

# Package ‘DrugUtilisation’

July 21, 2025

**Title** Summarise Patient-Level Drug Utilisation in Data Mapped to the OMOP Common Data Model

**Version** 1.0.4

**Description** Summarise patient-level drug utilisation cohorts using data mapped to the Observational Medical Outcomes Partnership (OMOP) common data model. New users and prevalent users cohorts can be generated and their characteristics, indication and drug use summarised.

**License** Apache License ( $\geq 2$ )

**Encoding** UTF-8

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**Suggests** bit64, CohortSurvival, covr, DBI, duckdb, flextable, ggplot2, ggtext, gt, here, knitr, odbc, rmarkdown, RPostgres, scales, testthat ( $\geq 3.1.5$ ), tibble, visOmopResults ( $\geq 1.0.0$ )

**Config/testthat/edition** 3

**Imports** CDMConnector ( $\geq 1.4.0$ ), cli, clock, CodelistGenerator ( $\geq 3.1.0$ ), dplyr, glue, omopgenerics ( $\geq 1.0.0$ ), PatientProfiles ( $\geq 1.0.0$ ), purrr, rlang, stringr, tidyr

**Depends** R ( $\geq 4.1$ )

**LazyData** true

**URL** <https://darwin-eu.github.io/DrugUtilisation/>

**BugReports** <https://github.com/darwin-eu/DrugUtilisation/issues>

**Config/testthat/parallel** true

**VignetteBuilder** knitr

**NeedsCompilation** no

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|                          |                                                                                                                       |
|--------------------------|-----------------------------------------------------------------------------------------------------------------------|
| <i>addCumulativeDose</i> | <i>To add a new column with the cumulative dose. To add multiple columns use addDrugUtilisation() for efficiency.</i> |
|--------------------------|-----------------------------------------------------------------------------------------------------------------------|

---

## Description

To add a new column with the cumulative dose. To add multiple columns use addDrugUtilisation() for efficiency.

## Usage

```
addCumulativeDose(  
  cohort,  
  ingredientConceptId,  
  conceptSet = NULL,  
  indexDate = "cohort_start_date",  
  censorDate = "cohort_end_date",  
  restrictIncident = TRUE,  
  nameStyle = "cumulative_dose_{concept_name}_{ingredient}",  
  name = NULL  
)
```

## Arguments

|                                  |                                                                                                                                                 |
|----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cohort</code>              | A <code>cohort_table</code> object.                                                                                                             |
| <code>ingredientConceptId</code> | Ingredient OMOP concept that we are interested for the study.                                                                                   |
| <code>conceptSet</code>          | List of concepts to be included.                                                                                                                |
| <code>indexDate</code>           | Name of a column that indicates the date to start the analysis.                                                                                 |
| <code>censorDate</code>          | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| <code>restrictIncident</code>    | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| <code>nameStyle</code>           | Character string to specify the nameStyle of the new columns.                                                                                   |

**name**                      Name of the new computed cohort table, if NULL a temporary table will be created.

### Value

The same cohort with the added column.

### Examples

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addCumulativeDose(ingredientConceptId = 1125315) |>
  glimpse()
```

---

`addCumulativeQuantity` *To add a new column with the cumulative quantity. To add multiple columns use `addDrugUtilisation()` for efficiency.*

---

### Description

To add a new column with the cumulative quantity. To add multiple columns use `addDrugUtilisation()` for efficiency.

### Usage

```
addCumulativeQuantity(
  cohort,
  conceptSet,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "cumulative_quantity_{concept_name}",
  name = NULL
)
```

**Arguments**

|                  |                                                                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort           | A cohort_table object.                                                                                                                          |
| conceptSet       | List of concepts to be included.                                                                                                                |
| indexDate        | Name of a column that indicates the date to start the analysis.                                                                                 |
| censorDate       | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| restrictIncident | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| nameStyle        | Character string to specify the nameStyle of the new columns.                                                                                   |
| name             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

**Value**

The same cohort with the added column.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addCumulativeQuantity(conceptSet = codelist) |>
  glimpse()
```

---

|                |                                                                                                                    |
|----------------|--------------------------------------------------------------------------------------------------------------------|
| addDaysExposed | <i>To add a new column with the days exposed. To add multiple columns use addDrugUtilisation() for efficiency.</i> |
|----------------|--------------------------------------------------------------------------------------------------------------------|

---

**Description**

To add a new column with the days exposed. To add multiple columns use addDrugUtilisation() for efficiency.

**Usage**

```
addDaysExposed(
  cohort,
  conceptSet,
  gapEra,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "days_exposed_{concept_name}",
  name = NULL
)
```

**Arguments**

|                               |                                                                                                                                                 |
|-------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cohort</code>           | A <code>cohort_table</code> object.                                                                                                             |
| <code>conceptSet</code>       | List of concepts to be included.                                                                                                                |
| <code>gapEra</code>           | Number of days between two continuous exposures to be considered in the same era.                                                               |
| <code>indexDate</code>        | Name of a column that indicates the date to start the analysis.                                                                                 |
| <code>censorDate</code>       | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| <code>restrictIncident</code> | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| <code>nameStyle</code>        | Character string to specify the nameStyle of the new columns.                                                                                   |
| <code>name</code>             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

**Value**

The same cohort with the added column.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addDaysExposed(conceptSet = codelist, gapEra = 1) |>
  glimpse()
```

---

|                   |                                                                                                                       |
|-------------------|-----------------------------------------------------------------------------------------------------------------------|
| addDaysPrescribed | <i>To add a new column with the days prescribed. To add multiple columns use addDrugUtilisation() for efficiency.</i> |
|-------------------|-----------------------------------------------------------------------------------------------------------------------|

---

## Description

To add a new column with the days prescribed. To add multiple columns use addDrugUtilisation() for efficiency.

## Usage

```
addDaysPrescribed(
  cohort,
  conceptSet,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "days_prescribed_{concept_name}",
  name = NULL
)
```

## Arguments

|                  |                                                                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort           | A cohort_table object.                                                                                                                          |
| conceptSet       | List of concepts to be included.                                                                                                                |
| indexDate        | Name of a column that indicates the date to start the analysis.                                                                                 |
| censorDate       | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| restrictIncident | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| nameStyle        | Character string to specify the nameStyle of the new columns.                                                                                   |
| name             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

## Value

The same cohort with the added columns.

## Examples

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

cdm <- mockDrugUtilisation()
```

```

codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addDaysPrescribed(conceptSet = codelist) |>
  glimpse()

```

---

|                |                                                                                   |
|----------------|-----------------------------------------------------------------------------------|
| addDrugRestart | <i>Add drug restart information as a column per follow-up period of interest.</i> |
|----------------|-----------------------------------------------------------------------------------|

---

## Description

Add drug restart information as a column per follow-up period of interest.

## Usage

```

addDrugRestart(
  cohort,
  switchCohortTable,
  switchCohortId = NULL,
  followUpDays = Inf,
  censorDate = NULL,
  incident = TRUE,
  nameStyle = "drug_restart_{follow_up_days}"
)

```

## Arguments

|                   |                                                                                                                                                     |
|-------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort            | A cohort_table object.                                                                                                                              |
| switchCohortTable | A cohort table in the cdm that contains possible alternative treatments.                                                                            |
| switchCohortId    | The cohort ids to be used from switchCohortTable. If NULL all cohort definition ids are used.                                                       |
| followUpDays      | A vector of number of days to follow up. It can be multiple values.                                                                                 |
| censorDate        | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                      |
| incident          | Whether the switch treatment has to be incident (start after discontinuation) or not (it can start before the discontinuation and last till after). |
| nameStyle         | Character string to specify the nameStyle of the new columns.                                                                                       |

**Value**

The cohort table given with additional columns with information on the restart, switch and not exposed per follow-up period of interest.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

conceptlist <- list(acetaminophen = 1125360, metformin = c(1503297, 1503327))
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "switch_cohort",
                                       conceptSet = conceptlist)

cdm$cohort1 |>
  addDrugRestart(switchCohortTable = "switch_cohort")
```

---

|                    |                                                          |
|--------------------|----------------------------------------------------------|
| addDrugUtilisation | <i>Add new columns with drug use related information</i> |
|--------------------|----------------------------------------------------------|

---

**Description**

Add new columns with drug use related information

**Usage**

