Package: DrugUtilisation (via r-universe)

September 10, 2024

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

Version 0.7.1

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 (>= 2)

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Suggests covr, testthat (>= 3.1.5), odbc, CohortSurvival, here, RPostgres, duckdb, knitr, rmarkdown, ggplot2, tibble, gt, flextable, ggtext, scales, tictoc, DBI

Config/testthat/edition 3

Imports CDMConnector (>= 1.4.0), CodelistGenerator (>= 3.1.0), checkmate, dbplyr, dplyr, glue, clock, tidyr, rlang, cli, PatientProfiles (>= 1.0.0), purrr, omopgenerics (>= 0.2.3), visOmopResults, lifecycle, stringr

Depends R (>= 2.10)

LazyData true

URL https://darwin-eu-dev.github.io/DrugUtilisation/

Config/testthat/parallel true

VignetteBuilder knitr

Repository https://darwin-eu-dev.r-universe.dev

RemoteUrl https://github.com/darwin-eu-dev/drugutilisation

RemoteRef HEAD

RemoteSha 08f7a3203c3f8bc90c2cec78056a66cb579280e6

Contents

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

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

`cohort`	Cohort in the cdm.
`ingredientConceptId`	Ingredient OMOP concept that we are interested for the study. It is a compulsory input, no default value is provided.
`conceptSet`	List of concepts to be included. If NULL all the descendants of ingredient concept id will be used.
`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 tables is created.

Value

The same cohort with the added column.

Examples

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

cdm$cohort1 |>
  addCumulativeDose(ingredientConceptId = 1125315)
```

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`	Cohort in the cdm.
`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 tables is created.

Value

The same cohort with the added column.

Examples

```
library(DrugUtilisation)

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

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

`addDailyDose` *add daily dose information to a drug_exposure table*

Description

[Deprecated]

Usage

```
addDailyDose(drugExposure, ingredientConceptId, name = NULL)
```

Arguments

`drugExposure`	drugExposure it must contain drug_concept_id, quantity, drug_exposure_start_date and drug_exposure_end_date as columns
`ingredientConceptId`	ingredientConceptId for which to filter the drugs of interest
`name`	Name of the computed table, if NULL a temporary table will be generated.

Value

same input table

Examples

```
library(DrugUtilisation)
library(dplyr)

cdm <- mockDrugUtilisation()

cdm[["drug_exposure"]] |>
```

```
  filter(drug_concept_id == 2905077) |>
  addDailyDose(ingredientConceptId = 1125315)
```

addDrugUse *Add new columns with drug use related information*

Description

[Deprecated]

Usage

```
addDrugUse(
  cohort,
  cdm = lifecycle::deprecated(),
  ingredientConceptId,
  conceptSet = NULL,
  duration = TRUE,
  quantity = TRUE,
  dose = TRUE,
  gapEra = 0,
  eraJoinMode = "zero",
  overlapMode = "sum",
  sameIndexMode = "sum",
  imputeDuration = "none",
  imputeDailyDose = "none",
  durationRange = c(1, Inf),
  dailyDoseRange = c(0, Inf)
)
```

Arguments

`cohort` Cohort in the cdm

`cdm` deprecated

`ingredientConceptId` Ingredient OMOP concept that we are interested for the study. It is a compulsory input, no default value is provided.

`conceptSet` List of concepts to be included. If NULL all the descendants of ingredient concept id will be used.

`duration` Whether to add duration related columns.

`quantity` Whether to add quantity related columns.

`dose` Whether to add dose related columns.

`gapEra` Number of days between two continuous exposures to be considered in the same era.

`eraJoinMode` How two different continuous exposures are joined in an era. There are four options: "zero" the exposures are joined considering that the period between both continuous exposures the subject is treated with a daily dose of zero. The time between both exposures contributes to the total exposed time. "join" the exposures are joined considering that the period between both continuous exposures the subject is treated with a daily dose of zero. The time between both exposures does not contribute to the total exposed time. "previous" the exposures are joined considering that the period between both continuous exposures the subject is treated with the daily dose of the previous subexposure. The time between both exposures contributes to the total exposed time. "subsequent" the exposures are joined considering that the period between both continuous exposures the subject is treated with the daily dose of the subsequent subexposure. The time between both exposures contributes to the total exposed time.

`overlapMode` How the overlapping between two exposures that do not start on the same day is solved inside a subexposure. There are five possible options: "previous" the considered daily_dose is the one of the earliest exposure. "subsequent" the considered daily_dose is the one of the new exposure that starts in that subexposure. "minimum" the considered daily_dose is the minimum of all of the exposures in the subexposure. "maximum" the considered daily_dose is the maximum of all of the exposures in the subexposure. "sum" the considered daily_dose is the sum of all the exposures present in the subexposure.

