <i>Restrict the cdm object to a subset of tables.</i> |
|-----------|-------------------------------------------------------|

---

### Description

Restrict the cdm object to a subset of tables.

### Usage

```
cdmSelect(cdm, ...)
```

### Arguments

|     |                                                                 |
|-----|-----------------------------------------------------------------|
| cdm | A cdm_reference object.                                         |
| ... | Selection of tables to use, it supports tidyselect expressions. |

### Value

A cdm\_reference with only the specified tables.

### Examples

```
cdm <- emptyCdmReference("my cdm")
cdm

cdm |>
  cdmSelect("person")
```

---

|           |                                        |
|-----------|----------------------------------------|
| cdmSource | <i>Get the cdmSource of an object.</i> |
|-----------|----------------------------------------|

---

### Description

Get the cdmSource of an object.

### Usage

```
cdmSource(x, cdm = lifecycle::deprecated())
```

### Arguments

|     |                                 |
|-----|---------------------------------|
| x   | Object to obtain the cdmSource. |
| cdm | Deprecated, use x please.       |



**Value**

A cdm\_source object.

**Examples**

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdmSource(cdm)
cdmSource(cdm$person)
```

---

cdmSourceType

---

*Get the source type of a cdm\_reference object.*


---

**Description**

**[Deprecated]**

**Usage**

```
cdmSourceType(cdm)
```

**Arguments**

cdm                    A cdm\_reference object.

**Value**

A character vector with the type of source of the cdm\_reference object.

## Examples

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdmSourceType(cdm)
```

---

|                    |                                                                                                                                                                                                                               |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cdmTableFromSource | <i>This is an internal developer focused function that creates a cdm_table from a table that shares the source but it is not a cdm_table. Please use insertTable if you want to insert a table to a cdm_reference object.</i> |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

## Description

This is an internal developer focused function that creates a cdm\_table from a table that shares the source but it is not a cdm\_table. Please use insertTable if you want to insert a table to a cdm\_reference object.

## Usage

```
cdmTableFromSource(src, value)
```

## Arguments

|       |                                                           |
|-------|-----------------------------------------------------------|
| src   | A cdm_source object.                                      |
| value | A table that shares source with the cdm_reference object. |

## Value

A cdm\_table.

---

|            |                                      |
|------------|--------------------------------------|
| cdmVersion | <i>Get the version of an object.</i> |
|------------|--------------------------------------|

---

## Description

Get the version of an object.

## Usage

```
cdmVersion(x)
```

## Arguments

x                      Object to know the cdm version of an object.

## Value

A character vector indicating the cdm version.

## Examples

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdmVersion(cdm)
cdmVersion(cdm$person)
```

---

checkCohortRequirements

*Check whether a cohort table satisfies requirements*


---

## Description

**[Deprecated]**

## Usage

```
checkCohortRequirements(
  cohort,
  checkEndAfterStart = TRUE,
  checkOverlappingEntries = TRUE,
  checkMissingValues = TRUE,
  checkInObservation = TRUE,
  type = "error",
  call = parent.frame()
)
```

## Arguments

|                         |                                                                                                                                                            |
|-------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort                  | cohort_table object.                                                                                                                                       |
| checkEndAfterStart      | If TRUE a check that all cohort end dates come on or after cohort start date will be performed.                                                            |
| checkOverlappingEntries | If TRUE a check that no individuals have overlapping cohort entries will be performed.                                                                     |
| checkMissingValues      | If TRUE a check that there are no missing values in required fields will be performed.                                                                     |
| checkInObservation      | If TRUE a check that cohort entries are within the individuals observation periods will be performed.                                                      |
| type                    | Can be either "error" or "warning". If "error" any check failure will result in an error, whereas if "warning" any check failure will result in a warning. |
| call                    | The call for which to return the error message.                                                                                                            |

## Value

An error will be returned if any of the selected checks fail.

---

|                |                                                 |
|----------------|-------------------------------------------------|
| cohortCodelist | <i>Get codelist from a cohort_table object.</i> |
|----------------|-------------------------------------------------|

---

## Description

Get codelist from a cohort\_table object.

## Usage

```
cohortCodelist(  
  cohort,  
  cohortId = NULL,  
  codelistType = c("index event", "inclusion criteria", "exit criteria"),  
  type = lifecycle::deprecated(),  
  cohortTable = lifecycle::deprecated()  
)
```

## Arguments

|              |                                                                                                                                |
|--------------|--------------------------------------------------------------------------------------------------------------------------------|
| cohort       | A cohort_table object.                                                                                                         |
| cohortId     | A particular cohort definition id that is present in the cohort table. If NULL the codelists of all cohorts will be retrieved. |
| codelistType | The reason for the codelist. Can be "index event", "inclusion criteria", or "exit criteria".                                   |
| type         | deprecated.                                                                                                                    |
| cohortTable  | deprecated.                                                                                                                    |

## Value

A table with the codelists used.

## Examples

```
library(omopgenerics)  
library(dplyr, warn.conflicts = FALSE)  
  
person <- tibble(  
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,  
  race_concept_id = 0, ethnicity_concept_id = 0  
)  
observation_period <- tibble(  
  observation_period_id = 1, person_id = 1,  
  observation_period_start_date = as.Date("2000-01-01"),  
  observation_period_end_date = as.Date("2023-12-31"),  
  period_type_concept_id = 0  
)  
cohort <- tibble(  
  cohort_id = 1, cohort_name = "Cohort 1", cohort_start_date = as.Date("2000-01-01"),  
  cohort_end_date = as.Date("2023-12-31"), cohort_type_concept_id = 0  
)
```

```

    cohort_definition_id = c(1, 1, 1, 2),
    subject_id = 1,
    cohort_start_date = as.Date(c(
      "2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01"
    )),
    cohort_end_date = as.Date(c(
      "2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01"
    ))
  )
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "my_example_cdm",
  cohortTables = list("cohort1" = cohort)
)
cdm$cohort1 <- newCohortTable(table = cdm$cohort1,
  cohortCodelistRef = dplyr::tibble(
    cohort_definition_id = c(1,1,1,2,2),
    codelist_name =c("disease X", "disease X", "disease X",
      "disease Y", "disease Y"),
    concept_id = c(1,2,3,4,5),
    codelist_type = "index event"
  ))
cohortCodelist(cdm$cohort1, cohortId = 1, codelistType = "index event")

```

---

cohortColumns

*Required columns for a generated cohort set.*


---

## Description

Required columns for a generated cohort set.

## Usage

```
cohortColumns(table, version = "5.3")
```

## Arguments

|         |                                               |
|---------|-----------------------------------------------|
| table   | Either cohort, cohort_set or cohort_attrition |
| version | Version of the OMOP Common Data Model.        |

## Value

Character vector with the column names

Required columns

**Examples**

```
library(omopgenerics)
cohortColumns("cohort")
```

---

cohortCount

*Get cohort counts from a cohort\_table object.*


---

**Description**

Get cohort counts from a cohort\_table object.

**Usage**

```
cohortCount(cohort)
```

**Arguments**

cohort                    A cohort\_table object.

**Value**

A table with the counts.

**Examples**

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cohort <- tibble(
  cohort_definition_id = c(1, 1, 1, 2),
  subject_id = 1,
  cohort_start_date = as.Date(c(
    "2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01"
  )),
  cohort_end_date = as.Date(c(
    "2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01"
  )),
)
```

```

cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "my_example_cdm",
  cohortTables = list("cohort1" = cohort)
)

cohortCount(cdm$cohort1)

```

---

|              |                                                                                      |
|--------------|--------------------------------------------------------------------------------------|
| cohortTables | <i>Cohort tables that a cdm reference can contain in the OMOP Common Data Model.</i> |
|--------------|--------------------------------------------------------------------------------------|

---

### Description

Cohort tables that a cdm reference can contain in the OMOP Common Data Model.

### Usage

```
cohortTables(version = "5.3")
```

### Arguments

|         |                                        |
|---------|----------------------------------------|
| version | Version of the OMOP Common Data Model. |
|---------|----------------------------------------|

### Value

cohort tables

### Examples

```

library(omopgenerics)
cohortTables()

```

---

|                       |                                                      |
|-----------------------|------------------------------------------------------|
| collect.cdm_reference | <i>Retrieves the cdm reference into a local cdm.</i> |
|-----------------------|------------------------------------------------------|

---

### Description

Retrieves the cdm reference into a local cdm.

### Usage

```

## S3 method for class 'cdm_reference'
collect(x, ...)

```



**Arguments**

x                    A cdm\_reference object.  
 ...                For compatibility only, not used.

**Value**

A local cdm\_reference.

**Examples**

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

cdm <- cdmFromTables(
  tables = list(
    "person" = dplyr::tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = dplyr::tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

collect(cdm)
```

---

collect.cohort\_table    *To collect a cohort\_table object.*

---

**Description**

To collect a cohort\_table object.

**Usage**

```
## S3 method for class 'cohort_table'
collect(x, ...)
```

**Arguments**

x                    cohort\_table object.  
 ...                Not used (for compatibility).

**Value**

A data frame with the cohort\_table

---

|               |                                                   |
|---------------|---------------------------------------------------|
| combineStrata | <i>Provide all combinations of strata levels.</i> |
|---------------|---------------------------------------------------|

---

**Description**

Provide all combinations of strata levels.

**Usage**

```
combineStrata(levels, overall = FALSE)
```

**Arguments**

|         |                                                  |
|---------|--------------------------------------------------|
| levels  | Vector of all strata levels to combine.          |
| overall | Whether to provide an empty element character(). |

**Value**

A vector of all combinations of strata.

**Examples**

```
combineStrata(character())
combineStrata(character(), overall = TRUE)
combineStrata(c("age", "sex"), overall = TRUE)
combineStrata(c("age", "sex", "year"))
```

---

|                   |                                  |
|-------------------|----------------------------------|
| compute.cdm_table | <i>Store results in a table.</i> |
|-------------------|----------------------------------|

---

**Description**

Store results in a table.

**Usage**

```
## S3 method for class 'cdm_table'
compute(
  x,
  name = NULL,
  temporary = NULL,
  overwrite = TRUE,
  logPrefix = NULL,
  ...
)
```

**Arguments**

|           |                                                                   |
|-----------|-------------------------------------------------------------------|
| x         | Table in the cdm.                                                 |
| name      | Name to store the table with.                                     |
| temporary | Whether to store table temporarily (TRUE) or permanently (FALSE). |
| overwrite | Whether to overwrite previously existing table with name same.    |
| logPrefix | Prefix to use when saving a log file.                             |
| ...       | For compatibility (not used).                                     |

**Value**

Reference to a table in the cdm

---

|               |                                   |
|---------------|-----------------------------------|
| createIndexes | <i>Create the missing indexes</i> |
|---------------|-----------------------------------|

---

**Description**

[Experimental]

**Usage**

```
createIndexes(cdm, name = NULL)
```

**Arguments**

|      |                            |
|------|----------------------------|
| cdm  | A cdm_reference object.    |
| name | Name(s) of the cdm tables. |

**Value**

Whether the process was completed successfully.

---

|               |                          |
|---------------|--------------------------|
| createLogFile | <i>Create a log file</i> |
|---------------|--------------------------|

---

**Description**

Create a log file

**Usage**

```
createLogFile(logFile = here::here("log_{date}_{time}"))
```

**Arguments**

|         |                                                                                                                       |
|---------|-----------------------------------------------------------------------------------------------------------------------|
| logFile | File path to write logging messages. You can use '{date}' and '{time}' to add the date and time in the log file name. |
|---------|-----------------------------------------------------------------------------------------------------------------------|

**Value**

Invisible TRUE if logger was created correctly.

**Examples**

```
library(dplyr)

logFile <- tempfile(pattern = "log_{date}_{time}", fileext = ".txt")
createLogFile(logFile = logFile)

logMessage("Starting analysis")
1 + 1
logMessage("Analysis finished")

res <- summariseLogFile()

glimpse(res)

tidy(res)
```

---

|                  |                             |
|------------------|-----------------------------|
| createTableIndex | <i>Create a table index</i> |
|------------------|-----------------------------|

---

**Description**

**[Experimental]**

**Usage**