```
addDrugUtilisation(
  cohort,
  gapEra,
  conceptSet = NULL,
  ingredientConceptId = NULL,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  numberExposures = TRUE,
  numberEras = TRUE,
  daysExposed = TRUE,
  daysPrescribed = TRUE,
  timeToExposure = TRUE,
  initialExposureDuration = TRUE,
  initialQuantity = TRUE,
  cumulativeQuantity = TRUE,
  initialDailyDose = TRUE,
  cumulativeDose = TRUE,
  nameStyle = "{value}_{concept_name}_{ingredient}",
  name = NULL
)
```

**Arguments**

|                         |                                                                                                                                                                                                                               |
|-------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort                  | A cohort_table object.                                                                                                                                                                                                        |
| gapEra                  | Number of days between two continuous exposures to be considered in the same era.                                                                                                                                             |
| conceptSet              | List of concepts to be included.                                                                                                                                                                                              |
| ingredientConceptId     | Ingredient OMOP concept that we are interested for the study.                                                                                                                                                                 |
| indexDate               | Name of a column that indicates the date to start the analysis.                                                                                                                                                               |
| censorDate              | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                                                                                                |
| restrictIncident        | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included.                                                                               |
| numberExposures         | Whether to include 'number_exposures' (number of drug exposure records between indexDate and censorDate).                                                                                                                     |
| numberEras              | Whether to include 'number_eras' (number of continuous exposure episodes between indexDate and censorDate).                                                                                                                   |
| daysExposed             | Whether to include 'days_exposed' (number of days that the individual is in a continuous exposure episode, including allowed treatment gaps, between indexDate and censorDate; sum of the length of the different drug eras). |
| daysPrescribed          | Whether to include 'days_prescribed' (sum of the number of days for each prescription that contribute in the analysis).                                                                                                       |
| timeToExposure          | Whether to include 'time_to_exposure' (number of days between indexDate and the first episode).                                                                                                                               |
| initialExposureDuration | Whether to include 'initial_exposure_duration' (number of prescribed days of the first drug exposure record).                                                                                                                 |
| initialQuantity         | Whether to include 'initial_quantity' (quantity of the first drug exposure record).                                                                                                                                           |
| cumulativeQuantity      | Whether to include 'cumulative_quantity' (sum of the quantity of the different exposures considered in the analysis).                                                                                                         |
| initialDailyDose        | Whether to include 'initial_daily_dose_{unit}' (daily dose of the first considered prescription).                                                                                                                             |
| cumulativeDose          | Whether to include 'cumulative_dose_{unit}' (sum of the cumulative dose of the analysed drug exposure records).                                                                                                               |
| nameStyle               | Character string to specify the nameStyle of the new columns.                                                                                                                                                                 |
| name                    | Name of the new computed cohort table, if NULL a temporary table will be created.                                                                                                                                             |

**Value**

The same cohort with the added columns.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")

cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addDrugUtilisation(ingredientConceptId = 1125315, gapEra = 30) |>
  glimpse()
```

---

|               |                                                          |
|---------------|----------------------------------------------------------|
| addIndication | <i>Add a variable indicating individuals indications</i> |
|---------------|----------------------------------------------------------|

---

**Description**

Add a variable to a drug cohort indicating their presence in an indication cohort in a specified time window. If an individual is not in one of the indication cohorts, they will be considered to have an unknown indication if they are present in one of the specified OMOP CDM clinical tables. If they are neither in an indication cohort or a clinical table they will be considered as having no observed indication.

**Usage**

```
addIndication(
  cohort,
  indicationCohortName,
  indicationCohortId = NULL,
  indicationWindow = list(c(0, 0)),
  unknownIndicationTable = NULL,
  indexDate = "cohort_start_date",
  censorDate = NULL,
  mutuallyExclusive = TRUE,
  nameStyle = NULL,
  name = NULL
)
```

**Arguments**

|                      |                                 |
|----------------------|---------------------------------|
| cohort               | A cohort_table object.          |
| indicationCohortName | Name of indication cohort table |

|                        |                                                                                                                                                                          |
|------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| indicationCohortId     | target cohort Id to add indication                                                                                                                                       |
| indicationWindow       | time window of interests                                                                                                                                                 |
| unknownIndicationTable | Tables to search unknown indications                                                                                                                                     |
| indexDate              | Name of a column that indicates the date to start the analysis.                                                                                                          |
| censorDate             | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                                           |
| mutuallyExclusive      | Whether to consider mutually exclusive categories (one column per window) or not (one column per window and indication).                                                 |
| nameStyle              | Name style for the indications. By default: 'indication_{window_name}' (mutuallyExclusive = TRUE), 'indication_{window_name}_{cohort_name}' (mutuallyExclusive = FALSE). |
| name                   | Name of the new computed cohort table, if NULL a temporary table will be created.                                                                                        |

### Value

The original table with a variable added that summarises the individual's indications.

### Examples

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

cdm <- mockDrugUtilisation()

indications <- list(headache = 378253, asthma = 317009)
cdm <- generateConceptCohortSet(cdm = cdm,
                              conceptSet = indications,
                              name = "indication_cohorts")

cdm <- generateIngredientCohortSet(cdm = cdm,
                                 name = "drug_cohort",
                                 ingredient = "acetaminophen")

cdm$drug_cohort |>
  addIndication(
    indicationCohortName = "indication_cohorts",
    indicationWindow = list(c(0, 0)),
    unknownIndicationTable = "condition_occurrence"
  ) |>
  glimpse()
```

---

`addInitialDailyDose`     *To add a new column with the initial daily dose. To add multiple columns use `addDrugUtilisation()` for efficiency.*

---

## Description

To add a new column with the initial daily dose. To add multiple columns use `addDrugUtilisation()` for efficiency.

## Usage

```
addInitialDailyDose(
  cohort,
  ingredientConceptId,
  conceptSet = NULL,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "initial_daily_dose_{concept_name}_{ingredient}",
  name = NULL
)
```

## Arguments

|                                  |                                                                                                                                                 |
|----------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cohort</code>              | A <code>cohort_table</code> object.                                                                                                             |
| <code>ingredientConceptId</code> | Ingredient OMOP concept that we are interested for the study.                                                                                   |
| <code>conceptSet</code>          | List of concepts to be included.                                                                                                                |
| <code>indexDate</code>           | Name of a column that indicates the date to start the analysis.                                                                                 |
| <code>censorDate</code>          | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| <code>restrictIncident</code>    | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| <code>nameStyle</code>           | Character string to specify the <code>nameStyle</code> of the new columns.                                                                      |
| <code>name</code>                | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

## Value

The same cohort with the added column.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addInitialDailyDose(ingredientConceptId = 1125315) |>
  glimpse()
```

---

addInitialExposureDuration

*To add a new column with the duration of the first exposure. To add multiple columns use addDrugUtilisation() for efficiency.*

---

**Description**

To add a new column with the duration of the first exposure. To add multiple columns use addDrugUtilisation() for efficiency.

**Usage**

```
addInitialExposureDuration(
  cohort,
  conceptSet,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "initial_exposure_duration_{concept_name}",
  name = NULL
)
```

**Arguments**

|            |                                                                                                                |
|------------|----------------------------------------------------------------------------------------------------------------|
| cohort     | A cohort_table object.                                                                                         |
| conceptSet | List of concepts to be included.                                                                               |
| indexDate  | Name of a column that indicates the date to start the analysis.                                                |
| censorDate | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used. |

|                  |                                                                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| restrictIncident | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| nameStyle        | Character string to specify the nameStyle of the new columns.                                                                                   |
| name             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

**Value**

The same cohort with the added column.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addInitialExposureDuration(conceptSet = codelist) |>
  glimpse()
```

---

|                    |                                                                                                                        |
|--------------------|------------------------------------------------------------------------------------------------------------------------|
| addInitialQuantity | <i>To add a new column with the initial quantity. To add multiple columns use addDrugUtilisation() for efficiency.</i> |
|--------------------|------------------------------------------------------------------------------------------------------------------------|

---

**Description**

To add a new column with the initial quantity. To add multiple columns use addDrugUtilisation() for efficiency.

**Usage**

```
addInitialQuantity(
  cohort,
  conceptSet,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "initial_quantity_{concept_name}",
  name = NULL
)
```

**Arguments**

|                  |                                                                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort           | A cohort_table object.                                                                                                                          |
| conceptSet       | List of concepts to be included.                                                                                                                |
| indexDate        | Name of a column that indicates the date to start the analysis.                                                                                 |
| censorDate       | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| restrictIncident | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| nameStyle        | Character string to specify the nameStyle of the new columns.                                                                                   |
| name             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

**Value**

The same cohort with the added column.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addInitialQuantity(conceptSet = codelist) |>
  glimpse()
```

---

|               |                                                                                                                      |
|---------------|----------------------------------------------------------------------------------------------------------------------|
| addNumberEras | <i>To add a new column with the number of eras. To add multiple columns use addDrugUtilisation() for efficiency.</i> |
|---------------|----------------------------------------------------------------------------------------------------------------------|

---

**Description**

To add a new column with the number of eras. To add multiple columns use addDrugUtilisation() for efficiency.