`sameIndexMode` How the overlapping between two exposures that start on the same day is solved inside a subexposure. There are three possible options: "minimum" the considered daily_dose is the minimum of all of the exposures in the subexposure. "maximum" the considered daily_dose is the maximum of all of the exposures in the subexposure. "sum" the considered daily_dose is the sum of all the exposures present in the subexposure.

`imputeDuration` Whether/how the duration should be imputed "none", "median", "mean", "mode" or a number

`imputeDailyDose`
Whether/how the daily_dose should be imputed "none", "median", "mean", "mode" or a number

`durationRange` Range between the duration must be comprised. It should be a numeric vector of length two, with no NAs and the first value should be equal or smaller than the second one. It must not be NULL if imputeDuration is not "none". If NULL no restrictions are applied.

`dailyDoseRange` Range between the daily_dose must be comprised. It should be a numeric vector of length two, with no NAs and the first value should be equal or smaller than the second one. It must not be NULL if imputeDailyDose is not "none". If NULL no restrictions are applied.

Value

The same cohort with the added columns.

Examples

```
library(DrugUtilisation)
```

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

cdm <- generateDrugUtilisationCohortSet(cdm, "dus_cohort", codelist)
cdm[["dus_cohort"]] |>
  addDrugUse(ingredientConceptId = 1125315)
```

addDrugUtilisation *Add new columns with drug use related information*

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,
  exposedTime = TRUE,
  timeToExposure = TRUE,
  initialQuantity = TRUE,
  cumulativeQuantity = TRUE,
  initialDailyDose = TRUE,
  cumulativeDose = TRUE,
  nameStyle = "{value}_{concept_name}_{ingredient}",
  name = NULL
)
```

Arguments

`cohort` Cohort in the cdm

`gapEra` Number of days between two continuous exposures to be considered in the same era.

conceptSet List of concepts to be included. If NULL all the descendants of ingredient concept id will be used.

ingredientConceptId Ingredient OMOP concept that we are interested for the study. It is a compulsory input, no default value is provided.

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 add a column with the number of exposures.

numberEras Whether to add a column with the number of eras.

exposedTime Whether to add a column with the number of exposed days.

timeToExposure Whether to add a column with the number of days between indexDate and start of the first exposure.

initialQuantity Whether to add a column with the initial quantity.

cumulativeQuantity Whether to add a column with the cumulative quantity of the identified prescription.

initialDailyDose Whether to add a column with the initial daily dose.

cumulativeDose Whether to add a column with the cumulative dose.

nameStyle Character string to specify the nameStyle of the new columns.

name Name of the new computed cohort table, if NULL a temporary tables is created.

Value

The same cohort with the added columns.

Examples

```
library(DrugUtilisation)

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

cdm <- generateDrugUtilisationCohortSet(cdm, "dus_cohort", codelist)
cdm[["dus_cohort"]] |>
  addDrugUtilisation(ingredientConceptId = 1125315, gapEra = 30)
```

addExposedTime — *To add a new column with the exposed time. To add multiple columns use* `addDrugUtilisation()` *for efficiency.*

Description

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

Usage

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

Arguments

`cohort`	Cohort in the cdm.
`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 tables is created.

Value

The same cohort with the added column.

Examples

```
library(DrugUtilisation)

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

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

addIndication *Add a variable indicating individuals indications*

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,
  name = NULL
)
```

Arguments

`cohort` A cohort table in the cdm.

`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` Date respect to indication will be calculated.

`censorDate` After that day no indication will be considered.

`name` name of permanant table

Value

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

Examples

```
library(DrugUtilisation)
library(CDMConnector)
library(dplyr)

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("indication_cohorts", indicationWindow = list(c(0, 0))) |>
  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

`cohort` Cohort in the cdm.

`ingredientConceptId` Ingredient OMOP concept that we are interested for the study. It is a compulsory input, no default value is provided.

`conceptSet` List of concepts to be included. If NULL all the descendants of ingredient concept id will be used.

`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 tables is created.

Value

The same cohort with the added column.

Examples

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

cdm$cohort1 |>
  addInitialDailyDose(ingredientConceptId = 1125315)
```

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

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`	Cohort in the cdm.
`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 tables is created.

Value

The same cohort with the added column.

Examples

```
library(DrugUtilisation)

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

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

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

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`	Cohort in the cdm.
`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 tables is created.

Value

The same cohort with the added column.

Examples

```
library(DrugUtilisation)

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

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

addNumberExposures

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

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` Cohort in the cdm

`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 tables is created.