```
createTableIndex(table, index)
```

**Arguments**

|       |                      |
|-------|----------------------|
| table | A cdm_table object.  |
| index | Index to be created. |

**Value**

Whether the index could be created

---

|                 |                                        |
|-----------------|----------------------------------------|
| dropSourceTable | <i>Drop a table from a cdm object.</i> |
|-----------------|----------------------------------------|

---

**Description**

Drop a table from a cdm object.

**Usage**

```
dropSourceTable(cdm, name)
```

**Arguments**

|      |                                                                        |
|------|------------------------------------------------------------------------|
| cdm  | A cdm reference.                                                       |
| name | Name(s) of the table(s) to insert. Tidymodel statements are supported. |

**Value**

The table in the cdm reference.

---

|           |                                                     |
|-----------|-----------------------------------------------------|
| dropTable | <i>Drop a table from a cdm object. [Deprecated]</i> |
|-----------|-----------------------------------------------------|

---

**Description**

Drop a table from a cdm object. **[Deprecated]**

**Usage**

```
dropTable(cdm, name)
```

**Arguments**

|      |                                                                     |
|------|---------------------------------------------------------------------|
| cdm  | A cdm reference.                                                    |
| name | Name(s) of the table(s) to drop Tidymodel statements are supported. |

**Value**

The cdm reference.

---

|                    |                                |
|--------------------|--------------------------------|
| emptyAchillesTable | Create an empty achilles table |
|--------------------|--------------------------------|

---

**Description**

Create an empty achilles table

**Usage**

```
emptyAchillesTable(cdm, name)
```

**Arguments**

|      |                                      |
|------|--------------------------------------|
| cdm  | A cdm_reference to create the table. |
| name | Name of the table to create.         |

**Value**

The cdm\_reference with an achilles empty table

**Examples**

```
library(omopgenerics)
cdm <- emptyCdmReference("my_example_cdm")
emptyAchillesTable(cdm = cdm, name = "achilles_results")
```

---

|                   |                               |
|-------------------|-------------------------------|
| emptyCdmReference | Create an empty cdm_reference |
|-------------------|-------------------------------|

---

**Description**

Create an empty cdm\_reference

**Usage**

```
emptyCdmReference(cdmName, cdmVersion = NULL)
```

**Arguments**

|            |                              |
|------------|------------------------------|
| cdmName    | Name of the cdm_reference    |
| cdmVersion | Version of the cdm_reference |

**Value**

An empty cdm\_reference

**Examples**

```
library(omopgenerics)
emptyCdmReference(cdmName = "my_example_cdm")
```

---

|               |                               |
|---------------|-------------------------------|
| emptyCodelist | <i>Empty codelist object.</i> |
|---------------|-------------------------------|

---

**Description**

Empty codelist object.

**Usage**

```
emptyCodelist()
```

**Value**

An empty codelist object.

**Examples**

```
emptyCodelist()
```

---

|                          |                               |
|--------------------------|-------------------------------|
| emptyCodelistWithDetails | <i>Empty codelist object.</i> |
|--------------------------|-------------------------------|

---

**Description**

Empty codelist object.

**Usage**

```
emptyCodelistWithDetails()
```

**Value**

An empty codelist object.

**Examples**

```
emptyCodelistWithDetails()
```

---

|                  |                                     |
|------------------|-------------------------------------|
| emptyCohortTable | Create an empty cohort_table object |
|------------------|-------------------------------------|

---

## Description

Create an empty cohort\_table object

## Usage

```
emptyCohortTable(cdm, name, overwrite = TRUE)
```

## Arguments

|           |                                         |
|-----------|-----------------------------------------|
| cdm       | A cdm_reference to create the table.    |
| name      | Name of the table to create.            |
| overwrite | Whether to overwrite an existent table. |

## Value

The cdm\_reference with an empty cohort table

## Examples

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test"
)

cdm <- emptyCohortTable(cdm, "my_empty_cohort")

cdm
cdm$my_empty_cohort
settings(cdm$my_empty_cohort)
attrition(cdm$my_empty_cohort)
cohortCount(cdm$my_empty_cohort)
```



---

|                           |                                             |
|---------------------------|---------------------------------------------|
| emptyConceptSetExpression | <i>Empty concept_set_expression object.</i> |
|---------------------------|---------------------------------------------|

---

**Description**

Empty concept\_set\_expression object.

**Usage**

emptyConceptSetExpression()

**Value**

An empty concept\_set\_expression object.

**Examples**

emptyConceptSetExpression()

---

|                |                                   |
|----------------|-----------------------------------|
| emptyOmopTable | <i>Create an empty omop table</i> |
|----------------|-----------------------------------|

---

**Description**

Create an empty omop table

**Usage**

emptyOmopTable(cdm, name)

**Arguments**

- |      |                                      |
|------|--------------------------------------|
| cdm  | A cdm_reference to create the table. |
| name | Name of the table to create.         |

**Value**

The cdm\_reference with an empty cohort table

## Examples

```
library(omopgenerics)

person <- dplyr::tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- dplyr::tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test"
)

cdm <- emptyOmopTable(cdm, "drug_exposure")

cdm$drug_exposure
```

---

`emptySummarisedResult` *Empty summarised\_result object.*

---

## Description

Empty summarised\_result object.

## Usage

```
emptySummarisedResult(settings = NULL)
```

## Arguments

|                       |                                                                                                                               |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------|
| <code>settings</code> | Tibble/data.frame with the settings of the empty summarised_result. It has to contain at least <code>result_id</code> column. |
|-----------------------|-------------------------------------------------------------------------------------------------------------------------------|

## Value

An empty summarised\_result object.

## Examples

```
library(omopgenerics)

emptySummarisedResult()
```

---

|                     |                                                             |
|---------------------|-------------------------------------------------------------|
| estimateTypeChoices | <i>Choices that can be present in estimate_type column.</i> |
|---------------------|-------------------------------------------------------------|

---

**Description**

Choices that can be present in estimate\_type column.

**Usage**

```
estimateTypeChoices()
```

**Value**

A character vector with the options that can be present in estimate\_type column in the summarised\_result objects.

**Examples**

```
library(omopgenerics)
estimateTypeChoices()
```

---

|                 |                                         |
|-----------------|-----------------------------------------|
| existingIndexes | <i>Existing indexes in a cdm object</i> |
|-----------------|-----------------------------------------|

---

**Description**

**[Experimental]**

**Usage**

```
existingIndexes(cdm, name)
```

**Arguments**

|      |                            |
|------|----------------------------|
| cdm  | A cdm_reference object.    |
| name | Name(s) of the cdm tables. |

**Value**

A tibble with 3 columns: table\_class class of the table, table\_name name of the table, and existing\_index index definition.

---

|                 |                                         |
|-----------------|-----------------------------------------|
| expectedIndexes | <i>Expected indexes in a cdm object</i> |
|-----------------|-----------------------------------------|

---

**Description****[Experimental]****Usage**

```
expectedIndexes(cdm, name)
```

**Arguments**

|      |                            |
|------|----------------------------|
| cdm  | A cdm_reference object.    |
| name | Name(s) of the cdm tables. |

**Value**

A tibble with 3 columns: `table_class` class of the table, `table_name` name of the table, and `expected_index` index definition.

---

|                |                                  |
|----------------|----------------------------------|
| exportCodelist | <i>Export a codelist object.</i> |
|----------------|----------------------------------|

---

**Description**

Export a codelist object.

**Usage**

```
exportCodelist(x, path, type = "json")
```

**Arguments**

|      |                                                                    |
|------|--------------------------------------------------------------------|
| x    | A codelist                                                         |
| path | Path to where files will be created.                               |
| type | Type of files to export. Currently 'json' and 'csv' are supported. |

**Value**

Files with codelists

---

`exportConceptSetExpression`*Export a concept set expression.*

---

**Description**

Export a concept set expression.

**Usage**

```
exportConceptSetExpression(x, path, type = "json")
```

**Arguments**

|                   |                                                                    |
|-------------------|--------------------------------------------------------------------|
| <code>x</code>    | A concept set expression                                           |
| <code>path</code> | Path to where files will be created.                               |
| <code>type</code> | Type of files to export. Currently 'json' and 'csv' are supported. |

**Value**

Files with concept set expressions

---

`exportSummarisedResult`*Export a summarised\_result object to a csv file.*

---

**Description**

Export a summarised\_result object to a csv file.

**Usage**

```
exportSummarisedResult(  
  ...,  
  minCellCount = 5,  
  fileName = "results_{cdm_name}_{date}.csv",  
  path = getwd(),  
  logFile = getOption("omopgenerics.logFile"),  
  logSqlPath = getOption("omopgenerics.log_sql_path"),  
  logExplainPath = lifecycle::deprecated()  
)
```

**Arguments**

|                |                                                                                                                                 |
|----------------|---------------------------------------------------------------------------------------------------------------------------------|
| ...            | A set of summarised_result objects.                                                                                             |
| minCellCount   | Minimum count for suppression purposes.                                                                                         |
| fileName       | Name of the file that will be created. Use {cdm_name} to refer to the cdmName of the objects and {date} to add the export date. |
| path           | Path where to create the csv file. It is ignored if fileName it is a full name with path included.                              |
| logFile        | Path to the log file to export.                                                                                                 |
| logSqlPath     | Path to the folder that contains the sql logs to export.                                                                        |
| logExplainPath | deprecated.                                                                                                                     |

---

|                  |                                                                                |
|------------------|--------------------------------------------------------------------------------|
| filterAdditional | <i>Filter the additional_name-additional_level pair in a summarised_result</i> |
|------------------|--------------------------------------------------------------------------------|

---

**Description**

Filter the additional\_name-additional\_level pair in a summarised\_result

**Usage**

```
filterAdditional(result, ...)
```

**Arguments**

|        |                                                                                                                                                                                                                                                                                                   |
|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| result | A <summarised_result> object.                                                                                                                                                                                                                                                                     |
| ...    | Expressions that return a logical value (additionalColumns() are used to evaluate the expression), and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept. |

**Value**

A <summarised\_result> object with only the rows that fulfill the required specified additional.

**Examples**

```
library(dplyr)
library(omopgenerics)

x <- tibble(
  "result_id" = 1L,
  "cdm_name" = "eunomia",
  "group_name" = "cohort_name",
  "group_level" = c("cohort1", "cohort2", "cohort3"),
  "strata_name" = "sex",
```

```

    "strata_level" = "Female",
    "variable_name" = "number subjects",
    "variable_level" = NA_character_,
    "estimate_name" = "count",
    "estimate_type" = "integer",
    "estimate_value" = c("100", "44", "14"),
    "additional_name" = c("year", "time_step", "year && time_step"),
    "additional_level" = c("2010", "4", "2015 && 5")
  ) |>
  newSummarisedResult()

x |>
  filterAdditional(year == "2010")

```

---

filterGroup

---

*Filter the group\_name-group\_level pair in a summarised\_result*


---

## Description

Filter the group\_name-group\_level pair in a summarised\_result

## Usage

```
filterGroup(result, ...)
```

## Arguments

|        |                                                                                                                                                                                                                                                                                              |
|--------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| result | A <summarised_result> object.                                                                                                                                                                                                                                                                |
| ...    | Expressions that return a logical value (groupColumns() are used to evaluate the expression), and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept. |

## Value

A <summarised\_result> object with only the rows that fulfill the required specified group.

## Examples

```

library(dplyr)
library(omopgenerics)

x <- tibble(
  "result_id" = 1L,
  "cdm_name" = "eunomia",
  "group_name" = c("cohort_name", "age_group && cohort_name", "age_group"),
  "group_level" = c("my_cohort", ">40 && second_cohort", "<40"),
  "strata_name" = "sex",

```

```

    "strata_level" = "Female",
    "variable_name" = "number subjects",
    "variable_level" = NA_character_,
    "estimate_name" = "count",
    "estimate_type" = "integer",
    "estimate_value" = c("100", "44", "14"),
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult()

x |>
  filterGroup(cohort_name == "second_cohort")

```

---

filterSettings

---

Filter a <summarised\_result> using the settings

---

## Description

Filter a <summarised\_result> using the settings

## Usage

```
filterSettings(result, ...)
```

## Arguments

|        |                                                                                                                                                                                                                                                                                                   |
|--------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| result | A <summarised_result> object.                                                                                                                                                                                                                                                                     |
| ...    | Expressions that return a logical value (columns in settings are used to evaluate the expression), and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept. |

## Value

A <summarised\_result> object with only the result\_id rows that fulfill the required specified settings.