**Usage**

```
addNumberEras(
  cohort,
  conceptSet,
  gapEra,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "number_eras_{concept_name}",
  name = NULL
)
```

**Arguments**

|                  |                                                                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort           | A cohort_table object.                                                                                                                          |
| conceptSet       | List of concepts to be included.                                                                                                                |
| gapEra           | Number of days between two continuous exposures to be considered in the same era.                                                               |
| indexDate        | Name of a column that indicates the date to start the analysis.                                                                                 |
| censorDate       | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| restrictIncident | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| nameStyle        | Character string to specify the nameStyle of the new columns.                                                                                   |
| name             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

**Value**

The same cohort with the added column.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addNumberEras(conceptSet = codelist, gapEra = 1) |>
  glimpse()
```

---

|                    |                                                                                                                           |
|--------------------|---------------------------------------------------------------------------------------------------------------------------|
| addNumberExposures | <i>To add a new column with the number of exposures. To add multiple columns use addDrugUtilisation() for efficiency.</i> |
|--------------------|---------------------------------------------------------------------------------------------------------------------------|

---

### Description

To add a new column with the number of exposures. To add multiple columns use addDrugUtilisation() for efficiency.

### Usage

```
addNumberExposures(
  cohort,
  conceptSet,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "number_exposures_{concept_name}",
  name = NULL
)
```

### Arguments

|                  |                                                                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort           | A cohort_table object.                                                                                                                          |
| conceptSet       | List of concepts to be included.                                                                                                                |
| indexDate        | Name of a column that indicates the date to start the analysis.                                                                                 |
| censorDate       | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| restrictIncident | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| nameStyle        | Character string to specify the nameStyle of the new columns.                                                                                   |
| name             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

### Value

The same cohort with the added columns.

### Examples

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

cdm <- mockDrugUtilisation()
```

```

codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addNumberExposures(conceptSet = codelist) |>
  glimpse()

```

---

|                   |                                                                                                                        |
|-------------------|------------------------------------------------------------------------------------------------------------------------|
| addTimeToExposure | <i>To add a new column with the time to exposure. To add multiple columns use addDrugUtilisation() for efficiency.</i> |
|-------------------|------------------------------------------------------------------------------------------------------------------------|

---

## Description

To add a new column with the time to exposure. To add multiple columns use addDrugUtilisation() for efficiency.

## Usage

```

addTimeToExposure(
  cohort,
  conceptSet,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  nameStyle = "time_to_exposure_{concept_name}",
  name = NULL
)

```

## Arguments

|                  |                                                                                                                                                 |
|------------------|-------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort           | A cohort_table object.                                                                                                                          |
| conceptSet       | List of concepts to be included.                                                                                                                |
| indexDate        | Name of a column that indicates the date to start the analysis.                                                                                 |
| censorDate       | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                  |
| restrictIncident | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included. |
| nameStyle        | Character string to specify the nameStyle of the new columns.                                                                                   |
| name             | Name of the new computed cohort table, if NULL a temporary table will be created.                                                               |

**Value**

The same cohort with the added column.

**Examples**

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

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

cdm$dus_cohort |>
  addTimeToExposure(conceptSet = codelist) |>
  glimpse()
```

---

addTreatment

---

*Add a variable indicating individuals medications*


---

**Description**

Add a variable to a drug cohort indicating their presence of a medication cohort in a specified time window.

**Usage**

```
addTreatment(
  cohort,
  treatmentCohortName,
  treatmentCohortId = NULL,
  window = list(c(0, 0)),
  indexDate = "cohort_start_date",
  censorDate = NULL,
  mutuallyExclusive = TRUE,
  nameStyle = NULL,
  name = NULL
)
```

**Arguments**

**cohort**                    A cohort\_table object.

**treatmentCohortName**      Name of treatment cohort table

|                   |                                                                                                                                                                              |
|-------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| treatmentCohortId | target cohort Id to add treatment                                                                                                                                            |
| window            | time window of interests.                                                                                                                                                    |
| indexDate         | Name of a column that indicates the date to start the analysis.                                                                                                              |
| censorDate        | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                                               |
| mutuallyExclusive | Whether to consider mutually exclusive categories (one column per window) or not (one column per window and treatment).                                                      |
| nameStyle         | Name style for the treatment columns. By default: 'treatment_{window_name}' (mutuallyExclusive = TRUE), 'treatment_{window_name}_{cohort_name}' (mutuallyExclusive = FALSE). |
| name              | Name of the new computed cohort table, if NULL a temporary table will be created.                                                                                            |

**Value**

The original table with a variable added that summarises the individual's indications.

**Examples**

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

cdm <- mockDrugUtilisation(numberIndividuals = 50)

cdm <- generateIngredientCohortSet(cdm = cdm,
                                  name = "drug_cohort",
                                  ingredient = "acetaminophen")

cdm <- generateIngredientCohortSet(cdm = cdm,
                                  name = "treatments",
                                  ingredient = c("metformin", "simvastatin"))

cdm$drug_cohort |>
  addTreatment("treatments", window = list(c(0, 0), c(1, 30), c(31, 60))) |>
  glimpse()
```

---

benchmarkDrugUtilisation

*Run benchmark of drug utilisation cohort generation*

---

**Description**

Run benchmark of drug utilisation cohort generation

**Usage**

```
benchmarkDrugUtilisation(
  cdm,
  ingredient = "acetaminophen",
  alternativeIngredient = c("ibuprofen", "aspirin", "diclofenac"),
  indicationCohort = NULL
)
```

**Arguments**

`cdm`                    A `cdm_reference` object.

`ingredient`           Name of ingredient to benchmark.

`alternativeIngredient`  
                      Name of ingredients to use as alternative treatments.

`indicationCohort`  
                      Name of a cohort in the `cdm_reference` object to use as indicationmn.

**Value**

A `summarise_result` object.

**Examples**

```
library(DrugUtilisation)
library(CDMConnector)
library(duckdb)

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

timings <- benchmarkDrugUtilisation(cdm)

timings
```

---

|              |                                               |
|--------------|-----------------------------------------------|
| cohortGapEra | <i>Get the gapEra used to create a cohort</i> |
|--------------|-----------------------------------------------|

---

**Description**

Get the `gapEra` used to create a cohort

**Usage**

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

**Arguments**

`cohort` A `cohort_table` object.

`cohortId` Integer vector referring to `cohortIds` from `cohort`. If `NULL` all cohort definition ids in settings will be used.

**Value**

gapEra values for the specific `cohortIds`

**Examples**

```
library(DrugUtilisation)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()

druglist <- getDrugIngredientCodes(cdm = cdm,
                                   name = c("acetaminophen", "metformin"))

cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "drug_cohorts",
                                       conceptSet = druglist,
                                       gapEra = 100)

cohortGapEra(cdm$drug_cohorts)
```

---

|                          |                                                                               |
|--------------------------|-------------------------------------------------------------------------------|
| <code>erafyCohort</code> | <i>Erafy a cohort_table collapsing records separated gapEra days or less.</i> |
|--------------------------|-------------------------------------------------------------------------------|

---

**Description**

Erafy a `cohort_table` collapsing records separated `gapEra` days or less.