Value

The same cohort with the added columns.

Examples

```
library(DrugUtilisation)

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

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

`addRoute` *add route column to a table containing drug_exposure information*

Description

[Deprecated]

Usage

```
addRoute(drugTable)
```

Arguments

`drugTable` Table in the cdm that must contain drug_concept_id

Value

It adds route to the current table

Examples

```
library(DrugUtilisation)
library(dplyr)

cdm <- mockDrugUtilisation()

cdm[["drug_exposure"]] |>
  addRoute()
```

---

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

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`	Cohort in the cdm.
`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 tables is created.

Value

The same cohort with the added column.

Examples

```
library(DrugUtilisation)

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

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

benchmarkDrugUtilisation

Run benchmark of drug utilisation cohort generation

Description

Run benchmark of drug utilisation cohort generation

Usage

```
benchmarkDrugUtilisation(
  cdm,
  numberOfCohort = 1:4,
  indicationCohortName = "cohort1",
  ingredientId = 1125315,
  drugExposureName = "drug_exposure"
)
```

Arguments

`cdm`	A CDM reference object
`numberOfCohort`	Number of cohort to generate for benchmarking. An integer or a vector of integers
`indicationCohortName`	Name of indication cohort table
`ingredientId`	Ingredient OMOP concept that we are interested for the study. It is a compulsory input, no default value is provided.

`drugExposureName`
: Name of drug_exposure table in cdm, the table must contain drug_concept_id, quantity, drug_exposure_start_date and drug_exposure_end_date as columns

Value

a tibble with time taken for different analyses

Examples

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

timings <- benchmarkDrugUtilisation(cdm)

timings
```

cohortGapEra *Get the gapEra used to create a cohort*

Description

Get the gapEra used to create a cohort

Usage

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

Arguments

`cohort`	A `cohort_table` object.
`cohortId`	Integer vector refering to cohortIds from cohort. If NULL all cohort definition ids in settings will be used.

Value

gapEra values for the specific cohortIds

Examples

```
library(CDMConnector)
library(DrugUtilisation)
library(dplyr)

cdm <- mockDrugUtilisation()

druglist <- CodelistGenerator::getDrugIngredientCodes(
  cdm, c("acetaminophen", "metformin")
)

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

cohortGapEra(cdm$drug_cohorts)
```

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

Description

[Deprecated]

Usage

```
dailyDoseCoverage(cdm, ingredientConceptId)
```

Arguments

`cdm`	A cdm reference created using CDMConnector
`ingredientConceptId`	Code indicating the ingredient of interest

Value

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

`defaultTableOptions` *Additional arguments for the table functions.*

Description

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

Usage

```
defaultTableOptions()
```

Value

The default .options named list.

Examples

```
{
  defaultTableOptions()
}
```

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,
  level = c("ATC 1st"),
  doseForm = NULL,
  gapEra = 1,
  durationRange = lifecycle::deprecated(),
  imputeDuration = lifecycle::deprecated(),
  priorUseWashout = lifecycle::deprecated(),
  priorObservation = lifecycle::deprecated(),
  cohortDateRange = lifecycle::deprecated(),
  limit = lifecycle::deprecated()
)
```

Arguments

cdm	A cdm reference.
name	The name of the new cohort table to add to the cdm reference.
atcName	Names of ATC classification of interest.

`level`	ATC level. Can be one or more of "ATC 1st", "ATC 2nd", "ATC 3rd", "ATC 4th", and "ATC 5th"
`doseForm`	Only descendants codes with the specified dose form will be returned. If NULL, descendant codes will be returned regardless of dose form.
`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.
`durationRange`	Deprecated.
`imputeDuration`	Deprecated.
`priorUseWashout`	Deprecated
`priorObservation`	Deprecated.
`cohortDateRange`	Deprecated.
`limit`	Deprecated.

Value

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

Examples

```
library(DrugUtilisation)
library(dplyr)

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,
  durationRange = lifecycle::deprecated(),
  imputeDuration = lifecycle::deprecated(),
  priorUseWashout = lifecycle::deprecated(),
  priorObservation = lifecycle::deprecated(),
  cohortDateRange = lifecycle::deprecated(),
  limit = lifecycle::deprecated()
)
```

Arguments

cdm A cdm reference.

name The name of the new cohort table to add to the cdm reference.

conceptSet The concepts used to create the cohort, provide as a codelist or concept set expression.