## Examples

```

library(dplyr)
library(omopgenerics)

x <- tibble(
  "result_id" = as.integer(c(1, 2)),
  "cdm_name" = c("cprd", "eunomia"),
  "group_name" = "cohort_name",
  "group_level" = "my_cohort",

```



```

      "strata_name" = "sex",
      "strata_level" = "male",
      "variable_name" = "Age group",
      "variable_level" = "10 to 50",
      "estimate_name" = "count",
      "estimate_type" = "numeric",
      "estimate_value" = "5",
      "additional_name" = "overall",
      "additional_level" = "overall"
    ) |>
    newSummarisedResult(settings = tibble(
      "result_id" = c(1, 2), "custom" = c("A", "B")
    ))

x

x |> filterSettings(custom == "A")

```

---

|              |                                                                        |
|--------------|------------------------------------------------------------------------|
| filterStrata | <i>Filter the strata_name-strata_level pair in a summarised_result</i> |
|--------------|------------------------------------------------------------------------|

---

## Description

Filter the strata\_name-strata\_level pair in a summarised\_result

## Usage

```
filterStrata(result, ...)
```

## Arguments

|        |                                                                                                                                                                                                                                                                                               |
|--------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| result | A <summarised_result> object.                                                                                                                                                                                                                                                                 |
| ...    | Expressions that return a logical value (strataColumns() are used to evaluate the expression), and are defined in terms of the variables in .data. If multiple expressions are included, they are combined with the & operator. Only rows for which all conditions evaluate to TRUE are kept. |

## Value

A <summarised\_result> object with only the rows that fulfill the required specified strata.

## Examples

```

library(dplyr)
library(omopgenerics)

x <- tibble(
  "result_id" = 1L,

```

```

    "cdm_name" = "eunomia",
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = c("sex", "sex &&& age_group", "sex &&& year"),
    "strata_level" = c("Female", "Male &&& <40", "Female &&& 2010"),
    "variable_name" = "number subjects",
    "variable_level" = NA_character_,
    "estimate_name" = "count",
    "estimate_type" = "integer",
    "estimate_value" = c("100", "44", "14"),
    "additional_name" = "overall",
    "additional_level" = "overall"
) |>
  newSummarisedResult()

x |>
  filterStrata(sex == "Female")

```

---

 getCohortId

*Get the cohort definition id of a certain name*


---

## Description

Get the cohort definition id of a certain name

## Usage

```
getCohortId(cohort, cohortName = NULL)
```

## Arguments

|            |                                                                      |
|------------|----------------------------------------------------------------------|
| cohort     | A cohort_table object.                                               |
| cohortName | Names of the cohort of interest. If NULL all cohort names are shown. |

## Value

Cohort definition ids

---

|               |                                                              |
|---------------|--------------------------------------------------------------|
| getCohortName | <i>Get the cohort name of a certain cohort definition id</i> |
|---------------|--------------------------------------------------------------|

---

**Description**

Get the cohort name of a certain cohort definition id

**Usage**

```
getCohortName(cohort, cohortId = NULL)
```

**Arguments**

|          |                                                                     |
|----------|---------------------------------------------------------------------|
| cohort   | A cohort_table object.                                              |
| cohortId | Cohort definition id of interest. If NULL all cohort ids are shown. |

**Value**

Cohort names

---

|                     |                                                                                                                                                             |
|---------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|
| getPersonIdentifier | <i>Get the column name with the person identifier from a table (either subject_id or person_id), it will throw an error if it contains both or neither.</i> |
|---------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

Get the column name with the person identifier from a table (either subject\_id or person\_id), it will throw an error if it contains both or neither.

**Usage**

```
getPersonIdentifier(x, call = parent.frame())
```

**Arguments**

|      |                                          |
|------|------------------------------------------|
| x    | A table.                                 |
| call | A call argument passed to cli functions. |

**Value**

Person identifier column.

---

|              |                                                |
|--------------|------------------------------------------------|
| groupColumns | <i>Identify variables in group_name column</i> |
|--------------|------------------------------------------------|

---

**Description**

Identifies and returns the unique values in group\_name column.

**Usage**

```
groupColumns(result)
```

**Arguments**

result            A tibble.

**Value**

Unique values of the group name column.

**Examples**

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))

  x

  x |> groupColumns()
}
```

---

|                |                           |
|----------------|---------------------------|
| importCodelist | <i>Import a codelist.</i> |
|----------------|---------------------------|

---

**Description**

Import a codelist.

**Usage**

```
importCodelist(path, type = "json")
```

**Arguments**

|      |                                                                    |
|------|--------------------------------------------------------------------|
| path | Path to where files will be created.                               |
| type | Type of files to export. Currently 'json' and 'csv' are supported. |

**Value**

A codelist

---

|                            |                                         |
|----------------------------|-----------------------------------------|
| importConceptSetExpression | <i>Import a concept set expression.</i> |
|----------------------------|-----------------------------------------|

---

**Description**

Import a concept set expression.

**Usage**

```
importConceptSetExpression(path, type = "json")
```

**Arguments**

|      |                                                                    |
|------|--------------------------------------------------------------------|
| path | Path to where files will be created.                               |
| type | Type of files to export. Currently 'json' and 'csv' are supported. |

**Value**

A concept set expression

---

```
importSummarisedResult
```

*Import a set of summarised results.*

---

### Description

Import a set of summarised results.

### Usage

```
importSummarisedResult(path, recursive = FALSE, ...)
```

### Arguments

|           |                                                                                                                    |
|-----------|--------------------------------------------------------------------------------------------------------------------|
| path      | Path to directory with CSV files containing summarised results or to a specific CSV file with a summarised result. |
| recursive | If TRUE and path is a directory, search for files will recurse into directories                                    |
| ...       | Passed to readr::read_csv.                                                                                         |

### Value

A summarised result

---

```
insertCdmTo
```

*Insert a cdm\_reference object to a different source.*

---

### Description

Insert a cdm\_reference object to a different source.

### Usage

```
insertCdmTo(cdm, to)
```

### Arguments

|     |                                                                 |
|-----|-----------------------------------------------------------------|
| cdm | A cdm_reference, if not local it will be collected into memory. |
| to  | A cdm_source or another cdm_reference, with a valid cdm_source. |

### Value

The first cdm\_reference object inserted to the source.

---

|                  |                                                                                                                                                                                                  |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| insertFromSource | <i>Convert a table that is not a cdm_table but have the same original source to a cdm_table. This Table is not meant to be used to insert tables in the cdm, please use insertTable instead.</i> |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description****[Deprecated]****Usage**

```
insertFromSource(cdm, value)
```

**Arguments**

|       |                                                           |
|-------|-----------------------------------------------------------|
| cdm   | A cdm_reference object.                                   |
| value | A table that shares source with the cdm_reference object. |

**Value**

A table in the cdm\_reference environment

---

|             |                                        |
|-------------|----------------------------------------|
| insertTable | <i>Insert a table to a cdm object.</i> |
|-------------|----------------------------------------|

---

**Description**

Insert a table to a cdm object.

**Usage**

```
insertTable(cdm, name, table, overwrite = TRUE, temporary = FALSE, ...)
```

**Arguments**

|           |                                                   |
|-----------|---------------------------------------------------|
| cdm       | A cdm reference or the source of a cdm reference. |
| name      | Name of the table to insert.                      |
| table     | Table to insert to the cdm.                       |
| overwrite | Whether to overwrite an existent table.           |
| temporary | Whether to create a temporary table.              |
| ...       | For compatibility.                                |

**Value**

```
The cdm reference. library(omopgenerics) library(dplyr, warn.conflicts = FALSE)
person <- tibble( person_id = 1, gender_concept_id = 0, year_of_birth = 1990, race_concept_id
= 0, ethnicity_concept_id = 0 ) observation_period <- tibble( observation_period_id = 1, per-
son_id = 1, observation_period_start_date = as.Date("2000-01-01"), observation_period_end_date
= as.Date("2023-12-31"), period_type_concept_id = 0 ) cdm <- cdmFromTables( tables = list("person"
= person, "observation_period" = observation_period), cdmName = "my_example_cdm" )
x <- tibble(a = 1)
cdm <- insertTable(cdm = cdm, name = "new_table", table = x)
cdm$new_table
```

---

|                    |                                                                                      |
|--------------------|--------------------------------------------------------------------------------------|
| isResultSuppressed | <i>To check whether an object is already suppressed to a certain min cell count.</i> |
|--------------------|--------------------------------------------------------------------------------------|

---

**Description**

To check whether an object is already suppressed to a certain min cell count.

**Usage**

```
isResultSuppressed(result, minCellCount = 5)
```

**Arguments**

|              |                                                |
|--------------|------------------------------------------------|
| result       | The suppressed result to check                 |
| minCellCount | Minimum count of records used when suppressing |

**Value**

Warning or message with check result

**Examples**

```
x <- dplyr::tibble(
  "result_id" = 1L,
  "cdm_name" = "eunomia",
  "group_name" = "cohort_name",
  "group_level" = "my_cohort",
  "strata_name" = c("sex", "sex &&& age_group", "sex &&& year"),
  "strata_level" = c("Female", "Male &&& <40", "Female &&& 2010"),
  "variable_name" = "number subjects",
  "variable_level" = NA_character_,
  "estimate_name" = "count",
  "estimate_type" = "integer",
  "estimate_value" = c("100", "44", "14"),
  "additional_name" = "overall",
```



```
    "additional_level" = "overall"  
  ) |>  
    newSummarisedResult()  
  
  isResultSuppressed(x)
```

---

|              |                                         |
|--------------|-----------------------------------------|
| isTableEmpty | <i>Check if a table is empty or not</i> |
|--------------|-----------------------------------------|

---

**Description**

Check if a table is empty or not

**Usage**

```
isTableEmpty(table)
```

**Arguments**

|       |         |
|-------|---------|
| table | a table |
|-------|---------|

**Value**

Boolean to indicate if a cdm\_table is empty (TRUE or FALSE).

---

|                  |                                                              |
|------------------|--------------------------------------------------------------|
| listSourceTables | <i>List tables that can be accessed though a cdm object.</i> |
|------------------|--------------------------------------------------------------|

---

**Description**

List tables that can be accessed though a cdm object.

**Usage**

```
listSourceTables(cdm)
```

**Arguments**

|     |                                                   |
|-----|---------------------------------------------------|
| cdm | A cdm reference or the source of a cdm reference. |
|-----|---------------------------------------------------|

**Value**

A character vector with the names of tables.

---

|            |                                   |
|------------|-----------------------------------|
| logMessage | <i>Log a message to a logFile</i> |
|------------|-----------------------------------|

---

### Description

The message is written to the logFile and displayed in the console, if logFile does not exist the message is only displayed in the console.

### Usage

```
logMessage(  
  message = "Start logging file",  
  logFile = getOption("omopgenerics.logFile")  
)
```

### Arguments

|         |                                                                             |
|---------|-----------------------------------------------------------------------------|
| message | Message to log.                                                             |
| logFile | File path to write logging messages. Create a logFile with createLogFile(). |

### Value

Invisible TRUE if the logging message is written to a log file.

### Examples

```
library(dplyr)  
  
logFile <- tempfile(pattern = "log_{date}_{time}", fileext = ".txt")  
createLogFile(logFile = logFile)  
  
logMessage("Starting analysis")  
1 + 1  
logMessage("Analysis finished")  
  
res <- summariseLogFile()  
  
glimpse(res)  
  
tidy(res)
```

---

|                  |                                            |
|------------------|--------------------------------------------|
| newAchillesTable | Create an achilles table from a cdm_table. |
|------------------|--------------------------------------------|

---

**Description**

Create an achilles table from a cdm\_table.

**Usage**

```
newAchillesTable(table, version = "5.3", cast = FALSE)
```

**Arguments**

|         |                                              |
|---------|----------------------------------------------|
| table   | A cdm_table.                                 |
| version | version of the cdm.                          |
| cast    | Whether to cast columns to the correct type. |

**Value**

An achilles\_table object

---

|                 |                                   |
|-----------------|-----------------------------------|
| newCdmReference | cdm_reference objects constructor |
|-----------------|-----------------------------------|

---

**Description**

cdm\_reference objects constructor

**Usage**

```
newCdmReference(tables, cdmName, cdmVersion = NULL, .softValidation = FALSE)
```

**Arguments**

|                 |                                                                                                                        |
|-----------------|------------------------------------------------------------------------------------------------------------------------|
| tables          | List of tables that are part of the OMOP Common Data Model reference.                                                  |
| cdmName         | Name of the cdm object.                                                                                                |
| cdmVersion      | Version of the cdm. Supported versions 5.3 and 5.4.                                                                    |
| .softValidation | Whether to perform a soft validation of consistency. If set to FALSE, non overlapping observation periods are ensured. |

**Value**

A cdm\_reference object.

**Examples**

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

cdmTables <- list(
  "person" = tibble(
    person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
    race_concept_id = 0, ethnicity_concept_id = 0
  ) |>
  newCdmTable(newLocalSource(), "person"),
  "observation_period" = tibble(
    observation_period_id = 1, person_id = 1,
    observation_period_start_date = as.Date("2000-01-01"),
    observation_period_end_date = as.Date("2023-12-31"),
    period_type_concept_id = 0
  ) |>
  newCdmTable(newLocalSource(), "observation_period")
)
cdm <- newCdmReference(tables = cdmTables, cdmName = "mock")

cdm
```

---

newCdmSource

---

*Create a cdm source object.*


---

**Description**

Create a cdm source object.