**Usage**

```
erafyCohort(
  cohort,
  gapEra,
  cohortId = NULL,
  nameStyle = "{cohort_name}_{gap_era}",
  name = omopgenerics::tableName(cohort)
)
```

**Arguments**

|           |                                                                                                                                                                 |
|-----------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort    | A cohort_table object.                                                                                                                                          |
| gapEra    | Number of days between two continuous exposures to be considered in the same era.                                                                               |
| cohortId  | A cohort definition id to restrict by. If NULL, all cohorts will be included.                                                                                   |
| nameStyle | String to create the new names of cohorts. Must contain '{cohort_name}' if more than one cohort is present and '{gap_era}' if more than one gapEra is provided. |
| name      | Name of the new cohort table, it must be a length 1 character vector.                                                                                           |

**Value**

A cohort\_table object.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

cdm$cohort2 <- cdm$cohort1 |>
  erafyCohort(gapEra = 30, name = "cohort2")

cdm$cohort2

settings(cdm$cohort2)

mockDisconnect(cdm)
```

---

generateAtcCohortSet    *Generate a set of drug cohorts based on ATC classification*

---

**Description**

Adds a new cohort table to the cdm reference with individuals who have drug exposure records that belong to the specified Anatomical Therapeutic Chemical (ATC) classification. Cohort start and end dates will be based on drug record start and end dates, respectively. Records that overlap or have fewer days between them than the specified gap era will be concatenated into a single cohort entry.

**Usage**

```
generateAtcCohortSet(
  cdm,
  name,
  atcName = NULL,
```

```

    gapEra = 1,
    subsetCohort = NULL,
    subsetCohortId = NULL,
    numberExposures = FALSE,
    daysPrescribed = FALSE,
    ...
  )

```

## Arguments

|                 |                                                                                                                                                                                             |
|-----------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cdm             | A cdm_reference object.                                                                                                                                                                     |
| name            | Name of the new cohort table, it must be a length 1 character vector.                                                                                                                       |
| atcName         | Names of ATC classification of interest.                                                                                                                                                    |
| gapEra          | Number of days between two continuous exposures to be considered in the same era. Records that have fewer days between them than this gap will be concatenated into the same cohort record. |
| subsetCohort    | Cohort table to subset.                                                                                                                                                                     |
| subsetCohortId  | Cohort id to subset.                                                                                                                                                                        |
| numberExposures | Whether to include 'number_exposures' (number of drug exposure records between indexDate and censorDate).                                                                                   |
| daysPrescribed  | Whether to include 'days_prescribed' (number of days prescribed used to create each era).                                                                                                   |
| ...             | Arguments to be passed to CodelistGenerator::getATCCodes().                                                                                                                                 |

## Value

The function returns the cdm reference provided with the addition of the new cohort table.

## Examples

```

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

cdm <- mockDrugUtilisation()

cdm <- generateAtcCohortSet(cdm = cdm,
                           atcName = "alimentary tract and metabolism",
                           name = "drugs")

cdm$drugs |>
  glimpse()

```

---

```
generateDrugUtilisationCohortSet
```

*Generate a set of drug cohorts based on given concepts*

---

## Description

Adds a new cohort table to the cdm reference with individuals who have drug exposure records with the specified concepts. Cohort start and end dates will be based on drug record start and end dates, respectively. Records that overlap or have fewer days between them than the specified gap era will be concatenated into a single cohort entry.

## Usage

```
generateDrugUtilisationCohortSet(
  cdm,
  name,
  conceptSet,
  gapEra = 1,
  subsetCohort = NULL,
  subsetCohortId = NULL,
  numberExposures = FALSE,
  daysPrescribed = FALSE
)
```

## Arguments

|                 |                                                                                                           |
|-----------------|-----------------------------------------------------------------------------------------------------------|
| cdm             | A cdm_reference object.                                                                                   |
| name            | Name of the new cohort table, it must be a length 1 character vector.                                     |
| conceptSet      | List of concepts to be included.                                                                          |
| gapEra          | Number of days between two continuous exposures to be considered in the same era.                         |
| subsetCohort    | Cohort table to subset.                                                                                   |
| subsetCohortId  | Cohort id to subset.                                                                                      |
| numberExposures | Whether to include 'number_exposures' (number of drug exposure records between indexDate and censorDate). |
| daysPrescribed  | Whether to include 'days_prescribed' (number of days prescribed used to create each era).                 |

## Value

The function returns the cdm reference provided with the addition of the new cohort table.

### Examples

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

cdm <- mockDrugUtilisation()

druglist <- getDrugIngredientCodes(cdm = cdm,
                                   name = c("acetaminophen", "metformin"),
                                   nameStyle = "{concept_name}")

cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "drug_cohorts",
                                       conceptSet = druglist,
                                       gapEra = 30,
                                       numberExposures = TRUE,
                                       daysPrescribed = TRUE)

cdm$drug_cohorts |>
  glimpse()
```

---

`generateIngredientCohortSet`*Generate a set of drug cohorts based on drug ingredients*

---

### Description

Adds a new cohort table to the cdm reference with individuals who have drug exposure records with the specified drug ingredient. Cohort start and end dates will be based on drug record start and end dates, respectively. Records that overlap or have fewer days between them than the specified gap era will be concatenated into a single cohort entry.

### Usage

```
generateIngredientCohortSet(
  cdm,
  name,
  ingredient = NULL,
  gapEra = 1,
  subsetCohort = NULL,
  subsetCohortId = NULL,
  numberExposures = FALSE,
  daysPrescribed = FALSE,
  ...
)
```

**Arguments**

|                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cdm</code>             | A <code>cdm_reference</code> object.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>name</code>            | Name of the new cohort table, it must be a length 1 character vector.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| <code>ingredient</code>      | Accepts both vectors and named lists of ingredient names. For a vector input, e.g., <code>c("acetaminophen", "codeine")</code> , it generates a cohort table with descendant concept codes for each ingredient, assigning unique <code>cohort_definition_id</code> . For a named list input, e.g., <code>list("test_1" = c("simvastatin", "acetaminophen"), "test_2" = "metformin")</code> , it produces a cohort table based on the structure of the input, where each name leads to a combined set of descendant concept codes for the specified ingredients, creating distinct <code>cohort_definition_id</code> for each named group. |
| <code>gapEra</code>          | Number of days between two continuous exposures to be considered in the same era.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| <code>subsetCohort</code>    | Cohort table to subset.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| <code>subsetCohortId</code>  | Cohort id to subset.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>numberExposures</code> | Whether to include 'number_exposures' (number of drug exposure records between <code>indexDate</code> and <code>censorDate</code> ).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| <code>daysPrescribed</code>  | Whether to include 'days_prescribed' (number of days prescribed used to create each era).                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| <code>...</code>             | Arguments to be passed to <code>CodelistGenerator::getDrugIngredientCodes()</code> .                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |

**Value**

The function returns the `cdm` reference provided with the addition of the new cohort table.

**Examples**

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

cdm <- mockDrugUtilisation()

cdm <- generateIngredientCohortSet(cdm = cdm,
                                  ingredient = "acetaminophen",
                                  name = "acetaminophen")

cdm$acetaminophen |>
  glimpse()
```

---

|                     |                                                                       |
|---------------------|-----------------------------------------------------------------------|
| mockDrugUtilisation | <i>It creates a mock database for testing DrugUtilisation package</i> |
|---------------------|-----------------------------------------------------------------------|

---

## Description

It creates a mock database for testing DrugUtilisation package

## Usage

```
mockDrugUtilisation(  
  con = NULL,  
  writeSchema = NULL,  
  numberIndividuals = 10,  
  seed = NULL,  
  ...  
)
```

## Arguments

|                   |                                                                                                                       |
|-------------------|-----------------------------------------------------------------------------------------------------------------------|
| con               | A DBIConnection object to a database. If NULL a new duckdb connection will be used.                                   |
| writeSchema       | A schema with writing permissions to copy there the cdm tables.                                                       |
| numberIndividuals | Number of individuals in the mock cdm.                                                                                |
| seed              | Seed for the random numbers. If NULL no seed is used.                                                                 |
| ...               | Tables to use as basis to create the mock. If some tables are provided they will be used to construct the cdm object. |

## Value

A cdm reference with the mock tables

## Examples

```
library(DrugUtilisation)  
  
cdm <- mockDrugUtilisation()  
  
cdm
```

---

|                     |                                                                          |
|---------------------|--------------------------------------------------------------------------|
| patternsWithFormula | <i>Patterns valid to compute daily dose with the associated formula.</i> |
|---------------------|--------------------------------------------------------------------------|

---

**Description**

Patterns valid to compute daily dose with the associated formula.

**Usage**

```
patternsWithFormula
```

**Format**

A data frame with eight variables: pattern\_id, amount, amount\_unit, numerator, numerator\_unit, denominator, denominator\_unit, formula\_name and formula.

---

|              |                                                                                       |
|--------------|---------------------------------------------------------------------------------------|
| patternTable | <i>Function to create a tibble with the patterns from current drug strength table</i> |
|--------------|---------------------------------------------------------------------------------------|

---

**Description**

Function to create a tibble with the patterns from current drug strength table

**Usage**

```
patternTable(cdm)
```

**Arguments**

|     |                         |
|-----|-------------------------|
| cdm | A cdm_reference object. |
|-----|-------------------------|

**Value**

The function creates a tibble with the different patterns found in the table, plus a column of potentially valid and invalid combinations.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

patternTable(cdm)
```

---

|                 |                                                                                                                  |
|-----------------|------------------------------------------------------------------------------------------------------------------|
| plotDrugRestart | <i>Generate a custom ggplot2 from a summarised_result object generated with summariseDrugRestart() function.</i> |
|-----------------|------------------------------------------------------------------------------------------------------------------|

---

## Description

Generate a custom ggplot2 from a summarised\_result object generated with summariseDrugRestart() function.