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.

durationRange Deprecated.

imputeDuration Deprecated.

priorUseWashout
Deprecated.

priorObservation
Deprecated.

cohortDateRange
Deprecated.

limit Deprecated.

Value

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

Examples

```
library(CDMConnector)
library(DrugUtilisation)
library(dplyr)

cdm <- mockDrugUtilisation()

druglist <- CodelistGenerator::getDrugIngredientCodes(
  cdm, c("acetaminophen", "metformin")
)

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

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,
  doseForm = NULL,
  doseUnit = NULL,
  routeCategory = NULL,
  ingredientRange = c(1, Inf),
  gapEra = 1,
  durationRange = lifecycle::deprecated(),
  imputeDuration = lifecycle::deprecated(),
  priorUseWashout = lifecycle::deprecated(),
  priorObservation = lifecycle::deprecated(),
  cohortDateRange = lifecycle::deprecated(),
  limit = lifecycle::deprecated()
)
```

Arguments

cdm	A cdm reference.
name	The name of the new cohort table to add to the cdm reference.

`ingredient` Accepts both vectors and named lists of ingredient names. For a vector input, e.g., c("acetaminophen", "codeine"), it generates a cohort table with descendant concept codes for each ingredient, assigning unique cohort_definition_id. For a named list input, e.g., list("test_1" = c("simvastatin", "acetaminophen"), "test_2" = "metformin"), 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 cohort_definition_id for each named group.

`doseForm` Only descendants codes with the specified dose form will be returned. If NULL, descendant codes will be returned regardless of dose form.

`doseUnit` Only descendants codes with the specified dose unit will be returned. If NULL, descendant codes will be returned regardless of dose unit

`routeCategory` Only descendants codes with the specified route will be returned. If NULL, descendant codes will be returned regardless of route category.

`ingredientRange`
Used to restrict descendant codes to those associated with a specific number of ingredients. Must be a vector of length two with the first element the minimum number of ingredients allowed and the second the maximum. A value of c(2, 2) would restrict to only concepts associated with two ingredients.

`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.

`durationRange` Deprecated.

`imputeDuration` Deprecated.

`priorUseWashout`
Deprecated

`priorObservation`
Deprecated.

`cohortDateRange`
Deprecated.

`limit` Deprecated.

Value

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

Examples

```
library(DrugUtilisation)
library(dplyr)

cdm <- mockDrugUtilisation()

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

cdm$acetaminophen |>
  glimpse()
```

`mockDrugUtilisation` *It creates a mock database for testing DrugUtilisation package*

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 *Patterns valid to compute daily dose with the associated formula.*

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

Description

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

Usage

```
patternTable(cdm)
```

Arguments

`cdm`	'cdm' object created with CDMConnector::cdm_from_con(). It must must contain 'drug_strength' and 'concept' tables.

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 *Generate a custom ggplot2 from a summarised_result object generated with summariseDrugRestart() function.*

Description

Generate a custom ggplot2 from a summarised_result object generated with summariseDrugRestart() function.

Usage

```
plotDrugRestart(
  result,
  facetX = "variable_name",
  facetY = c("cdm_name", "cohort_name", "strata"),
  colour = "variable_level",
  splitStrata = TRUE
)
```

Arguments

result	A summarised_result object with results from summariseDrugRestart().
facetX	Vector of variables to facet by horizontally. Allowed options are: "cdm_name", "cohort_name", "strata", "variable_name"
facetY	Vector of variables to facet by vertically Allowed options are: "cdm_name", "cohort_name", "strata", "variable_name".
colour	Vector of variables to distinct by colour. Allowed options are: "cdm_name", "cohort_name", "strata", "variable_name", and "variable_level".
splitStrata	Whether to split strata columns.

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)

CDMConnector::cdmDisconnect(cdm = cdm)

## End(Not run)
```

---

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

Description

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

Usage

```
plotIndication(
  result,
  x = "window",
  facet = c("cdm_name", "cohort_name", "strata"),
  color = c("indication"),
  splitStrata = TRUE
)
```

Arguments

`result`	A summarised_result object.
`x`	Variables to be used in the x axis.
`facet`	Variables to be used to facet the plot.
`color`	Variables to be used to color the plot.
`splitStrata`	Whether to split strata.

Value

A ggplot2 object

Examples