**Usage**

```
newCdmSource(src, sourceType)
```

**Arguments**

|            |                            |
|------------|----------------------------|
| src        | Source to a cdm object.    |
| sourceType | Type of the source object. |

**Value**

A validated cdm source object.

---

|             |                      |
|-------------|----------------------|
| newCdmTable | Create an cdm table. |
|-------------|----------------------|

---

**Description**

Create an cdm table.

**Usage**

newCdmTable(table, src, name)

**Arguments**

- |       |                                |
|-------|--------------------------------|
| table | A table that is part of a cdm. |
| src   | The source of the table.       |
| name  | The name of the table.         |

**Value**

A cdm\_table object

---

|             |                               |
|-------------|-------------------------------|
| newCodelist | 'codelist' object constructor |
|-------------|-------------------------------|

---

**Description**

'codelist' object constructor

**Usage**

newCodelist(x)

**Arguments**

- |   |                                                                   |
|---|-------------------------------------------------------------------|
| x | A named list where each element contains a vector of concept IDs. |
|---|-------------------------------------------------------------------|

**Value**

A codelist object.

---

|                                      |  |
|--------------------------------------|--|
| newCodelistWithDetails               |  |
| <i>'codelist' object constructor</i> |  |

---

|                               |                                                                              |
|-------------------------------|------------------------------------------------------------------------------|
| <b>Description</b>            |                                                                              |
| 'codelist' object constructor |                                                                              |
| <b>Usage</b>                  |                                                                              |
| newCodelistWithDetails(x)     |                                                                              |
| <b>Arguments</b>              |                                                                              |
| x                             | A named list where each element contains a tibble with the column concept_id |
| <b>Value</b>                  |                                                                              |
| A codelist object.            |                                                                              |

---

|                |                                          |
|----------------|------------------------------------------|
| newCohortTable | <i>cohort_table objects constructor.</i> |
|----------------|------------------------------------------|

---

**Description**

cohort\_table objects constructor.

**Usage**

```
newCohortTable(  
  table,  
  cohortSetRef = attr(table, "cohort_set"),  
  cohortAttritionRef = attr(table, "cohort_attrition"),  
  cohortCodelistRef = attr(table, "cohort_codelist"),  
  .softValidation = FALSE  
)
```

**Arguments**

- table            cdm\_table object with at least: cohort\_definition\_id, subject\_id, cohort\_start\_date, cohort\_end\_date.
- cohortSetRef    Table with at least: cohort\_definition\_id, cohort\_name
- cohortAttritionRef    Table with at least: cohort\_definition\_id, number\_subjects, number\_records, reason\_id, reason, excluded\_subjects, excluded\_records.

cohortCodelistRef  
Table with at least: cohort\_definition\_id, codelist\_name, concept\_id and codelist\_type.

.softValidation  
Whether to perform a soft validation of consistency. If set to FALSE four additional checks will be performed: 1) a check that cohort end date is not before cohort start date, 2) a check that there are no missing values in required columns, 3) a check that cohort duration is all within observation period, and 4) that there are no overlapping cohort entries

## Value

A cohort\_table object

## Examples

```
person <- dplyr::tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- dplyr::tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cohort1 <- dplyr::tibble(
  cohort_definition_id = 1, subject_id = 1,
  cohort_start_date = as.Date("2020-01-01"),
  cohort_end_date = as.Date("2020-01-10")
)
cdm <- cdmFromTables(
  tables = list(
    "person" = person,
    "observation_period" = observation_period,
    "cohort1" = cohort1
  ),
  cdmName = "test"
)
cdm
cdm$cohort1 <- newCohortTable(table = cdm$cohort1)
cdm
settings(cdm$cohort1)
attrition(cdm$cohort1)
cohortCount(cdm$cohort1)
```

---

newConceptSetExpression

*'concept\_set\_expression' object constructor*

---

**Description**

'concept\_set\_expression' object constructor

**Usage**

`newConceptSetExpression(x)`

**Arguments**

`x` a named list of tibbles, each of which containing concept set definitions

**Value**

A `concept_set_expression`

---

|                             |                                       |
|-----------------------------|---------------------------------------|
| <code>newLocalSource</code> | <i>A new local source for the cdm</i> |
|-----------------------------|---------------------------------------|

---

**Description**

A new local source for the cdm

**Usage**

`newLocalSource()`

**Value**

A list in the format of a cdm source

**Examples**

```
library(omopgenerics)
newLocalSource()
```



---

|              |                                        |
|--------------|----------------------------------------|
| newOmopTable | Create an omop table from a cdm table. |
|--------------|----------------------------------------|

---

**Description**

Create an omop table from a cdm table.

**Usage**

```
newOmopTable(table, version = "5.3", cast = FALSE)
```

**Arguments**

|         |                                              |
|---------|----------------------------------------------|
| table   | A cdm_table.                                 |
| version | version of the cdm.                          |
| cast    | Whether to cast columns to the correct type. |

**Value**

An omop\_table object

---

|                     |                                         |
|---------------------|-----------------------------------------|
| newSummarisedResult | 'summarised_results' object constructor |
|---------------------|-----------------------------------------|

---

**Description**

'summarised\_results' object constructor

**Usage**

```
newSummarisedResult(x, settings = attr(x, "settings"))
```

**Arguments**

|          |                                            |
|----------|--------------------------------------------|
| x        | Table.                                     |
| settings | Settings for the summarised_result object. |

**Value**

A summarised\_result object

**Examples**

```

library(dplyr)
library(omopgenerics)

x <- tibble(
  "result_id" = 1L,
  "cdm_name" = "cprd",
  "group_name" = "cohort_name",
  "group_level" = "acetaminophen",
  "strata_name" = "sex &&& age_group",
  "strata_level" = c("male &&& <40", "male &&& >=40"),
  "variable_name" = "number_subjects",
  "variable_level" = NA_character_,
  "estimate_name" = "count",
  "estimate_type" = "integer",
  "estimate_value" = c("5", "15"),
  "additional_name" = "overall",
  "additional_level" = "overall"
) |>
  newSummarisedResult()

x
settings(x)
summary(x)

x <- tibble(
  "result_id" = 1L,
  "cdm_name" = "cprd",
  "group_name" = "cohort_name",
  "group_level" = "acetaminophen",
  "strata_name" = "sex &&& age_group",
  "strata_level" = c("male &&& <40", "male &&& >=40"),
  "variable_name" = "number_subjects",
  "variable_level" = NA_character_,
  "estimate_name" = "count",
  "estimate_type" = "integer",
  "estimate_value" = c("5", "15"),
  "additional_name" = "overall",
  "additional_level" = "overall"
) |>
  newSummarisedResult(settings = tibble(
    result_id = 1L, result_type = "custom_summary", mock = TRUE, value = 5
  ))

x
settings(x)
summary(x)

```

---

numberRecords

---

*Count the number of records that a cdm\_table has.*


---

**Description**

Count the number of records that a `cdm_table` has.

**Usage**

```
numberRecords(x)
```

**Arguments**

`x`                      A `cdm_table`.

**Value**

An integer with the number of records in the table.

**Examples**

```
person <- dplyr::tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- dplyr::tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test"
)

numberRecords(cdm$observation_period)
```

---

|                             |                                                                        |
|-----------------------------|------------------------------------------------------------------------|
| <code>numberSubjects</code> | <i>Count the number of subjects that a <code>cdm_table</code> has.</i> |
|-----------------------------|------------------------------------------------------------------------|

---

**Description**

Count the number of subjects that a `cdm_table` has.

**Usage**

```
numberSubjects(x)
```

**Arguments**

`x`                      A `cdm_table`.

**Value**

An integer with the number of subjects in the table.

**Examples**

```
person <- dplyr::tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- dplyr::tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test"
)

numberSubjects(cdm$observation_period)
```

---

|             |                                                                                           |
|-------------|-------------------------------------------------------------------------------------------|
| omopColumns | <i>Required columns that the standard tables in the OMOP Common Data Model must have.</i> |
|-------------|-------------------------------------------------------------------------------------------|

---

**Description**

Required columns that the standard tables in the OMOP Common Data Model must have.

**Usage**

```
omopColumns(
  table,
  field = NULL,
  version = "5.3",
  onlyRequired = lifecycle::deprecated()
)
```

**Arguments**

|              |                                        |
|--------------|----------------------------------------|
| table        | Table to see required columns.         |
| field        | Name of the specific field.            |
| version      | Version of the OMOP Common Data Model. |
| onlyRequired | deprecated                             |

**Value**

Character vector with the column names

**Examples**

```
library(omopgenerics)

omopColumns("person")
```

---

|                |                                                                                 |
|----------------|---------------------------------------------------------------------------------|
| omopDataFolder | <i>Check or set the OMOP_DATA_FOLDER where the OMOP related data is stored.</i> |
|----------------|---------------------------------------------------------------------------------|

---

**Description**

Check or set the OMOP\_DATA\_FOLDER where the OMOP related data is stored.

**Usage**

```
omopDataFolder(path = NULL)
```

**Arguments**

|      |                                                                                                    |
|------|----------------------------------------------------------------------------------------------------|
| path | Path to a folder to store the OMOP related data. If NULL the current OMOP_DATA_FOLDER is returned. |
|------|----------------------------------------------------------------------------------------------------|

**Value**

The OMOP data folder.

**Examples**

```
omopDataFolder()
omopDataFolder(file.path(tempdir(), "OMOP_DATA"))
omopDataFolder()
```

---

|                 |                                                       |
|-----------------|-------------------------------------------------------|
| omopTableFields | <i>Return a table of omop cdm fields informations</i> |
|-----------------|-------------------------------------------------------|

---

**Description**

Return a table of omop cdm fields informations

**Usage**

```
omopTableFields(cdmVersion = "5.3")
```

**Arguments**

cdmVersion      cdm version of the omop cdm.

**Value**

a tibble contain informations on all the different fields in omop cdm.

---

|            |                                                                                        |
|------------|----------------------------------------------------------------------------------------|
| omopTables | <i>Standard tables that a cdm reference can contain in the OMOP Common Data Model.</i> |
|------------|----------------------------------------------------------------------------------------|

---

**Description**

Standard tables that a cdm reference can contain in the OMOP Common Data Model.

**Usage**

```
omopTables(version = "5.3")
```

**Arguments**

version            Version of the OMOP Common Data Model.

**Value**

Standard tables

**Examples**

```
library(omopgenerics)

omopTables()
```

---

|                |                                 |
|----------------|---------------------------------|
| pivotEstimates | <i>Set estimates as columns</i> |
|----------------|---------------------------------|

---

**Description**

Pivot the estimates as new columns in result table.

**Usage**

```
pivotEstimates(result, pivotEstimatesBy = "estimate_name", nameStyle = NULL)
```

**Arguments**

|                  |                                                                                                                                                    |
|------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|
| result           | A <summarised_result>.                                                                                                                             |
| pivotEstimatesBy | Names from which pivot wider the estimate values. If NULL the table will not be pivotted.                                                          |
| nameStyle        | Name style (glue package specifications) to customise names when pivotting estimates. If NULL standard tidyr::pivot_wider formatting will be used. |

**Value**

A tibble.