## Usage

```
plotDrugRestart(  
  result,  
  facet = cdm_name + cohort_name ~ follow_up_days,  
  colour = "variable_level"  
)
```

## Arguments

|        |                                                                                                                          |
|--------|--------------------------------------------------------------------------------------------------------------------------|
| result | A summarised_result object.                                                                                              |
| facet  | Columns to facet by. See options with availablePlotColumns(result). Formula is also allowed to specify rows and columns. |
| colour | Columns to color by. See options with availablePlotColumns(result).                                                      |

## Value

A ggplot2 object.

## Examples

```
## Not run:  
library(DrugUtilisation)  
  
cdm <- mockDrugUtilisation()  
  
conceptlist <- list("a" = 1125360, "b" = c(1503297, 1503327))  
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,  
                                       name = "switch_cohort",  
                                       conceptSet = conceptlist)  
  
result <- cdm$cohort1 |>  
  summariseDrugRestart(switchCohortTable = "switch_cohort")  
  
plotDrugRestart(result)  
  
## End(Not run)
```

---

plotDrugUtilisation     *Plot the results of summariseDrugUtilisation*

---

## Description

Plot the results of summariseDrugUtilisation

## Usage

```
plotDrugUtilisation(
  result,
  variable = "number exposures",
  plotType = "barplot",
  facet = strataColumns(result),
  colour = "cohort_name"
)
```

## Arguments

|          |                                                                                                                          |
|----------|--------------------------------------------------------------------------------------------------------------------------|
| result   | A summarised_result object.                                                                                              |
| variable | Variable to plot. See unique(result\$variable_name) for options.                                                         |
| plotType | Must be a choice between: 'scatterplot', 'barplot', 'densityplot', and 'boxplot'.                                        |
| facet    | Columns to facet by. See options with availablePlotColumns(result). Formula is also allowed to specify rows and columns. |
| colour   | Columns to color by. See options with availablePlotColumns(result).                                                      |

## Value

A ggplot2 object.

## Examples

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

cdm <- mockDrugUtilisation(numberIndividuals = 100)
codes <- list(aceta = c(1125315, 1125360, 2905077, 43135274))
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "cohort",
                                       conceptSet = codes)

result <- cdm$cohort |>
  addSex() |>
  summariseDrugUtilisation(
    strata = "sex",
    ingredientConceptId = 1125315,
```

```

      estimates = c("min", "q25", "median", "q75", "max", "density")
    )

result |>
  filter(estimate_name == "median") |>
  plotDrugUtilisation(
    variable = "days prescribed",
    plotType = "barplot"
  )

result |>
  plotDrugUtilisation(
    variable = "days exposed",
    facet = cohort_name ~ cdm_name,
    colour = "sex",
    plotType = "boxplot"
  )

result |>
  plotDrugUtilisation(
    variable = "cumulative dose milligram",
    plotType = "densityplot",
    facet = "cohort_name",
    colour = "sex"
  )

mockDisconnect(cdm)

```

---

|                |                                                                                       |
|----------------|---------------------------------------------------------------------------------------|
| plotIndication | <i>Generate a plot visualisation (ggplot2) from the output of summariseIndication</i> |
|----------------|---------------------------------------------------------------------------------------|

---

## Description

Generate a plot visualisation (ggplot2) from the output of summariseIndication

## Usage

```

plotIndication(
  result,
  facet = cdm_name + cohort_name ~ window_name,
  colour = "variable_level"
)

```

## Arguments

**result**                    A summarised\_result object.

|        |                                                                                                                          |
|--------|--------------------------------------------------------------------------------------------------------------------------|
| facet  | Columns to facet by. See options with availablePlotColumns(result). Formula is also allowed to specify rows and columns. |
| colour | Columns to color by. See options with availablePlotColumns(result).                                                      |

**Value**

A ggplot2 object

**Examples**

```
library(DrugUtilisation)
library(CDMConnector)

cdm <- mockDrugUtilisation()

indications <- list(headache = 378253, asthma = 317009)
cdm <- generateConceptCohortSet(cdm = cdm,
                              conceptSet = indications,
                              name = "indication_cohorts")

cdm <- generateIngredientCohortSet(cdm = cdm,
                                  name = "drug_cohort",
                                  ingredient = "acetaminophen")

result <- cdm$drug_cohort |>
  summariseIndication(
    indicationCohortName = "indication_cohorts",
    unknownIndicationTable = "condition_occurrence",
    indicationWindow = list(c(-Inf, 0), c(-365, 0))
  )

plotIndication(result)
```

---

plotProportionOfPatientsCovered

*Plot proportion of patients covered*

---

**Description**

Plot proportion of patients covered

**Usage**

```
plotProportionOfPatientsCovered(
  result,
  facet = "cohort_name",
  colour = strataColumns(result),
  ribbon = TRUE
)
```

**Arguments**

|        |                                                                                                                          |
|--------|--------------------------------------------------------------------------------------------------------------------------|
| result | A summarised_result object.                                                                                              |
| facet  | Columns to facet by. See options with availablePlotColumns(result). Formula is also allowed to specify rows and columns. |
| colour | Columns to color by. See options with availablePlotColumns(result).                                                      |
| ribbon | Whether to plot a ribbon with the confidence intervals.                                                                  |

**Value**

Plot of proportion Of patients covered over time

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "my_cohort",
                                       conceptSet = list(drug_of_interest = c(1503297, 1503327)))

result <- cdm$my_cohort |>
  summariseProportionOfPatientsCovered(followUpDays = 365)

plotProportionOfPatientsCovered(result)
```

---

|               |                                                                                                              |
|---------------|--------------------------------------------------------------------------------------------------------------|
| plotTreatment | <i>Generate a custom ggplot2 from a summarised_result object generated with summariseTreatment function.</i> |
|---------------|--------------------------------------------------------------------------------------------------------------|

---

**Description**

Generate a custom ggplot2 from a summarised\_result object generated with summariseTreatment function.

**Usage**

```
plotTreatment(
  result,
  facet = cdm_name + cohort_name ~ window_name,
  colour = "variable_level"
)
```

**Arguments**

|        |                                                                                                                          |
|--------|--------------------------------------------------------------------------------------------------------------------------|
| result | A summarised_result object.                                                                                              |
| facet  | Columns to facet by. See options with availablePlotColumns(result). Formula is also allowed to specify rows and columns. |
| colour | Columns to color by. See options with availablePlotColumns(result).                                                      |

**Value**

A ggplot2 object.

**Examples**

```
## Not run:
library(DrugUtilisation)

cdm <- mockDrugUtilisation()
result <- cdm$cohort1 |>
  summariseTreatment(
    treatmentCohortName = "cohort2",
    window = list(c(0, 30), c(31, 365))
  )

plotTreatment(result)

## End(Not run)
```

---

requireDrugInDateRange

*Restrict cohort to only cohort records within a certain date range*

---

**Description**

Filter the cohort table keeping only the cohort records for which the specified index date is within a specified date range.

**Usage**

```
requireDrugInDateRange(
  cohort,
  dateRange,
  indexDate = "cohort_start_date",
  cohortId = NULL,
  name = omopgenerics::tableName(cohort)
)
```

**Arguments**

|           |                                                                                                   |
|-----------|---------------------------------------------------------------------------------------------------|
| cohort    | A cohort_table object.                                                                            |
| dateRange | Date interval to consider. Any records with the index date outside of this range will be dropped. |
| indexDate | The column containing the date that will be checked against the date range.                       |
| cohortId  | A cohort definition id to restrict by. If NULL, all cohorts will be included.                     |
| name      | Name of the new cohort table, it must be a length 1 character vector.                             |

**Value**

The cohort table having applied the date requirement.