```
library(DrugUtilisation)
library(CDMConnector)
library(dplyr)

cdm <- mockDrugUtilisation()
```

```
indications <- list("headache" = 378253, "asthma" = 317009)
cdm <- generateConceptCohortSet(cdm, indications, "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,
  ylim = c(0, NA),
  facet = NULL,
  colour = NULL,
  colour_name = NULL
)
```

Arguments

`result`	Output of summariseProportionOfPatientsCovered
`ylim`	Limits for the Y axis
`facet`	Variables to use for facets
`colour`	Variables to use for colours
`colour_name`	Colour legend name

Value

Plot of proportion Of patients covered over time

plotTreatment *Generate a custom ggplot2 from a summarised_result object generated with summariseTreatment function.*

Description

Generate a custom ggplot2 from a summarised_result object generated with summariseTreatment function.

Usage

```
plotTreatment(
  result,
  facetX = "window_name",
  facetY = c("cdm_name", "cohort_name", "strata"),
  splitStrata = TRUE,
  colour = "treatment"
)
```

Arguments

`result` A summarised_result object with results from summariseDrugRestart().

`facetX` Vector of variables to facet by horizontally. Allowed options are: "cdm_name", "cohort_name", "strata", "variable_name"

`facetY` Vector of variables to facet by vertically Allowed options are: "cdm_name", "cohort_name", "strata", "variable_name".

`splitStrata` Whether to split strata columns.

`colour` Vector of variables to distinct by colour. Allowed options are: "cdm_name", "cohort_name", "strata", "variable_name", and "variable_level".

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)
```

readConceptList *Get concept ids from a provided path to json files*

Description

[Deprecated]

Usage

```
readConceptList(path, cdm)
```

Arguments

path	path to a file or folder containing jsons to be read
cdm	A cdm reference created with CDMConnector

Value

list of concept_ids and respective concept_ids of interest

Examples

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

codelist <- readConceptList(
  path = system.file("concepts", package = "DrugUtilisation"), cdm = cdm
)
```

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 in a cdm reference.

`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` IDs of the cohorts to modify. The default is NULL meaning all cohorts will be used; otherwise, only the specified cohorts will be modified, and the rest will remain unchanged.

`name` Name of the table with the filtered cohort records. The default name is the original cohort name, where the original table will be overwritten.

Value

The cohort table having applied the date requirement.

Examples

```
library(DrugUtilisation)
library(dplyr)

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 in a cdm reference.
`cohortId`	IDs of the cohorts to modify. The default is NULL meaning all cohorts will be used; otherwise, only the specified cohorts will be modified, and the rest will remain unchanged.
`name`	Name of the table with the filtered cohort records. The default name is the original cohort name, where the original table will be overwritten.

Value

The cohort table having applied the first entry requirement.

Examples

```
library(DrugUtilisation)
library(dplyr)

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 in a cdm reference.
days	Number of days of prior observation required before cohort start date. Any records with fewer days will be dropped.
cohortId	IDs of the cohorts to modify. The default is NULL meaning all cohorts will be used; otherwise, only the specified cohorts will be modified, and the rest will remain unchanged.
name	Name of the table with the filtered cohort records. The default name is the original cohort name, where the original table will be overwritten.

Value

The cohort table having applied the prior observation requirement.

Examples

```
library(DrugUtilisation)
library(dplyr)

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

`cohort` A cohort table in a cdm reference.

`days` 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 Inf will lead to the same result as that from using the `requireIsFirstDrugEntry` function (with only an individual´s first cohort record kept).

`cohortId` IDs of the cohorts to modify. The default is NULL meaning all cohorts will be used; otherwise, only the specified cohorts will be modified, and the rest will remain unchanged.

`name` Name of the table with the filtered cohort records. The default name is the original cohort name, where the original table will be overwritten.

Value

The cohort table having applied the washout requirement.

Examples

```
library(DrugUtilisation)
library(dplyr)

cdm <- mockDrugUtilisation()

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

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

`stratifyByUnit` *Function to stratify a conceptSet by unit*

Description

[Deprecated]

Usage

```
stratifyByUnit(conceptSet, cdm, ingredientConceptId)
```

Arguments

conceptSet	List of concept sets
cdm	cdm reference
ingredientConceptId	ConceptId that refers to an ingredient

Value

The conceptSet stratified by unit

Examples

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

codelist <- CodelistGenerator::getDrugIngredientCodes(cdm, "acetaminophen")

codelistStratified <- stratifyByUnit(codelist, cdm, 1125315)

codelistStratified
```

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

`cdm`	A cdm reference created using CDMConnector.
`ingredientConceptId`	Code indicating the ingredient of interest.
`estimates`	Estimates to obtain.
`sampleSize`	Maximum number of records of an ingredient to estimate dose coverage. If an ingredient has more, a random sample equal to `sampleSize` will be considered. If NULL, 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, 1125315)
```

summariseDrugRestart *Summarise the drug restart per window.*

Description

[Experimental]

Usage

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

Arguments

`cohort` A cohort table.

`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.

`strata` List with column names or vectors of column names groups to stratify results by.

`followUpDays` A vector of number of days to follow up. It can be multiple values.

`censorDate` Date of censoring. Individuals are always censored at the end of observation.

`restrictToFirstDiscontinuation` 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 window.

Examples