**Examples**

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = 1L,
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
    newSummarisedResult()

  x |>
    pivotEstimates()
```

```
}
```

---

```
print.cdm_reference
```

*Print a CDM reference object*

---

## Description

Print a CDM reference object

## Usage

```
## S3 method for class 'cdm_reference'  
print(x, ...)
```

## Arguments

|     |                                                    |
|-----|----------------------------------------------------|
| x   | A cdm_reference object                             |
| ... | Included for compatibility with generic. Not used. |

## Value

Invisibly returns the input

## Examples

```
library(omopgenerics)  
  
cdm <- cdmFromTables(  
  tables = list(  
    "person" = dplyr::tibble(  
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,  
      race_concept_id = 0, ethnicity_concept_id = 0  
    ),  
    "observation_period" = dplyr::tibble(  
      observation_period_id = 1:3, person_id = 1:3,  
      observation_period_start_date = as.Date("2000-01-01"),  
      observation_period_end_date = as.Date("2023-12-31"),  
      period_type_concept_id = 0  
    )  
  ),  
  cdmName = "mock"  
)  
  
print(cdm)
```



---

|                |                         |
|----------------|-------------------------|
| print.codelist | <i>Print a codelist</i> |
|----------------|-------------------------|

---

**Description**

Print a codelist

**Usage**

```
## S3 method for class 'codelist'  
print(x, ...)
```

**Arguments**

|     |                                                    |
|-----|----------------------------------------------------|
| x   | A codelist                                         |
| ... | Included for compatibility with generic. Not used. |

**Value**

Invisibly returns the input

**Examples**

```
codes <- list("disease X" = c(1, 2, 3), "disease Y" = c(4, 5))  
codes <- newCodelist(codes)  
print(codes)
```

---

|                             |                                      |
|-----------------------------|--------------------------------------|
| print.codelist_with_details | <i>Print a codelist with details</i> |
|-----------------------------|--------------------------------------|

---

**Description**

Print a codelist with details

**Usage**

```
## S3 method for class 'codelist_with_details'  
print(x, ...)
```

**Arguments**

|     |                                                    |
|-----|----------------------------------------------------|
| x   | A codelist with details                            |
| ... | Included for compatibility with generic. Not used. |

**Value**

Invisibly returns the input

**Examples**

```
codes <- list("disease X" = dplyr::tibble(
  concept_id = c(1, 2, 3),
  other = c("a", "b", "c")
))
codes <- newCodelistWithDetails(codes)
print(codes)
```

---

```
print.conceptSetExpression
```

*Print a concept set expression*

---

**Description**

Print a concept set expression

**Usage**

```
## S3 method for class 'conceptSetExpression'
print(x, ...)
```

**Arguments**

|     |                                                    |
|-----|----------------------------------------------------|
| x   | A concept set expression                           |
| ... | Included for compatibility with generic. Not used. |

**Value**

Invisibly returns the input

**Examples**

```
asthma_cs <- list(
  "asthma_narrow" = dplyr::tibble(
    "concept_id" = 1,
    "excluded" = FALSE,
    "descendants" = TRUE,
    "mapped" = FALSE
  ),
  "asthma_broad" = dplyr::tibble(
    "concept_id" = c(1, 2),
    "excluded" = FALSE,
    "descendants" = TRUE,
```

```

      "mapped" = FALSE
    )
  )
  asthma_cs <- newConceptSetExpression(asthma_cs)
  print(asthma_cs)

```

---

|                 |                                                                |
|-----------------|----------------------------------------------------------------|
| readSourceTable | <i>Read a table from the cdm_source and add it to the cdm.</i> |
|-----------------|----------------------------------------------------------------|

---

### Description

Read a table from the cdm\_source and add it to the cdm.

### Usage

```
readSourceTable(cdm, name)
```

### Arguments

|      |                                                  |
|------|--------------------------------------------------|
| cdm  | A cdm reference.                                 |
| name | Name of a table to read in the cdm_source space. |

### Value

A cdm\_reference with new table.

---

|                       |                                 |
|-----------------------|---------------------------------|
| recordCohortAttrition | <i>Update cohort attrition.</i> |
|-----------------------|---------------------------------|

---

### Description

Update cohort attrition.

### Usage

```
recordCohortAttrition(cohort, reason, cohortId = NULL)
```

### Arguments

|          |                                                                                                       |
|----------|-------------------------------------------------------------------------------------------------------|
| cohort   | A cohort_table object.                                                                                |
| reason   | A character string.                                                                                   |
| cohortId | Cohort definition id of the cohort to update attrition. If NULL all cohort_definition_id are updated. |

**Value**

cohort\_table with updated attrition.

**Examples**

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cohort <- tibble(
  cohort_definition_id = c(1, 1, 1, 2),
  subject_id = 1,
  cohort_start_date = as.Date(c("2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01")),
  cohort_end_date = as.Date(c("2020-01-01", "2021-01-01", "2022-01-01", "2022-01-01")),
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "my_example_cdm",
  cohortTables = list("cohort1" = cohort)
)

cdm$cohort1
attrition(cdm$cohort1)

cdm$cohort1 <- cdm$cohort1 |>
  group_by(cohort_definition_id, subject_id) |>
  filter(cohort_start_date == min(cohort_start_date)) |>
  ungroup() |>
  compute(name = "cohort1", temporary = FALSE) |>
  recordCohortAttrition("Restrict to first observation")

cdm$cohort1
attrition(cdm$cohort1)
```

---

resultColumns

*Required columns that the result tables must have.*


---

**Description**

Required columns that the result tables must have.

**Usage**

```
resultColumns(table = "summarised_result")
```

**Arguments**

table            Table to see required columns.

**Value**

Required columns

**Examples**

```
library(omopgenerics)

resultColumns()
```

---

|                      |                                                                                  |
|----------------------|----------------------------------------------------------------------------------|
| resultPackageVersion | <i>Check if different packages version are used for summarise_results object</i> |
|----------------------|----------------------------------------------------------------------------------|

---

**Description**

Check if different packages version are used for summarise\_results object

**Usage**

```
resultPackageVersion(result)
```

**Arguments**

result            a summarised results object

**Value**

a summarised results object

---

|          |                                     |
|----------|-------------------------------------|
| settings | <i>Get settings from an object.</i> |
|----------|-------------------------------------|

---

**Description**

Get settings from an object.

**Usage**

```
settings(x)
```

**Arguments**

x                      Object

**Value**

A table with the settings of the object.

---

|                       |                                                        |
|-----------------------|--------------------------------------------------------|
| settings.cohort_table | <i>Get cohort settings from a cohort_table object.</i> |
|-----------------------|--------------------------------------------------------|

---

**Description**

Get cohort settings from a cohort\_table object.

**Usage**

```
## S3 method for class 'cohort_table'  
settings(x)
```

**Arguments**

x                      A cohort\_table object.

**Value**

A table with the details of the cohort settings.

## Examples

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cohort <- tibble(
  cohort_definition_id = 1,
  subject_id = 1,
  cohort_start_date = as.Date("2010-01-01"),
  cohort_end_date = as.Date("2012-01-01")
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test",
  cohortTables = list("my_cohort" = cohort)
)

settings(cdm$my_cohort)

cdm$my_cohort <- cdm$my_cohort |>
  newCohortTable(cohortSetRef = tibble(
    cohort_definition_id = 1, cohort_name = "new_name"
  ))

settings(cdm$my_cohort)
```

---

settings.summarised\_result

*Get settings from a summarised\_result object.*

---

## Description

Get settings from a summarised\_result object.

## Usage

```
## S3 method for class 'summarised_result'
settings(x)
```

**Arguments**

x                      A summarised\_result object.

**Value**

A table with the settings.

**Examples**

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cohort <- tibble(
  cohort_definition_id = 1,
  subject_id = 1,
  cohort_start_date = as.Date("2010-01-01"),
  cohort_end_date = as.Date("2012-01-01")
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test",
  cohortTables = list("my_cohort" = cohort)
)

result <- summary(cdm$my_cohort)

settings(result)
```

---

|                 |                                                                 |
|-----------------|-----------------------------------------------------------------|
| settingsColumns | <i>Identify settings columns of a &lt;summarised_result&gt;</i> |
|-----------------|-----------------------------------------------------------------|

---

**Description**

Identifies and returns the columns of the settings table obtained by using settings() in a <summarised\_result> object.

**Usage**

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



**Arguments**

result            A <summarised\_result>.

metadata         Whether to include metadata columns in settings or not.

**Value**

Vector with names of the settings columns

**Examples**

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))

  x

  x |> settingsColumns()
}
```

---

|            |                                          |
|------------|------------------------------------------|
| sourceType | <i>Get the source type of an object.</i> |
|------------|------------------------------------------|

---

**Description**

Get the source type of an object.

**Usage**

```
sourceType(x)
```

Arguments

x                                    Object to know the source type.

Value

A character vector that defines the type of cdm\_source.

---

|                 |                                                           |
|-----------------|-----------------------------------------------------------|
| splitAdditional | <i>Split additional_name and additional_level columns</i> |
|-----------------|-----------------------------------------------------------|

---

Description

Pivots the input dataframe so the values of the column additional\_name are transformed into columns that contain values from the additional\_level column.

Usage

```
splitAdditional(result, keep = FALSE, fill = "overall")
```

Arguments

result                    A dataframe with at least the columns additional\_name and additional\_level.  
keep                      Whether to keep the original group\_name and group\_level columns.  
fill                       Optionally, a character that specifies what value should be filled in with when missing.

Value

A dataframe.

Examples

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
```

```

      "additional_name" = "overall",
      "additional_level" = "overall"
    ) |>
    newSummarisedResult(settings = tibble(
      "result_id" = c(1, 2), "custom" = c("A", "B")
    ))

x

x |> splitAdditional()
}

```

splitAll

*Split all pairs name-level into columns.***Description**

Pivots the input dataframe so any pair name-level columns are transformed into columns (name) that contain values from the corresponding level.

**Usage**

```
splitAll(result, keep = FALSE, fill = "overall", exclude = "variable")
```

**Arguments**

|         |                                                                         |
|---------|-------------------------------------------------------------------------|
| result  | A data.frame.                                                           |
| keep    | Whether to keep the original name-level columns.                        |
| fill    | A character that specifies what value should be filled in when missing. |
| exclude | Name of a column pair to exclude.                                       |

**Value**

A dataframe with group, strata and additional as columns.

**Examples**

```

{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
  )
}

```

```

    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))

x

x |> splitAll()
}

```

---

splitGroup

*Split group\_name and group\_level columns*


---

### Description

Pivots the input dataframe so the values of the column `group_name` are transformed into columns that contain values from the `group_level` column.

### Usage

```
splitGroup(result, keep = FALSE, fill = "overall")
```

### Arguments

|                     |                                                                                              |
|---------------------|----------------------------------------------------------------------------------------------|
| <code>result</code> | A dataframe with at least the columns <code>group_name</code> and <code>group_level</code> . |
| <code>keep</code>   | Whether to keep the original <code>group_name</code> and <code>group_level</code> columns.   |
| <code>fill</code>   | Optionally, a character that specifies what value should be filled in with when missing.     |

### Value

A dataframe.

### Examples

```

{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),

```

```

      "cdm_name" = c("cprd", "eunomia"),
      "group_name" = "cohort_name",
      "group_level" = "my_cohort",
      "strata_name" = "sex",
      "strata_level" = "male",
      "variable_name" = "Age group",
      "variable_level" = "10 to 50",
      "estimate_name" = "count",
      "estimate_type" = "numeric",
      "estimate_value" = "5",
      "additional_name" = "overall",
      "additional_level" = "overall"
    ) |>
    newSummarisedResult(settings = tibble(
      "result_id" = c(1, 2), "custom" = c("A", "B")
    ))

x

x |> splitGroup()
}

```

splitStrata

*Split strata\_name and strata\_level columns***Description**

Pivots the input dataframe so the values of the column `strata_name` are transformed into columns that contain values from the `strata_level` column.