**Examples**

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

cdm <- mockDrugUtilisation()

cdm$cohort1 <- cdm$cohort1 |>
  requireDrugInDateRange(dateRange = as.Date(c("2020-01-01", NA)))

attrition(cdm$cohort1) |>
  glimpse()
```

---

requireIsFirstDrugEntry

*Restrict cohort to only the first cohort record per subject*

---

**Description**

Filter the cohort table keeping only the first cohort record per subject.

**Usage**

```
requireIsFirstDrugEntry(
  cohort,
  cohortId = NULL,
  name = omopgenerics::tableName(cohort)
)
```

**Arguments**

|          |                                                                               |
|----------|-------------------------------------------------------------------------------|
| cohort   | A cohort_table object.                                                        |
| cohortId | A cohort definition id to restrict by. If NULL, all cohorts will be included. |
| name     | Name of the new cohort table, it must be a length 1 character vector.         |

**Value**

The cohort table having applied the first entry requirement.

**Examples**

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

cdm <- mockDrugUtilisation()

cdm$cohort1 <- cdm$cohort1 |>
  requireIsFirstDrugEntry()

attrition(cdm$cohort1) |>
  glimpse()
```

---

requireObservationBeforeDrug

*Restrict cohort to only cohort records with the given amount of prior observation time in the database*

---

**Description**

Filter the cohort table keeping only the cohort records for which the individual has the required observation time in the database prior to their cohort start date.

**Usage**

```
requireObservationBeforeDrug(
  cohort,
  days,
  cohortId = NULL,
  name = omopgenerics::tableName(cohort)
)
```

**Arguments**

|          |                                                                                                                     |
|----------|---------------------------------------------------------------------------------------------------------------------|
| cohort   | A cohort_table object.                                                                                              |
| days     | Number of days of prior observation required before cohort start date. Any records with fewer days will be dropped. |
| cohortId | A cohort definition id to restrict by. If NULL, all cohorts will be included.                                       |
| name     | Name of the new cohort table, it must be a length 1 character vector.                                               |

**Value**

The cohort table having applied the prior observation requirement.

**Examples**

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

cdm <- mockDrugUtilisation()

cdm$cohort1 <- cdm$cohort1 |>
  requireObservationBeforeDrug(days = 365)

attrition(cdm$cohort1) |>
  glimpse()
```

---

```
requirePriorDrugWashout
```

*Restrict cohort to only cohort records with a given amount of time since the last cohort record ended*

---

**Description**

Filter the cohort table keeping only the cohort records for which the required amount of time has passed since the last cohort entry ended for that individual.

**Usage**

```
requirePriorDrugWashout(
  cohort,
  days,
  cohortId = NULL,
  name = omopgenerics::tableName(cohort)
)
```

**Arguments**

|                       |                                                                                                                                                                                                                                                                                                                                             |
|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cohort</code>   | A <code>cohort_table</code> object.                                                                                                                                                                                                                                                                                                         |
| <code>days</code>     | The number of days required to have passed since the last cohort record finished. Any records with fewer days than this will be dropped. Note that setting days to <code>Inf</code> will lead to the same result as that from using the <code>requireIsFirstDrugEntry</code> function (with only an individual's first cohort record kept). |
| <code>cohortId</code> | A cohort definition id to restrict by. If <code>NULL</code> , all cohorts will be included.                                                                                                                                                                                                                                                 |
| <code>name</code>     | Name of the new cohort table, it must be a length 1 character vector.                                                                                                                                                                                                                                                                       |

**Value**

The cohort table having applied the washout requirement.

**Examples**

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

cdm <- mockDrugUtilisation()

cdm$cohort1 <- cdm$cohort1 |>
  requirePriorDrugWashout(days = 90)

attrition(cdm$cohort1) |>
  glimpse()
```

---

`summariseDoseCoverage` *Check coverage of daily dose computation in a sample of the cdm for selected concept sets and ingredient*

---

**Description**

Check coverage of daily dose computation in a sample of the cdm for selected concept sets and ingredient

**Usage**

```
summariseDoseCoverage(
  cdm,
  ingredientConceptId,
  estimates = c("count_missing", "percentage_missing", "mean", "sd", "q25", "median",
    "q75"),
  sampleSize = NULL
)
```

**Arguments**

|                                  |                                                                                                                                                                                                                        |
|----------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cdm</code>                 | A <code>cdm_reference</code> object.                                                                                                                                                                                   |
| <code>ingredientConceptId</code> | Ingredient OMOP concept that we are interested for the study.                                                                                                                                                          |
| <code>estimates</code>           | Estimates to obtain.                                                                                                                                                                                                   |
| <code>sampleSize</code>          | Maximum number of records of an ingredient to estimate dose coverage. If an ingredient has more, a random sample equal to <code>sampleSize</code> will be considered. If <code>NULL</code> , all records will be used. |

**Value**

The function returns information of the coverage of `computeDailyDose.R` for the selected ingredients and concept sets

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

summariseDoseCoverage(cdm = cdm, ingredientConceptId = 1125315)
```

---

`summariseDrugRestart`    *Summarise the drug restart for each follow-up period of interest.*

---

**Description**

Summarise the drug restart for each follow-up period of interest.

**Usage**

```
summariseDrugRestart(
  cohort,
  cohortId = NULL,
  switchCohortTable,
  switchCohortId = NULL,
  strata = list(),
  followUpDays = Inf,
  censorDate = NULL,
  incident = TRUE,
  restrictToFirstDiscontinuation = TRUE
)
```

**Arguments**

|                                             |                                                                                                                                                     |
|---------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cohort</code>                         | A <code>cohort_table</code> object.                                                                                                                 |
| <code>cohortId</code>                       | A cohort definition id to restrict by. If NULL, all cohorts will be included.                                                                       |
| <code>switchCohortTable</code>              | A cohort table in the cdm that contains possible alternative treatments.                                                                            |
| <code>switchCohortId</code>                 | The cohort ids to be used from <code>switchCohortTable</code> . If NULL all cohort definition ids are used.                                         |
| <code>strata</code>                         | A list of variables to stratify results. These variables must have been added as additional columns in the cohort table.                            |
| <code>followUpDays</code>                   | A vector of number of days to follow up. It can be multiple values.                                                                                 |
| <code>censorDate</code>                     | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                      |
| <code>incident</code>                       | Whether the switch treatment has to be incident (start after discontinuation) or not (it can start before the discontinuation and last till after). |
| <code>restrictToFirstDiscontinuation</code> | Whether to consider only the first discontinuation episode or all of them.                                                                          |

**Value**

A summarised\_result object with the percentages of restart, switch and not exposed per follow-up period given.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

conceptlist <- list(acetaminophen = 1125360, metformin = c(1503297, 1503327))
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "switch_cohort",
                                       conceptSet = conceptlist)

result <- cdm$cohort1 |>
  summariseDrugRestart(switchCohortTable = "switch_cohort")

tableDrugRestart(result)
```

---

summariseDrugUtilisation

*This function is used to summarise the dose utilisation table over multiple cohorts.*

---

**Description**

This function is used to summarise the dose utilisation table over multiple cohorts.