```
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")

tableDrugRestart(result)

CDMConnector::cdmDisconnect(cdm = cdm)
```

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

Description

[Deprecated]

Usage

```
summariseDrugUse(
  cohort,
  cdm = lifecycle::deprecated(),
  strata = list(),
  estimates = c("min", "q05", "q25", "median", "q75", "q95", "max", "mean", "sd",
    "count_missing", "percentage_missing"),
  minCellCount = lifecycle::deprecated()
)
```

Arguments

`cohort`	Cohort with drug use variables and strata.
`cdm`	Deprecated.
`strata`	Stratification list.
`estimates`	Estimates that we want for the columns.
`minCellCount`	Deprecated.

Value

A summary of the drug use stratified by cohort_name and strata_name

Examples

```
library(DrugUtilisation)
library(PatientProfiles)

cdm <- mockDrugUtilisation()
codelist <- CodelistGenerator::getDrugIngredientCodes(cdm, "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(
  cdm, "dus_cohort", codelist
)
cdm[["dus_cohort"]] <- cdm[["dus_cohort"]] |>
  addDrugUse(ingredientConceptId = 1125315)
result <- summariseDrugUse(cdm[["dus_cohort"]])
print(result)

cdm[["dus_cohort"]] <- cdm[["dus_cohort"]] |>
  addSex() |>
  addAge(ageGroup = list("<40" = c(0, 39), ">=40" = c(40, 150)))

cdm[["dus_cohort"]] |>
  summariseDrugUse(strata = list("age_group", "sex", c("age_group", "sex")))
```

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,
  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,
  exposedTime = TRUE,
  timeToExposure = TRUE,
  initialQuantity = TRUE,
  cumulativeQuantity = TRUE,
  initialDailyDose = TRUE,
  cumulativeDose = TRUE
)
```

Arguments

`cohort`	Cohort with drug use variables and strata.
`strata`	Stratification list.
`estimates`	Estimates that we want for the columns.
`ingredientConceptId`	Ingredient OMOP concept that we are interested for the study. It is a compulsory input, no default value is provided.
`conceptSet`	List of concepts to be included. If NULL all the descendants of ingredient concept id will be used.
`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.

`gapEra` Number of days between two continuous exposures to be considered in the same era.

`numberExposures`
Whether to add a column with the number of exposures.

`numberEras` Whether to add a column with the number of eras.

`exposedTime` Whether to add a column with the number of exposed days.

`timeToExposure` Whether to add a column with the number of days between indexDate and start of the first exposure.

`initialQuantity`
Whether to add a column with the initial quantity.

`cumulativeQuantity`
Whether to add a column with the cumulative quantity of the identified prescription.

`initialDailyDose`
Whether to add a column with the initial daily dose.

`cumulativeDose` Whether to add a column with the cumulative dose.

Value

A summary of drug utilisation stratified by cohort_name and strata_name

Examples

```
library(DrugUtilisation)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()
codelist <- CodelistGenerator::getDrugIngredientCodes(cdm, "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(
  cdm, "dus_cohort", codelist
)
cdm[["dus_cohort"]] %>%
  summariseDrugUtilisation(ingredientConceptId = 1125315)
```

`summariseIndication` *Summarise the indications of individuals in a drug cohort*

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,
  indicationCohortId = NULL,
  indicationWindow = list(c(0, 0)),
  unknownIndicationTable = NULL,
  indexDate = "cohort_start_date",
  censorDate = NULL
)
```

Arguments

`cohort` A cohort table in a cdm reference.

`strata` List of variables to stratify results by. These variables must be present in the cohort table.

`indicationCohortName` Name of the cohort table with potential indications.

`indicationCohortId` The target cohort ID to add indication. If NULL all cohorts will be considered.

`indicationWindow` The time window over which to identify indications.

`unknownIndicationTable` Tables in the OMOP CDM to search for unknown indications.

`indexDate` A date variable in the cohort table for which indications will be found relative to.

`censorDate` After that day no indication will be considered.

Value

A summarised result

Examples

```
library(DrugUtilisation)
library(CDMConnector)
library(dplyr)

cdm <- mockDrugUtilisation()