**Usage**

```
splitStrata(result, keep = FALSE, fill = "overall")
```

**Arguments**

|                     |                                                                                                |
|---------------------|------------------------------------------------------------------------------------------------|
| <code>result</code> | A dataframe with at least the columns <code>strata_name</code> and <code>strata_level</code> . |
| <code>keep</code>   | Whether to keep the original <code>group_name</code> and <code>group_level</code> columns.     |
| <code>fill</code>   | Optionally, a character that specifies what value should be filled in with when missing.       |

**Value**

A dataframe.

Examples

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))

  x

  x |> splitStrata()
}
```

---

|               |                              |
|---------------|------------------------------|
| statusIndexes | <i>Status of the indexes</i> |
|---------------|------------------------------|

---

Description

[Experimental]

Usage

```
statusIndexes(cdm, name = NULL)
```

Arguments

|      |                            |
|------|----------------------------|
| cdm  | A cdm_reference object.    |
| name | Name(s) of the cdm tables. |

Value

A tibble with 3 columns: table\_class class of the table, table\_name name of the table, index index definition, and index\_status status of the index, either: 'missing', 'extra', 'present'.

---

|               |                                                 |
|---------------|-------------------------------------------------|
| strataColumns | <i>Identify variables in strata_name column</i> |
|---------------|-------------------------------------------------|

---

**Description**

Identifies and returns the unique values in strata\_name column.

**Usage**

```
strataColumns(result)
```

**Arguments**

result            A tibble.

**Value**

Unique values of the strata name column.

**Examples**

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))

  x

  x |> strataColumns()
}
```

---

|                  |                                                                                             |
|------------------|---------------------------------------------------------------------------------------------|
| summariseLogFile | <i>Summarise and extract the information of a log file into a summarised_result object.</i> |
|------------------|---------------------------------------------------------------------------------------------|

---

## Description

Summarise and extract the information of a log file into a summarised\_result object.

## Usage

```
summariseLogFile(  
  logFile = getOption("omopgenerics.logFile"),  
  cdmName = "unknown"  
)
```

## Arguments

|         |                                                                                |
|---------|--------------------------------------------------------------------------------|
| logFile | File path to the log file to summarise. Create a logFile with createLogFile(). |
| cdmName | Name of the cdm for the summarise_result object.                               |

## Value

A summarise\_result with the information of the log file.

## Examples

```
library(dplyr)  
  
logFile <- tempfile(pattern = "log_{date}_{time}", fileext = ".txt")  
createLogFile(logFile = logFile)  
  
logMessage("Starting analysis")  
1 + 1  
logMessage("Analysis finished")  
  
res <- summariseLogFile()  
  
glimpse(res)  
  
tidy(res)
```



---

summary.cdm\_reference *Summary a cdm reference*

---

## Description

Summary a cdm reference

## Usage

```
## S3 method for class 'cdm_reference'  
summary(object, ...)
```

## Arguments

|        |                               |
|--------|-------------------------------|
| object | A cdm reference object.       |
| ...    | For compatibility (not used). |

## Value

A summarised\_result object with a summary of the data contained in the cdm.

## Examples

```
library(dplyr, warn.conflicts = FALSE)  
  
person <- tibble(  
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,  
  race_concept_id = 0, ethnicity_concept_id = 0  
)  
observation_period <- tibble(  
  observation_period_id = 1, person_id = 1,  
  observation_period_start_date = as.Date("2000-01-01"),  
  observation_period_end_date = as.Date("2023-12-31"),  
  period_type_concept_id = 0  
)  
cdm <- cdmFromTables(  
  tables = list("person" = person, "observation_period" = observation_period),  
  cdmName = "test"  
)  
  
summary(cdm)
```

---

|                    |                                      |
|--------------------|--------------------------------------|
| summary.cdm_source | <i>Summarise a cdm_source object</i> |
|--------------------|--------------------------------------|

---

**Description**

Summarise a cdm\_source object

**Usage**

```
## S3 method for class 'cdm_source'  
summary(object, ...)
```

**Arguments**

|        |                                |
|--------|--------------------------------|
| object | A generated cohort set object. |
| ...    | For compatibility (not used).  |

**Value**

A list of properties of the cdm\_source object.

**Examples**

```
summary(newLocalSource())
```

---

|                      |                                       |
|----------------------|---------------------------------------|
| summary.cohort_table | <i>Summary a generated cohort set</i> |
|----------------------|---------------------------------------|

---

**Description**

Summary a generated cohort set

**Usage**

```
## S3 method for class 'cohort_table'  
summary(object, ...)
```

**Arguments**

|        |                                |
|--------|--------------------------------|
| object | A generated cohort set object. |
| ...    | For compatibility (not used).  |

**Value**

A summarised\_result object with a summary of a cohort\_table.

**Examples**

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test",
  cohortTables = list("cohort1" = tibble(
    cohort_definition_id = 1,
    subject_id = 1,
    cohort_start_date = as.Date("2010-01-01"),
    cohort_end_date = as.Date("2010-01-05")
  ))
)

summary(cdm$cohort1)
```

---

summary.summarised\_result

*Summary a summarised\_result*


---

**Description**

Summary a summarised\_result

**Usage**

```
## S3 method for class 'summarised_result'
summary(object, ...)
```

**Arguments**

|        |                               |
|--------|-------------------------------|
| object | A summarised_result object.   |
| ...    | For compatibility (not used). |

**Value**

A summary of the result\_types contained in a summarised\_result object.

## Examples

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

person <- tibble(
  person_id = 1, gender_concept_id = 0, year_of_birth = 1990,
  race_concept_id = 0, ethnicity_concept_id = 0
)
observation_period <- tibble(
  observation_period_id = 1, person_id = 1,
  observation_period_start_date = as.Date("2000-01-01"),
  observation_period_end_date = as.Date("2023-12-31"),
  period_type_concept_id = 0
)
cdm <- cdmFromTables(
  tables = list("person" = person, "observation_period" = observation_period),
  cdmName = "test"
)

result <- summary(cdm)

summary(result)
```

---

suppress

*Function to suppress counts in result objects*

---

## Description

Function to suppress counts in result objects

## Usage

```
suppress(result, minCellCount = 5)
```

## Arguments

|              |                                             |
|--------------|---------------------------------------------|
| result       | Result object                               |
| minCellCount | Minimum count of records to report results. |

## Value

Table with suppressed counts

---

 suppress.summarised\_result

*Function to suppress counts in result objects*


---

## Description

Function to suppress counts in result objects

## Usage

```
## S3 method for class 'summarised_result'
suppress(result, minCellCount = 5)
```

## Arguments

`result` summarised\_result object.  
`minCellCount` Minimum count of records to report results.

## Value

summarised\_result with suppressed counts.

## Examples

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

my_result <- tibble(
  "result_id" = "1",
  "cdm_name" = "mock",
  "result_type" = "summarised_characteristics",
  "package_name" = "omopgenerics",
  "package_version" = as.character(utils::packageVersion("omopgenerics")),
  "group_name" = "overall",
  "group_level" = "overall",
  "strata_name" = c(rep("overall", 6), rep("sex", 3)),
  "strata_level" = c(rep("overall", 6), "male", "female", "female"),
  "variable_name" = c(
    "number records", "age_group", "age_group",
    "age_group", "age_group", "my_variable", "number records", "age_group",
    "age_group"
  ),
  "variable_level" = c(
    NA, "<50", "<50", ">=50", ">=50", NA, NA,
    "<50", "<50"
  ),
  "estimate_name" = c(
    "count", "count", "percentage", "count", "percentage",
    "random", "count", "count", "percentage"
  )
)
```

```

),
"estimate_type" = c(
  "integer", "integer", "percentage", "integer",
  "percentage", "numeric", "integer", "integer", "percentage"
),
"estimate_value" = c("10", "5", "50", "3", "30", "1", "3", "12", "6"),
"additional_name" = "overall",
"additional_level" = "overall"
)
my_result <- newSummarisedResult(my_result)
my_result |> glimpse()
my_result <- suppress(my_result, minCellCount = 5)
my_result |> glimpse()

```

---

|           |                                           |
|-----------|-------------------------------------------|
| tableName | <i>Get the table name of a cdm_table.</i> |
|-----------|-------------------------------------------|

---

## Description

Get the table name of a cdm\_table.

## Usage

```
tableName(table)
```

## Arguments

table            A cdm\_table.

## Value

A character with the name.

## Examples

```

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  )

```

```

    )
  },
  cdmName = "mock"
)

tableName(cdm$person)

```

---

|             |                                             |
|-------------|---------------------------------------------|
| tableSource | <i>Get the table source of a cdm_table.</i> |
|-------------|---------------------------------------------|

---

### Description

Get the table source of a cdm\_table.

### Usage

```
tableSource(table)
```

### Arguments

table                    A cdm\_table.

### Value

A cdm\_source object.

### Examples

```

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

tableSource(cdm$person)

```

---

tidy.summarised\_result

*Turn a <summarised\_result> object into a tidy tibble*


---

## Description

**[Experimental]** Provides tools for obtaining a tidy version of a <summarised\_result> object. This tidy version will include the settings as columns, estimate\_value will be pivotted into columns using estimate\_name as names, and group, strata, and additional will be splitted.

## Usage

```
## S3 method for class 'summarised_result'
tidy(x, ...)
```

## Arguments

x                    A <summarised\_result>.  
 ...                For compatibility (not used).

## Value

A tibble.

## Examples

```
{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))
```



```

x

x |> tidy()
}

```

---

|             |                                                             |
|-------------|-------------------------------------------------------------|
| tidyColumns | <i>Identify tidy columns of a &lt;summarised_result&gt;</i> |
|-------------|-------------------------------------------------------------|

---

### Description

Identifies and returns the columns that the tidy version of the <summarised\_result> will have.

### Usage

```
tidyColumns(result)
```

### Arguments

result            A <summarised\_result>.

### Value

Table columns after applying tidy() function to a <summarised\_result>.

### Examples

```

{
  library(dplyr)
  library(omopgenerics)

  x <- tibble(
    "result_id" = as.integer(c(1, 2)),
    "cdm_name" = c("cprd", "eunomia"),
    "group_name" = "cohort_name",
    "group_level" = "my_cohort",
    "strata_name" = "sex",
    "strata_level" = "male",
    "variable_name" = "Age group",
    "variable_level" = "10 to 50",
    "estimate_name" = "count",
    "estimate_type" = "numeric",
    "estimate_value" = "5",
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult(settings = tibble(
    "result_id" = c(1, 2), "custom" = c("A", "B")
  ))
}

```

```
x
x |> tidyColumns()
}
```

---

|           |                                                                                           |
|-----------|-------------------------------------------------------------------------------------------|
| tmpPrefix | Create a temporary prefix for tables, that contains a unique prefix that starts with tmp. |
|-----------|-------------------------------------------------------------------------------------------|

---

**Description**

Create a temporary prefix for tables, that contains a unique prefix that starts with tmp.

**Usage**

```
tmpPrefix()
```

**Value**

A temporary prefix.

**Examples**

```
library(omopgenerics)
tmpPrefix()
```

---

|             |                                          |
|-------------|------------------------------------------|
| toSnakeCase | Convert a character vector to snake case |
|-------------|------------------------------------------|

---

**Description**

Convert a character vector to snake case

**Usage**

```
toSnakeCase(x)
```

**Arguments**

x                      Character vector to convert

**Value**

A snake\_case vector

**Examples**

```
toSnakeCase("myVariable")

toSnakeCase(c("cohort1", "Cohort22b"))
```

---

```
transformToSummarisedResult
```

*Create a <summarised\_result> object from a data.frame, given a set of specifications.*

---

**Description**

Create a <summarised\_result> object from a data.frame, given a set of specifications.

**Usage**

```
transformToSummarisedResult(
  x,
  group = character(),
  strata = character(),
  additional = character(),
  estimates = character(),
  settings = character()
)
```

**Arguments**

|            |                                                                                |
|------------|--------------------------------------------------------------------------------|
| x          | A data.frame.                                                                  |
| group      | Columns in x to be used in group_name-group_level formatting.                  |
| strata     | Columns in x to be used in strata_name-strata_level formatting.                |
| additional | Columns in x to be used in additional_name-additional_level formatting.        |
| estimates  | Columns in x to be formatted into: estimate_name-estimate_type-estimate_value. |
| settings   | Columns in x thta form the settings of the <summarised_result> object.         |

**Value**

A <summarised\_result> object.

**Examples**