**Usage**

```
summariseDrugUtilisation(
  cohort,
  cohortId = NULL,
  strata = list(),
  estimates = c("q25", "median", "q75", "mean", "sd", "count_missing",
               "percentage_missing"),
  ingredientConceptId = NULL,
  conceptSet = NULL,
  indexDate = "cohort_start_date",
  censorDate = "cohort_end_date",
  restrictIncident = TRUE,
  gapEra = 1,
  numberExposures = TRUE,
  numberEras = TRUE,
  daysExposed = TRUE,
  daysPrescribed = TRUE,
```

```

    timeToExposure = TRUE,
    initialExposureDuration = TRUE,
    initialQuantity = TRUE,
    cumulativeQuantity = TRUE,
    initialDailyDose = TRUE,
    cumulativeDose = TRUE
)

```

## Arguments

|                         |                                                                                                                                                                                                                               |
|-------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| cohort                  | A cohort_table object.                                                                                                                                                                                                        |
| cohortId                | A cohort definition id to restrict by. If NULL, all cohorts will be included.                                                                                                                                                 |
| strata                  | A list of variables to stratify results. These variables must have been added as additional columns in the cohort table.                                                                                                      |
| estimates               | Estimates that we want for the columns.                                                                                                                                                                                       |
| ingredientConceptId     | Ingredient OMOP concept that we are interested for the study.                                                                                                                                                                 |
| conceptSet              | List of concepts to be included.                                                                                                                                                                                              |
| indexDate               | Name of a column that indicates the date to start the analysis.                                                                                                                                                               |
| sensorDate              | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.                                                                                                                |
| restrictIncident        | Whether to include only incident prescriptions in the analysis. If FALSE all prescriptions that overlap with the study period will be included.                                                                               |
| gapEra                  | Number of days between two continuous exposures to be considered in the same era.                                                                                                                                             |
| numberExposures         | Whether to include 'number_exposures' (number of drug exposure records between indexDate and sensorDate).                                                                                                                     |
| numberEras              | Whether to include 'number_eras' (number of continuous exposure episodes between indexDate and sensorDate).                                                                                                                   |
| daysExposed             | Whether to include 'days_exposed' (number of days that the individual is in a continuous exposure episode, including allowed treatment gaps, between indexDate and sensorDate; sum of the length of the different drug eras). |
| daysPrescribed          | Whether to include 'days_prescribed' (sum of the number of days for each prescription that contribute in the analysis).                                                                                                       |
| timeToExposure          | Whether to include 'time_to_exposure' (number of days between indexDate and the first episode).                                                                                                                               |
| initialExposureDuration | Whether to include 'initial_exposure_duration' (number of prescribed days of the first drug exposure record).                                                                                                                 |
| initialQuantity         | Whether to include 'initial_quantity' (quantity of the first drug exposure record).                                                                                                                                           |
| cumulativeQuantity      | Whether to include 'cumulative_quantity' (sum of the quantity of the different exposures considered in the analysis).                                                                                                         |

`initialDailyDose` Whether to include 'initial\_daily\_dose\_{unit}' (daily dose of the first considered prescription).

`cumulativeDose` Whether to include 'cumulative\_dose\_{unit}' (sum of the cumulative dose of the analysed drug exposure records).

### Value

A summary of drug utilisation stratified by `cohort_name` and `strata_name`

### Examples

```
library(DrugUtilisation)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()
cdm <- generateIngredientCohortSet(cdm = cdm,
                                  ingredient = "acetaminophen",
                                  name = "dus_cohort")

cdm$dus_cohort |>
  summariseDrugUtilisation(ingredientConceptId = 1125315)
```

---

|                     |                                                                  |
|---------------------|------------------------------------------------------------------|
| summariseIndication | <i>Summarise the indications of individuals in a drug cohort</i> |
|---------------------|------------------------------------------------------------------|

---

### Description

Summarise the observed indications of patients in a drug cohort based on their presence in an indication cohort in a specified time window. If an individual is not in one of the indication cohorts, they will be considered to have an unknown indication if they are present in one of the specified OMOP CDM clinical tables. Otherwise, if they are neither in an indication cohort or a clinical table they will be considered as having no observed indication.

### Usage

```
summariseIndication(
  cohort,
  strata = list(),
  indicationCohortName,
  cohortId = NULL,
  indicationCohortId = NULL,
  indicationWindow = list(c(0, 0)),
  unknownIndicationTable = NULL,
  indexDate = "cohort_start_date",
  mutuallyExclusive = TRUE,
  censorDate = NULL
)
```

**Arguments**

|                                     |                                                                                                                          |
|-------------------------------------|--------------------------------------------------------------------------------------------------------------------------|
| <code>cohort</code>                 | A <code>cohort_table</code> object.                                                                                      |
| <code>strata</code>                 | A list of variables to stratify results. These variables must have been added as additional columns in the cohort table. |
| <code>indicationCohortName</code>   | Name of the cohort table with potential indications.                                                                     |
| <code>cohortId</code>               | A cohort definition id to restrict by. If NULL, all cohorts will be included.                                            |
| <code>indicationCohortId</code>     | The target cohort ID to add indication. If NULL all cohorts will be considered.                                          |
| <code>indicationWindow</code>       | The time window over which to identify indications.                                                                      |
| <code>unknownIndicationTable</code> | Tables in the OMOP CDM to search for unknown indications.                                                                |
| <code>indexDate</code>              | Name of a column that indicates the date to start the analysis.                                                          |
| <code>mutuallyExclusive</code>      | Whether to report indications as mutually exclusive or report them as independent results.                               |
| <code>censorDate</code>             | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.           |

**Value**

A summarised result

**Examples**

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

cdm <- mockDrugUtilisation()

indications <- list(headache = 378253, asthma = 317009)
cdm <- generateConceptCohortSet(cdm = cdm,
                              conceptSet = indications,
                              name = "indication_cohorts")

cdm <- generateIngredientCohortSet(cdm = cdm,
                                 name = "drug_cohort",
                                 ingredient = "acetaminophen")

cdm$drug_cohort |>
  summariseIndication(
    indicationCohortName = "indication_cohorts",
    unknownIndicationTable = "condition_occurrence",
    indicationWindow = list(c(-Inf, 0))
  ) |>
  glimpse()
```

---

```
summariseProportionOfPatientsCovered
```

*Summarise proportion Of patients covered*

---

## Description

Gives the proportion of patients still in observation who are in the cohort on any given day following their first cohort entry. This is known as the “proportion of patients covered” (PPC) method for assessing treatment persistence.

## Usage

```
summariseProportionOfPatientsCovered(
  cohort,
  cohortId = NULL,
  strata = list(),
  followUpDays = NULL
)
```

## Arguments

|                           |                                                                                                                                                                                     |
|---------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| <code>cohort</code>       | A <code>cohort_table</code> object.                                                                                                                                                 |
| <code>cohortId</code>     | A cohort definition id to restrict by. If <code>NULL</code> , all cohorts will be included.                                                                                         |
| <code>strata</code>       | A list of variables to stratify results. These variables must have been added as additional columns in the cohort table.                                                            |
| <code>followUpDays</code> | Number of days to follow up individuals for. If <code>NULL</code> the maximum amount of days from an individuals first cohort start date to their last cohort end date will be used |

## Value

A summarised result

## Examples

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation(numberIndividuals = 100)

result <- cdm$cohort1 |>
  summariseProportionOfPatientsCovered(followUpDays = 365)

tidy(result)
```

---

|                    |                                                               |
|--------------------|---------------------------------------------------------------|
| summariseTreatment | <i>This function is used to summarise treatments received</i> |
|--------------------|---------------------------------------------------------------|

---

## Description

This function is used to summarise treatments received

## Usage

```
summariseTreatment(  
  cohort,  
  window,  
  treatmentCohortName,  
  cohortId = NULL,  
  treatmentCohortId = NULL,  
  strata = list(),  
  indexDate = "cohort_start_date",  
  censorDate = NULL,  
  mutuallyExclusive = FALSE  
)
```

## Arguments

|                     |                                                                                                                          |
|---------------------|--------------------------------------------------------------------------------------------------------------------------|
| cohort              | A cohort_table object.                                                                                                   |
| window              | Time window over which to summarise the treatments.                                                                      |
| treatmentCohortName | Name of a cohort in the cdm that contains the treatments of interest.                                                    |
| cohortId            | A cohort definition id to restrict by. If NULL, all cohorts will be included.                                            |
| treatmentCohortId   | Cohort definition id of interest from treatmentCohortName.                                                               |
| strata              | A list of variables to stratify results. These variables must have been added as additional columns in the cohort table. |
| indexDate           | Name of a column that indicates the date to start the analysis.                                                          |
| censorDate          | Name of a column that indicates the date to stop the analysis, if NULL end of individuals observation is used.           |
| mutuallyExclusive   | Whether to include mutually exclusive treatments or not.                                                                 |

## Value

A summary of treatments stratified by cohort\_name and strata\_name

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()
cdm$cohort1 |>
  summariseTreatment(
    treatmentCohortName = "cohort2",
    window = list(c(0, 30), c(31, 365))
  )
```

---

|                   |                                                           |
|-------------------|-----------------------------------------------------------|
| tableDoseCoverage | <i>Format a dose_coverage object into a visual table.</i> |
|-------------------|-----------------------------------------------------------|

---

**Description**

Format a dose\_coverage object into a visual table.

**Usage**

```
tableDoseCoverage(
  result,
  header = c("variable_name", "estimate_name"),
  groupColumn = c("cdm_name", "ingredient_name"),
  type = "gt",
  hide = c("variable_level", "sample_size"),
  .options = list()
)
```

**Arguments**

|             |                                                                                                                                  |
|-------------|----------------------------------------------------------------------------------------------------------------------------------|
| result      | A summarised_result object.                                                                                                      |
| header      | Columns to use as header. See options with availableTableColumns(result).                                                        |
| groupColumn | Columns to group by. See options with availableTableColumns(result).                                                             |
| type        | Type of table. Check supported types with visOmoResults::tableType().                                                            |
| hide        | Columns to hide from the visualisation. See options with availableTableColumns(result).                                          |
| .options    | A named list with additional formatting options. visOmoResults::tableOptions() shows allowed arguments and their default values. |

**Value**

A table with a formatted version of summariseDrugCoverage() results.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

result <- summariseDoseCoverage(cdm, 1125315)

tableDoseCoverage(result)
```

---

|                  |                                                          |
|------------------|----------------------------------------------------------|
| tableDrugRestart | <i>Format a drug_restart object into a visual table.</i> |
|------------------|----------------------------------------------------------|

---

**Description**

Format a drug\_restart object into a visual table.