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

cohort	A cohort table
cohortId	Cohort definition ID of interest. If NUll, results for all cohorts will be returned.
strata	List of variables to stratify by.
followUpDays	Number of days to follow up individuals for. If NULL 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

summariseTreatment *This function is used to summarise treatments received*

Description

This function is used to summarise treatments received

Usage

```
summariseTreatment(
  cohort,
  window,
  treatmentCohortName,
  treatmentCohortId = NULL,
  strata = list(),
  indexDate = "cohort_start_date",
  censorDate = NULL,
  minCellCount = lifecycle::deprecated()
)
```

Arguments

`cohort`	A cohort table in a cdm reference.
`window`	Time window over which to summarise the treatments.
`treatmentCohortName`	Name of a cohort in the cdm that contains the treatments of interest.
`treatmentCohortId`	Cohort definition id of interest from treatmentCohortName.
`strata`	List with column names or vectors of column names groups to stratify results by.
`indexDate`	Variable in x that contains the date to compute the intersection.
`censorDate`	Whether to censor overlap events at a specific date or a column date of x. If NULL, end of observation will be used.
`minCellCount`	`\ifelse{html}{\href{https://lifecycle.r-lib.org/articles/stages.html#deprecated}{\fi`

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 *Format a dose_coverage object into a visual table.*

Description

[Experimental]

Usage

```
tableDoseCoverage(
  result,
  header = c("variable", "estimate"),
  splitStrata = TRUE,
  ingridientName = TRUE,
  cdmName = TRUE,
  groupColumn = NULL,
  type = "gt",
  formatEstimateName = c(`N (%)` = "<count_missing> (<percentage_missing> %)", N =
    "<count>", `Mean (SD)` = "<mean> (<sd>)", `Median (Q25 - Q75)` =
    "<median> (<q25> - <q75>)"),
  .options = list()
)
```

Arguments

`result` A summarised_result object with results from summariseDoseCoverage().

`header` A vector containing which elements should go into the header in order. Allowed are: `cdm_name`, `group`, `strata`, `variable`, and `estimate`.

`splitStrata` If TRUE strata columns will be split.

`ingridientName` If TRUE cohort names will be displayed.

`cdmName` If TRUE database names will be displayed.

`groupColumn` Column to use as group labels.

`type` Type of desired formatted table, possibilities: "gt", "flextable", "tibble".

`formatEstimateName`
Named list of estimate name's to join, sorted by computation order. Indicate estimate_name's between <...>.

`.options` Named list with additional formatting options. DrugUtilisation::defaultTableOptions() 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 *Format a drug_restart object into a visual table.*

Description

[Experimental]

Usage

```
tableDrugRestart(
  result,
  header = c("strata"),
  splitStrata = TRUE,
  cohortName = TRUE,
  cdmName = TRUE,
  groupColumn = c("cdm_name", "cohort_name"),
  type = "gt",
  formatEstimateName = c(`N (%)` = "<count> (<percentage> %)"),
  .options = list()
)
```

Arguments

`result`	A summarised_result object with results from summariseDrugRestart().
`header`	A vector containing which elements should go into the header in order. Allowed values: `cdm_name`, `cohort_name`, `strata`, `variable`, `estimate`.
`splitStrata`	If TRUE strata columns will be split.
`cohortName`	If TRUE cohort names will be displayed.
`cdmName`	If TRUE database names will be displayed.
`groupColumn`	Column to use as group labels. Allowed values: `cdm_name`, `cohort_name`, `strata`, `variable_name`, `variable_level`, `estimate_name`.

`type` Type of desired formatted table, possibilities: "gt", "flextable", "tibble".

`formatEstimateName` Named list of estimate name's to join, sorted by computation order. Indicate estimate_name's between <...>.

`.options` Named list with additional formatting options. DrugUtilisation::defaultTableOptions() shows allowed arguments and their default values.

Value

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

Examples

```
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")

tableDrugRestart(result)

CDMConnector::cdmDisconnect(cdm = cdm)
```

tableDrugUtilisation *Format a drug_utilisation object into a visual table.*

Description

[Experimental]

Usage

```
tableDrugUtilisation(
  result,
  header = c("group", "strata"),
  splitStrata = TRUE,
  cohortName = TRUE,
  cdmName = TRUE,
  conceptSet = TRUE,
  ingredient = TRUE,
  groupColumn = NULL,
  type = "gt",
 formatEstimateName = c(`N (%)` = "<count_missing> (<percentage_missing> %)", N =
    "<count>", `Mean (SD)` = "<mean> (<sd>)", `Median (Q25 - Q75)` =
    "<median> (<q25> - <q75>)"),
  .options = list()
)
```