```
x <- dplyr::tibble(
  cohort_name = c("cohort1", "cohort2"),
  variable_name = "age",
  mean = c(50, 45.3),
  median = c(55L, 44L)
```

```
)

transformToSummarisedResult(
  x = x,
  group = c("cohort_name"),
  estimates = c("mean", "median")
)
```

---

|          |                                                                                  |
|----------|----------------------------------------------------------------------------------|
| uniqueId | <i>Get a unique Identifier with a certain number of characters and a prefix.</i> |
|----------|----------------------------------------------------------------------------------|

---

**Description**

Get a unique Identifier with a certain number of characters and a prefix.

**Usage**

```
uniqueId(n = 1, exclude = character(), nChar = 3, prefix = "id_")
```

**Arguments**

|         |                               |
|---------|-------------------------------|
| n       | Number of identifiers.        |
| exclude | Columns to exclude.           |
| nChar   | Number of characters.         |
| prefix  | A prefix for the identifiers. |

**Value**

A character vector with n unique identifiers.

---

|                 |                                   |
|-----------------|-----------------------------------|
| uniqueTableName | <i>Create a unique table name</i> |
|-----------------|-----------------------------------|

---

**Description**

Create a unique table name

**Usage**

```
uniqueTableName(prefix = "")
```

**Arguments**

|        |                             |
|--------|-----------------------------|
| prefix | Prefix for the table names. |
|--------|-----------------------------|

**Value**

A string that can be used as a dbplyr temp table name

**Examples**

```
library(omopgenerics)
uniqueTableName()
```

---

|                 |                                                                             |
|-----------------|-----------------------------------------------------------------------------|
| uniteAdditional | <i>Unite one or more columns in additional_name-additional_level format</i> |
|-----------------|-----------------------------------------------------------------------------|

---

**Description**

Unites targeted table columns into additional\_name-additional\_level columns.

**Usage**

```
uniteAdditional(
  x,
  cols = character(0),
  keep = FALSE,
  ignore = c(NA, "overall")
)
```

**Arguments**

- x                   Tibble or dataframe.
- cols               Columns to aggregate.
- keep               Whether to keep the original columns.
- ignore             Level values to ignore.

**Value**

A tibble with the new columns.

**Examples**

```
x <- dplyr::tibble(
  variable = "number subjects",
  value = c(10, 15, 40, 78),
  sex = c("Male", "Female", "Male", "Female"),
  age_group = c("<40", ">40", ">40", "<40")
)

x |>
  uniteAdditional(c("sex", "age_group"))
```

---

|            |                                                                   |
|------------|-------------------------------------------------------------------|
| uniteGroup | <i>Unite one or more columns in group_name-group_level format</i> |
|------------|-------------------------------------------------------------------|

---

**Description**

Unites targeted table columns into group\_name-group\_level columns.

**Usage**

```
uniteGroup(x, cols = character(0), keep = FALSE, ignore = c(NA, "overall"))
```

**Arguments**

- x                    Tibble or dataframe.
- cols                Columns to aggregate.
- keep                Whether to keep the original columns.
- ignore              Level values to ignore.

**Value**

A tibble with the new columns.

**Examples**

```
x <- dplyr::tibble(
  variable = "number subjects",
  value = c(10, 15, 40, 78),
  sex = c("Male", "Female", "Male", "Female"),
  age_group = c("<40", ">40", ">40", "<40")
)

x |>
  uniteGroup(c("sex", "age_group"))
```

---

|             |                                                                     |
|-------------|---------------------------------------------------------------------|
| uniteStrata | <i>Unite one or more columns in strata_name-strata_level format</i> |
|-------------|---------------------------------------------------------------------|

---

**Description**

Unites targeted table columns into strata\_name-strata\_level columns.

**Usage**

```
uniteStrata(x, cols = character(0), keep = FALSE, ignore = c(NA, "overall"))
```

**Arguments**

|        |                                       |
|--------|---------------------------------------|
| x      | Tibble or dataframe.                  |
| cols   | Columns to aggregate.                 |
| keep   | Whether to keep the original columns. |
| ignore | Level values to ignore.               |

**Value**

A tibble with the new columns.

**Examples**

```
x <- dplyr::tibble(
  variable = "number subjects",
  value = c(10, 15, 40, 78),
  sex = c("Male", "Female", "Male", "Female"),
  age_group = c("<40", ">40", ">40", "<40")
)

x |>
  uniteStrata(c("sex", "age_group"))
```

---

validateAchillesTable *Validate if a cdm\_table is a valid achilles table.*

---

**Description**

Validate if a cdm\_table is a valid achilles table.

**Usage**

```
validateAchillesTable(
  table,
  version = NULL,
  cast = FALSE,
  call = parent.frame()
)
```

**Arguments**

|         |                                           |
|---------|-------------------------------------------|
| table   | A cdm_table to validate.                  |
| version | The cdm vocabulary version.               |
| cast    | Whether to cast columns to required type. |
| call    | Passed to cli call.                       |

**Value**

invisible achilles table

---

validateAgeGroupArgument

*Validate the ageGroup argument. It must be a list of two integerish numbers lower age and upper age, both of the must be greater or equal to 0 and lower age must be lower or equal to the upper age. If not named automatic names will be given in the output list.*

---

**Description**

Validate the ageGroup argument. It must be a list of two integerish numbers lower age and upper age, both of the must be greater or equal to 0 and lower age must be lower or equal to the upper age. If not named automatic names will be given in the output list.

**Usage**

```
validateAgeGroupArgument(
  ageGroup,
  multipleAgeGroup = TRUE,
  overlap = FALSE,
  null = TRUE,
  ageGroupName = "age_group",
  call = parent.frame()
)
```

**Arguments**

|                  |                                       |
|------------------|---------------------------------------|
| ageGroup         | age group in a list.                  |
| multipleAgeGroup | allow mutiple age group.              |
| overlap          | allow overlapping ageGroup.           |
| null             | null age group allowed true or false. |
| ageGroupName     | Name of the default age group.        |
| call             | parent frame.                         |

**Value**

validate ageGroup

**Examples**

```
validateAgeGroupArgument(list(c(0, 39), c(40, Inf)))
```



---

|                     |                                                        |
|---------------------|--------------------------------------------------------|
| validateCdmArgument | <i>Validate if an object in a valid cdm_reference.</i> |
|---------------------|--------------------------------------------------------|

---

## Description

Validate if an object in a valid cdm\_reference.

## Usage

```
validateCdmArgument(
  cdm,
  checkOverlapObservation = FALSE,
  checkStartBeforeEndObservation = FALSE,
  checkPlausibleObservationDates = FALSE,
  checkPerson = FALSE,
  requiredTables = character(),
  validation = "error",
  call = parent.frame()
)
```

## Arguments

|                                |                                                                                                                                              |
|--------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| cdm                            | A cdm_reference object                                                                                                                       |
| checkOverlapObservation        | TRUE to perform check on no overlap observation period                                                                                       |
| checkStartBeforeEndObservation | TRUE to perform check on correct observational start and end date                                                                            |
| checkPlausibleObservationDates | TRUE to perform check that there are no implausible observation period start dates (before 1800-01-01) or end dates (after the current date) |
| checkPerson                    | TRUE to perform check on person id in all clinical table are in person table                                                                 |
| requiredTables                 | Name of tables that are required to be part of the cdm_reference object.                                                                     |
| validation                     | How to perform validation: "error", "warning".                                                                                               |
| call                           | A call argument to pass to cli functions.                                                                                                    |

## Value

A cdm\_reference object

## Examples

```
cdm <- cdmFromTables(
  tables = list(
    "person" = dplyr::tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    )
  )
)
```

```
    ),
    "observation_period" = dplyr::tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

validateCdmArgument(cdm)
```

---

|                  |                                                         |
|------------------|---------------------------------------------------------|
| validateCdmTable | <i>Validate if a table is a valid cdm_table object.</i> |
|------------------|---------------------------------------------------------|

---

**Description**

Validate if a table is a valid cdm\_table object.

**Usage**

```
validateCdmTable(table, name = NULL, call = parent.frame())
```

**Arguments**

|       |                                                            |
|-------|------------------------------------------------------------|
| table | Object to validate.                                        |
| name  | If we want to validate that the table has a specific name. |
| call  | Call argument that will be passed to cli.                  |

**Value**

The table or an error message.

---

|                        |                                       |
|------------------------|---------------------------------------|
| validateCohortArgument | <i>Validate a cohort table input.</i> |
|------------------------|---------------------------------------|

---

**Description**

Validate a cohort table input.

**Usage**

```
validateCohortArgument(
  cohort,
  checkEndAfterStart = FALSE,
  checkOverlappingEntries = FALSE,
  checkMissingValues = FALSE,
  checkInObservation = FALSE,
  checkAttributes = FALSE,
  checkPermanentTable = FALSE,
  dropExtraColumns = FALSE,
  validation = "error",
  call = parent.frame()
)
```

**Arguments**

|                         |                                                                                                       |
|-------------------------|-------------------------------------------------------------------------------------------------------|
| cohort                  | Object to be validated as a valid cohort input.                                                       |
| checkEndAfterStart      | If TRUE a check that all cohort end dates come on or after cohort start date will be performed.       |
| checkOverlappingEntries | If TRUE a check that no individuals have overlapping cohort entries will be performed.                |
| checkMissingValues      | If TRUE a check that there are no missing values in required fields will be performed.                |
| checkInObservation      | If TRUE a check that cohort entries are within the individuals observation periods will be performed. |
| checkAttributes         | Whether to check if attributes are present and populated correctly.                                   |
| checkPermanentTable     | Whether to check if the table has to be a permanent table.                                            |
| dropExtraColumns        | Whether to drop extra columns that are not the required ones.                                         |
| validation              | How to perform validation: "error", "warning".                                                        |
| call                    | A call argument to pass to cli functions.                                                             |

**Examples**

```
cdm <- cdmFromTables(
  tables = list(
    "person" = dplyr::tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = dplyr::tibble(
```

```

      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cohortTables = list(
    cohort = dplyr::tibble(
      cohort_definition_id = 1L,
      subject_id = 1L,
      cohort_start_date = as.Date("2020-01-01"),
      cohort_end_date = as.Date("2021-02-10")
    )
  ),
  cdmName = "mock"
)

validateCohortArgument(cdm$cohort)

```

---

### validateCohortIdArgument

*Validate cohortId argument. CohortId can either be a cohort\_definition\_id value, a cohort\_name or a tidysselect expression referinc to cohort\_names. If you want to support tidysselect expressions please use the function as: validateCohortIdArgument({{cohortId}}, cohort).*

---

### Description

Validate cohortId argument. CohortId can either be a cohort\_definition\_id value, a cohort\_name or a tidysselect expression referinc to cohort\_names. If you want to support tidysselect expressions please use the function as: validateCohortIdArgument({{cohortId}}, cohort).

### Usage

```

validateCohortIdArgument(
  cohortId,
  cohort,
  null = TRUE,
  validation = "error",
  call = parent.frame()
)

```

### Arguments

|          |                                    |
|----------|------------------------------------|
| cohortId | A cohortId vector to be validated. |
| cohort   | A cohort_table object.             |

|            |                                                                  |
|------------|------------------------------------------------------------------|
| null       | Whether NULL is accepted. If NULL all cohortId will be returned. |
| validation | How to perform validation: "error", "warning".                   |
| call       | A call argument to pass to cli functions.                        |

### Examples

```
cdm <- cdmFromTables(
  tables = list(
    "person" = dplyr::tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = dplyr::tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cohortTables = list(
    cohort = dplyr::tibble(
      cohort_definition_id = 1L,
      subject_id = 1L,
      cohort_start_date = as.Date("2020-01-01"),
      cohort_end_date = as.Date("2021-02-10")
    )
  ),
  cdmName = "mock"
)

validateCohortIdArgument(NULL, cdm$cohort)
validateCohortIdArgument(1L, cdm$cohort)
validateCohortIdArgument(2L, cdm$cohort, validation = "warning")
```

---

|                |                                                                                   |
|----------------|-----------------------------------------------------------------------------------|
| validateColumn | <i>Validate whether a variable points to a certain exiting column in a table.</i> |
|----------------|-----------------------------------------------------------------------------------|

---

### Description

Validate whether a variable points to a certain exiting column in a table.

### Usage