**Usage**

```
tableDrugRestart(
  result,
  header = c("cdm_name", "cohort_name"),
  groupColumn = "variable_name",
  type = "gt",
  hide = c("censor_date", "restrict_to_first_discontinuation", "follow_up_days",
    "cohort_table_name", "incident", "switch_cohort_table"),
  .options = list()
)
```

**Arguments**

|             |                                                                                                                                   |
|-------------|-----------------------------------------------------------------------------------------------------------------------------------|
| result      | A summarised_result object.                                                                                                       |
| header      | Columns to use as header. See options with availableTableColumns(result).                                                         |
| groupColumn | Columns to group by. See options with availableTableColumns(result).                                                              |
| type        | Type of table. Check supported types with visOmopResults::tableType().                                                            |
| hide        | Columns to hide from the visualisation. See options with availableTableColumns(result).                                           |
| .options    | A named list with additional formatting options. visOmopResults::tableOptions() shows allowed arguments and their default values. |

**Value**

A table with a formatted version of summariseDrugRestart() results.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

conceptlist <- list(acetaminophen = 1125360, metformin = c(1503297, 1503327))
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "switch_cohort",
                                       conceptSet = conceptlist)

result <- cdm$cohort1 |>
  summariseDrugRestart(switchCohortTable = "switch_cohort")

tableDrugRestart(result)
```

---

|                      |                                                              |
|----------------------|--------------------------------------------------------------|
| tableDrugUtilisation | <i>Format a drug_utilisation object into a visual table.</i> |
|----------------------|--------------------------------------------------------------|

---

**Description**

Format a drug\_utilisation object into a visual table.

**Usage**

```
tableDrugUtilisation(
  result,
  header = c("cdm_name"),
  groupColumn = c("cohort_name", strataColumns(result)),
  type = "gt",
  hide = c("variable_level", "censor_date", "cohort_table_name", "gap_era", "index_date",
           "restrict_incident"),
  .options = list()
)
```

**Arguments**

|             |                                                                                                                                  |
|-------------|----------------------------------------------------------------------------------------------------------------------------------|
| result      | A summarised_result object.                                                                                                      |
| header      | Columns to use as header. See options with availableTableColumns(result).                                                        |
| groupColumn | Columns to group by. See options with availableTableColumns(result).                                                             |
| type        | Type of table. Check supported types with visOmpResults::tableType().                                                            |
| hide        | Columns to hide from the visualisation. See options with availableTableColumns(result).                                          |
| .options    | A named list with additional formatting options. visOmpResults::tableOptions() shows allowed arguments and their default values. |

Value

A table with a formatted version of summariseIndication() results.

Examples

```
library(DrugUtilisation)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()
codelist <- getDrugIngredientCodes(cdm = cdm, name = "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "dus_cohort",
                                       conceptSet = codelist)

drugUse <- cdm$dus_cohort |>
  summariseDrugUtilisation(ingredientConceptId = 1125315)

tableDrugUtilisation(drugUse)
```

---

|                 |                                           |
|-----------------|-------------------------------------------|
| tableIndication | Create a table showing indication results |
|-----------------|-------------------------------------------|

---

Description

Create a table showing indication results

Usage

```
tableIndication(
  result,
  header = c("cdm_name", "cohort_name", strataColumns(result)),
  groupColumn = "variable_name",
  hide = c("window_name", "mutually_exclusive", "unknown_indication_table",
           "censor_date", "cohort_table_name", "index_date", "indication_cohort_name"),
  type = "gt",
  .options = list()
)
```

Arguments

- |             |                                                                                                                                   |
|-------------|-----------------------------------------------------------------------------------------------------------------------------------|
| result      | A summarised_result object.                                                                                                       |
| header      | Columns to use as header. See options with availableTableColumns(result).                                                         |
| groupColumn | Columns to group by. See options with availableTableColumns(result).                                                              |
| hide        | Columns to hide from the visualisation. See options with availableTableColumns(result).                                           |
| type        | Type of table. Check supported types with visOmapResults::tableType().                                                            |
| .options    | A named list with additional formatting options. visOmapResults::tableOptions() shows allowed arguments and their default values. |

**Value**

A table with a formatted version of summariseIndication() results.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

result <- cdm$cohort1 |>
  summariseIndication(
    indicationCohortName = "cohort2",
    indicationWindow = list(c(-30, 0)),
    unknownIndicationTable = "condition_occurrence"
  )

tableIndication(result)
```

---



*Create a table with proportion of patients covered results*

---

**Description**

Create a table with proportion of patients covered results

**Usage**

```
tableProportionOfPatientsCovered(
  result,
  header = c("cohort_name", strataColumns(result)),
  groupColumn = "cdm_name",
  type = "gt",
  hide = c("variable_name", "variable_level", "cohort_table_name"),
  .options = list()
)
```

**Arguments**

|             |                                                                                                                                  |
|-------------|----------------------------------------------------------------------------------------------------------------------------------|
| result      | A summarised_result object.                                                                                                      |
| header      | Columns to use as header. See options with availableTableColumns(result).                                                        |
| groupColumn | Columns to group by. See options with availableTableColumns(result).                                                             |
| type        | Type of table. Check supported types with visOmoResults::tableType().                                                            |
| hide        | Columns to hide from the visualisation. See options with availableTableColumns(result).                                          |
| .options    | A named list with additional formatting options. visOmoResults::tableOptions() shows allowed arguments and their default values. |

**Value**

A table with a formatted version of summariseProportionOfPatientsCovered() results.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

cdm <- generateDrugUtilisationCohortSet(cdm = cdm,
                                       name = "my_cohort",
                                       conceptSet = list(drug_of_interest = c(1503297, 1503327)))

result <- cdm$my_cohort |>
  summariseProportionOfPatientsCovered(followUpDays = 365)

tableProportionOfPatientsCovered(result)
```

---

|                |                                                                  |
|----------------|------------------------------------------------------------------|
| tableTreatment | <i>Format a summarised_treatment result into a visual table.</i> |
|----------------|------------------------------------------------------------------|

---

**Description**

Format a summarised\_treatment result into a visual table.

**Usage**

```
tableTreatment(
  result,
  header = c("cdm_name", "cohort_name"),
  groupColumn = "variable_name",
  type = "gt",
  hide = c("window_name", "mutually_exclusive", "censor_date", "cohort_table_name",
           "index_date", "treatment_cohort_name"),
  .options = list()
)
```

**Arguments**

|             |                                                                                                                                  |
|-------------|----------------------------------------------------------------------------------------------------------------------------------|
| result      | A summarised_result object.                                                                                                      |
| header      | Columns to use as header. See options with availableTableColumns(result).                                                        |
| groupColumn | Columns to group by. See options with availableTableColumns(result).                                                             |
| type        | Type of table. Check supported types with visOmpResults::tableType().                                                            |
| hide        | Columns to hide from the visualisation. See options with availableTableColumns(result).                                          |
| .options    | A named list with additional formatting options. visOmpResults::tableOptions() shows allowed arguments and their default values. |

**Value**

A table with a formatted version of summariseTreatment() results.

**Examples**

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

result <- cdm$cohort1 |>
  summariseTreatment(
    treatmentCohortName = "cohort2",
    window = list(c(0, 30), c(31, 365))
  )

tableTreatment(result)
```

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