Arguments

`result`	A summarised_result object with results from summariseDrugUtilisation().
`header`	A vector containing which elements should go into the header in order. Allowed are: `cdm_name`, `group`, `strata`, `variable`, `estimate`.
`splitStrata`	If TRUE strata columns will be split.
`cohortName`	If TRUE cohort names will be displayed.
`cdmName`	If TRUE database names will be displayed.
`conceptSet`	If TRUE concept sets name will be displayed.
`ingredient`	If TRUE ingredients names will be displayed for dose calculation.
`groupColumn`	Column to use as group labels, these can be: "cdm_name", "cohort_name", "concept_set", "variable_name", and/or "ingredient". If strata is split, any of the levels can be used, otherwise "strata_name" and "strata_level" can be used for table group format.
`type`	Type of desired formatted table, possibilities: "gt", "flextable", "tibble".
`formatEstimateName`	Named list of estimate name's to join, sorted by computation order. Indicate estimate_name's between <...>.
`.options`	Named list with additional formatting options. DrugUtilisation::defaultTableOptions() 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 <- CodelistGenerator::getDrugIngredientCodes(cdm, "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm, "dus_cohort", codelist)
cdm[["dus_cohort"]] %>%
  summariseDrugUtilisation(ingredientConceptId = 1125315) |>
  tableDrugUtilisation()
```

tableIndication *Create a table showing indication results*

Description

[Experimental]

Usage

```
tableIndication(
  result,
  header = c("group", "strata"),
  splitStrata = TRUE,
  cohortName = TRUE,
  cdmName = TRUE,
  groupColumn = "variable_name",
  type = "gt",
  .options = list()
)
```

Arguments

`result`	A summarised_result created by summariseIndication().
`header`	A vector containing which elements should go into the header in order. Allowed are: `cdm_name`, `group`, `strata`, `variable`.
`splitStrata`	If TRUE strata columns will be split.
`cohortName`	If TRUE cohort names will be displayed.
`cdmName`	If TRUE database names will be displayed.
`groupColumn`	Column to use as group labels.
`type`	Type of desired formatted table, possibilities: "gt", "flextable", "tibble".
`.options`	Named list with additional formatting options. DrugUtilisation::defaultTableOptions() 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, type = "tibble")
```

---

tableProportionOfPatientsCovered

Create a table with proportion of patients covered results

Description

[Experimental]

Usage

```
tableProportionOfPatientsCovered(
  result,
  times = NULL,
  header = c("group", "strata"),
  splitStrata = TRUE,
  cohortName = TRUE,
  cdmName = TRUE,
  groupColumn = "variable_name",
  type = "gt",
  .options = list()
)
```

Arguments

`result`	A summarised_result object with results from summariseProportionOfPatientsCovered().
`times`	Days to include in the table. If NULL all days will be included.
`header`	A vector containing which elements should go into the header in order. Allowed are: `cdm_name`, `group`, `strata`, `variable`.
`splitStrata`	If TRUE strata columns will be split.

`cohortName` If TRUE cohort names will be displayed.

`cdmName` If TRUE database names will be displayed.

`groupColumn` Column to use as group labels.

`type` Type of desired formatted table, possibilities: "gt", "flextable", "tibble".

`.options` Named list with additional formatting options. DrugUtilisation::defaultTableOptions() shows allowed arguments and their default values.

Value

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

`tableTreatment` *Format a summarised_treatment result into a visual table.*

Description

[Experimental]

Usage

```
tableTreatment(
  result,
  header = c("window_name"),
  splitStrata = TRUE,
  cdmName = TRUE,
  groupColumn = c("cdm_name", "cohort_name"),
  type = "gt",
  formatEstimateName = c(`N (%)` = "<count> (<percentage> %)"),
  .options = list()
)
```

Arguments

`result` A summarised_result object with results from summariseTreatmentFromCohort() or summariseTreatmentFromConceptSet().

`header` A vector containing which elements should go into the header in order. Allowed values: `cdm_name`, `cohort_name`, `strata`, `variable`, `estimate` and `window_name`.

`splitStrata` If TRUE strata columns will be split.

`cdmName` If TRUE database names will be displayed.

`groupColumn` Column to use as group labels. Allowed values: `cdm_name`, `cohort_name`, `strata`, `variable`, `estimate` and `window_name`.

`type` Type of desired formatted table, possibilities: "gt", "flextable", "tibble".

`formatEstimateName`
Named list of estimate name's to join, sorted by computation order. Indicate estimate_name's between <...>.

`.options` Named list with additional formatting options. DrugUtilisation::defaultTableOptions() 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)
```

Index