```
validateColumn(
  column,
  x,
  type = c("character", "date", "logical", "numeric", "integer"),
```

```

    validation = "error",
    call = parent.frame()
  )

```

### Arguments

|            |                                                                |
|------------|----------------------------------------------------------------|
| column     | Name of a column that you want to check that exist in x table. |
| x          | Table to check if the column exist.                            |
| type       | Type of the column.                                            |
| validation | Whether to throw warning or error.                             |
| call       | Passed to cli functions.                                       |

### Value

the validated name

### Examples

```

x <- dplyr::tibble(a = 1, b = "xxx")

validateColumn("a", x, validation = "warning")
validateColumn("a", x, type = "character", validation = "warning")
validateColumn("a", x, type = "numeric", validation = "warning")
validateColumn("not_existing", x, type = "numeric", validation = "warning")

```

---

### validateConceptSetArgument

*Validate conceptSet argument. It can either be a list, a codelist, a concept set expression or a codelist with details. The output will always be a codelist.*

---

### Description

Validate conceptSet argument. It can either be a list, a codelist, a concept set expression or a codelist with details. The output will always be a codelist.

### Usage

```

validateConceptSetArgument(
  conceptSet,
  cdm = NULL,
  validation = "error",
  call = parent.frame()
)

```

**Arguments**

|            |                                                                                                                  |
|------------|------------------------------------------------------------------------------------------------------------------|
| conceptSet | It can be either a named list of concepts or a codelist, codelist_with_details or concept_set_expression object. |
| cdm        | A cdm_reference object, needed if a concept_set_expression is provided.                                          |
| validation | How to perform validation: "error", "warning".                                                                   |
| call       | A call argument to pass to cli functions.                                                                        |

**Value**

A codelist object.

**Examples**

```
conceptSet <- list(disease_x = c(1L, 2L))
validateConceptSetArgument(conceptSet)
```

---

|                      |                                                                                                                                                      |
|----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|
| validateNameArgument | <i>Validate name argument. It must be a snake_case character vector. You can add the a cdm object to check name is not already used in that cdm.</i> |
|----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------|

---

**Description**

Validate name argument. It must be a snake\_case character vector. You can add the a cdm object to check name is not already used in that cdm.

**Usage**

```
validateNameArgument(
  name,
  cdm = NULL,
  validation = "error",
  null = FALSE,
  call = parent.frame()
)
```

**Arguments**

|            |                                                                                        |
|------------|----------------------------------------------------------------------------------------|
| name       | Name of a new table to be added to a cdm object.                                       |
| cdm        | A cdm_reference object. It will check if a table named name already exists in the cdm. |
| validation | How to perform validation: "error", "warning".                                         |
| null       | If TRUE, name can be NULL                                                              |
| call       | A call argument to pass to cli functions.                                              |

Examples

```
# this is a validate name
name <- "my_new_table"
validateNameArgument(name)

# this is not
name <- "myTableNAME"
validateNameArgument(name, validation = "warning")
```

---

|                   |                                                    |
|-------------------|----------------------------------------------------|
| validateNameLevel | Validate if two columns are valid Name-Level pair. |
|-------------------|----------------------------------------------------|

---

Description

Validate if two columns are valid Name-Level pair.

Usage

```
validateNameLevel(
  x,
  prefix,
  sep = " &&& ",
  validation = "error",
  call = parent.frame()
)
```

Arguments

|            |                                                                                  |
|------------|----------------------------------------------------------------------------------|
| x          | A tibble.                                                                        |
| prefix     | Prefix for the name-level pair, e.g. 'strata' for strata_name-strata_level pair. |
| sep        | Separation pattern.                                                              |
| validation | Either 'error', 'warning' or 'message'.                                          |
| call       | Will be used by cli to report errors.                                            |

---

|                   |                                                                                                                                                               |
|-------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|
| validateNameStyle | Validate nameStyle argument. If any of the element in ... has length greater than 1 it must be contained in nameStyle. Note that snake case notation is used. |
|-------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|

---

Description

Validate nameStyle argument. If any of the element in ... has length greater than 1 it must be contained in nameStyle. Note that snake case notation is used.



**Usage**

```
validateNameStyle(nameStyle, ..., call = parent.frame())
```

**Arguments**

|           |                                                                                               |
|-----------|-----------------------------------------------------------------------------------------------|
| nameStyle | A character vector. It must contain all the ... elements in snake_case format and between {}. |
| ...       | Elements to be included.                                                                      |
| call      | Passed to cli functions.                                                                      |

**Value**

invisible nameStyle.

**Examples**

```
validateNameStyle(
  nameStyle = "hi_{cohort_name}",
  cohortName = c("cohort1", "cohort2"),
  otherVariable = c("only 1 value")
)

## Not run:
validateNameStyle(
  nameStyle = "hi_{cohort_name}",
  cohortName = c("cohort1", "cohort2"),
  otherVariable = c("value1", "value2")
)

## End(Not run)
validateNameStyle(
  nameStyle = "{other_variable}_hi_{cohort_name}",
  cohortName = c("cohort1", "cohort2"),
  otherVariable = c("value1", "value2")
)
```

---

|                   |                                         |
|-------------------|-----------------------------------------|
| validateNewColumn | <i>Validate a new column of a table</i> |
|-------------------|-----------------------------------------|

---

**Description**

Validate a new column of a table

**Usage**

```
validateNewColumn(table, column, validation = "warning", call = parent.frame())
```

**Arguments**

|            |                                                         |
|------------|---------------------------------------------------------|
| table      | The table to check if the column already exists.        |
| column     | Character vector with the name(s) of the new column(s). |
| validation | Whether to throw warning or error.                      |
| call       | Passed to cli functions.                                |

**Value**

table without conflicting columns.

**Examples**

```
x <- dplyr::tibble(
  column1 = c(1L, 2L),
  column2 = c("a", "b")
)
validateNewColumn(x, "not_exiting_column")
validateNewColumn(x, "column1")
```

---

|                   |                               |
|-------------------|-------------------------------|
| validateOmopTable | <i>Validate an omop_table</i> |
|-------------------|-------------------------------|

---

**Description**

Validate an omop\_table

**Usage**

```
validateOmopTable(
  omopTable,
  version = NULL,
  cast = FALSE,
  call = parent.frame()
)
```

**Arguments**

|           |                                                         |
|-----------|---------------------------------------------------------|
| omopTable | An omop_table to check.                                 |
| version   | The version of the cdm.                                 |
| cast      | Whether to cast columns to the correct type.            |
| call      | Call argument that will be passed to cli error message. |

**Value**

An omop\_table object.

---

 validateResultArgument

*Validate if a an object is a valid 'summarised\_result' object.*


---

## Description

Validate if a an object is a valid 'summarised\_result' object.

## Usage

```
validateResultArgument(
  result,
  checkNoDuplicates = FALSE,
  checkNameLevel = FALSE,
  checkSuppression = FALSE,
  validation = "error",
  call = parent.frame()
)
```

## Arguments

|                   |                                                                   |
|-------------------|-------------------------------------------------------------------|
| result            | summarised_result object to validate.                             |
| checkNoDuplicates | Whether there are not allowed duplicates in the result object.    |
| checkNameLevel    | Whether the name-level paired columns are can be correctly split. |
| checkSuppression  | Whether the suppression in the result object is well defined.     |
| validation        | Only error is supported at the moment.                            |
| call              | parent.frame                                                      |

## Value

summarise result object

## Examples

```
x <- dplyr::tibble(
  "result_id" = 1L,
  "cdm_name" = "eunomia",
  "group_name" = "cohort_name",
  "group_level" = "my_cohort",
  "strata_name" = c("sex", "sex &&& age_group", "sex &&& year"),
  "strata_level" = c("Female", "Male &&& <40", "Female &&& 2010"),
  "variable_name" = "number subjects",
  "variable_level" = NA_character_,
  "estimate_name" = "count",
  "estimate_type" = "integer",
```

```

    "estimate_value" = c("100", "44", "14"),
    "additional_name" = "overall",
    "additional_level" = "overall"
  ) |>
  newSummarisedResult()

validateResultArgument(x)

```

---

validateStrataArgument

*To validate a strata list. It makes sure that elements are unique and point to columns in table.*

---

## Description

To validate a strata list. It makes sure that elements are unique and point to columns in table.

## Usage

```
validateStrataArgument(strata, table, call = parent.frame())
```

## Arguments

|        |                                                      |
|--------|------------------------------------------------------|
| strata | A list of characters that point to columns in table. |
| table  | A table with columns.                                |
| call   | Passed to cli functions.                             |

## Value

The same strata input or an error if the input is incorrect.

## Examples

```

strata <- list("age", "sex", c("age", "sex"))
x <- dplyr::tibble(age = 30L, sex = "Female")

validateStrataArgument(strata, x)

```

---

```
validateWindowArgument
```

*Validate a window argument. It must be a list of two elements (window start and window end), both must be integerish and window start must be lower or equal than window end.*

---

### Description

Validate a window argument. It must be a list of two elements (window start and window end), both must be integerish and window start must be lower or equal than window end.

### Usage

```
validateWindowArgument(window, snakeCase = TRUE, call = parent.frame())
```

### Arguments

|           |                                                  |
|-----------|--------------------------------------------------|
| window    | time window                                      |
| snakeCase | return default window name in snake case if TRUE |
| call      | A call argument to pass to cli functions.        |

### Value

time window

### Examples

```
validateWindowArgument(list(c(0, 15), c(-Inf, Inf)))
validateWindowArgument(list(c(0, 15), c(-Inf, Inf)), snakeCase = FALSE)
```

---

```
[[.cdm_reference
```

*Subset a cdm reference object.*

---

### Description

Subset a cdm reference object.

### Usage

```
## S3 method for class 'cdm_reference'
x[[name]]
```

**Arguments**

|      |                                                                |
|------|----------------------------------------------------------------|
| x    | A cdm reference                                                |
| name | The name or index of the table to extract from the cdm object. |

**Value**

A single cdm table reference

**Examples**

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdm[["person"]]
```

---

[[<-.cdm\_reference      *Assign a table to a cdm reference.*

---

**Description**

Assign a table to a cdm reference.

**Usage**

```
## S3 replacement method for class 'cdm_reference'
cdm[[name]] <- value
```

**Arguments**

|       |                                                 |
|-------|-------------------------------------------------|
| cdm   | A cdm reference.                                |
| name  | Name where to assign the new table.             |
| value | Table with the same source than the cdm object. |

Value

The cdm reference.

---

|                  |                                       |
|------------------|---------------------------------------|
| \$.cdm_reference | <i>Subset a cdm reference object.</i> |
|------------------|---------------------------------------|

---

Description

Subset a cdm reference object.

Usage

```
## S3 method for class 'cdm_reference'
x$name
```

Arguments

- x                   A cdm reference.
- name                The name of the table to extract from the cdm object.

Value

A single cdm table reference

Examples

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

cdm <- cdmFromTables(
  tables = list(
    "person" = tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdm$person
```

---

|                    |                                            |
|--------------------|--------------------------------------------|
| \$<-.cdm_reference | <i>Assign an table to a cdm reference.</i> |
|--------------------|--------------------------------------------|

---

## Description

Assign an table to a cdm reference.

## Usage

```
## S3 replacement method for class 'cdm_reference'
cdm$name <- value
```

## Arguments

|       |                                                 |
|-------|-------------------------------------------------|
| cdm   | A cdm reference.                                |
| name  | Name where to assign the new table.             |
| value | Table with the same source than the cdm object. |

## Value

The cdm reference.

## Examples

```
library(omopgenerics)

cdm <- cdmFromTables(
  tables = list(
    "person" = dplyr::tibble(
      person_id = c(1, 2, 3), gender_concept_id = 0, year_of_birth = 1990,
      race_concept_id = 0, ethnicity_concept_id = 0
    ),
    "observation_period" = dplyr::tibble(
      observation_period_id = 1:3, person_id = 1:3,
      observation_period_start_date = as.Date("2000-01-01"),
      observation_period_end_date = as.Date("2023-12-31"),
      period_type_concept_id = 0
    )
  ),
  cdmName = "mock"
)

cdm$person
```



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