

Package ‘DrugUtilisation’

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

Version 0.5.0

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.

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addDailyDose	<i>add daily dose information to a drug_exposure table</i>
--------------	--

Description

add daily dose information to a drug_exposure table

Usage

```
addDailyDose(
  drugExposure,
  cdm = attr(drugExposure, "cdm_reference"),
  ingredientConceptId
)
```

Arguments

drugExposure drugExposure it must contain drug_concept_id, quantity, drug_exposure_start_date and drug_exposure_end_date as columns

cdm A cdm reference

ingredientConceptId ingredientConceptId for which to filter the drugs of interest

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

Add new columns with drug use related information

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)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()
cdm <- generateDrugUtilisationCohortSet(
  cdm, "dus_cohort", getDrugIngredientCodes(cdm, name = "acetaminophen")
)
cdm[["dus_cohort"]] %>%
  addDrugUse(cdm, ingredientConceptId = 1125315)
  
```

addIndication *Get indication for a target cohort*

Description

Get indication for a target cohort

Usage

```

addIndication(
  x,
  cdm = lifecycle::deprecated(),
  indicationCohortName,
  indicationGap = 0,
  unknownIndicationTable = NULL,
  indicationDate = "cohort_start_date"
)
  
```

Arguments

x Table in the cdm
cdm A cdm reference created using CDMConnector
indicationCohortName Name of indication cohort table
indicationGap Gap between the event and the indication
unknownIndicationTable Tables to search unknown indications
indicationDate Date of the indication

Value

Same cohort adding the indications

Examples

```

library(DrugUtilisation)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()

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

acetaminophen <- getDrugIngredientCodes(cdm, "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm, "drug_cohort", acetaminophen)

cdm[["drug_cohort"]] %>%
  addIndication(cdm, "indication_cohorts", indicationGap = c(0, 30, 365))
  
```

addRoute

add route column to a table containing drug_exposure information

Description

add route column to a table containing drug_exposure information

Usage

```
addRoute(drugTable, cdm = attr(drugTable, "cdm_reference"))
```

Arguments

drugTable Table in the cdm that must contain drug_concept_id
cdm 'cdm' object created with CDMConnector::cdm_from_con(). It must contain 'concept_relationship' table.

Value

It adds route to the current table

Examples

```
library(DrugUtilisation)
library(dplyr)

cdm <- mockDrugUtilisation()

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

benchmarkDUS

Run benchmark of drug utilisation cohort generation

Description

Run benchmark of drug utilisation cohort generation

Usage

```
benchmarkDUS(  
  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

```
cdm <- DrugUtilisation::mockDrugUtilisation()
timings <- DrugUtilisation::benchmarkDUS(cdm)
```

<code>dailyDoseCoverage</code>	<i>Check coverage of daily dose computation in a sample of the cdm for selected concept sets and ingredient</i>
--------------------------------	---

Description

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

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

Examples

```
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

dailyDoseCoverage(cdm, 1125315)
```

```
generateDrugUtilisationCohortSet
```

Generates a cohort of the drug use of a certain list of concepts.

Description

Generates a cohort of the drug use of a certain list of concepts.

Usage

```
generateDrugUtilisationCohortSet(
  cdm,
  name,
  conceptSet,
  durationRange = c(1, Inf),
  imputeDuration = "none",
  gapEra = 0,
  priorUseWashout = 0,
  priorObservation = 0,
  cohortDateRange = as.Date(c(NA, NA)),
  limit = "all"
)
```

Arguments

cdm	A cdm_reference object.
name	Name of the GeneratedCohortSet
conceptSet	Named list of concept sets.
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 is only required if imputeDuration = TRUE. If NULL no restrictions are applied.
imputeDuration	Whether/how the duration should be imputed "none", "median", "mean", "mode", or it can be a count
gapEra	Number of days between two continuous exposures to be considered in the same era.

priorUseWashout	Prior days without exposure.
priorObservation	Minimum number of days of prior observation required for the incident eras to be considered.
cohortDateRange	Range for cohort_start_date and cohort_end_date
limit	Choice on how to summarise the exposures. There are two options: "all" we summarise the output will be a summary of the exposed eras of each individual. Each individual can contribute multiple times. "first" we only consider the first observable era of each individual that fulfills the criteria provided in previous parameters. In this case each individual can not contribute with multiple rows.

Value

The function returns the 'cdm' object with the created tables as references of the object.

Examples

```
library(CodelistGenerator)
library(CDMConnector)
library(DrugUtilisation)

cdm <- mockDrugUtilisation()

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

cdm <- generateDrugUtilisationCohortSet(
  cdm = cdm,
  name = "drug_cohorts",
  conceptSet = druglist,
  priorObservation = 365
)

cdm[["drug_cohorts"]]

cohortSet(cdm[["drug_cohorts"]])

cohortCount(cdm[["drug_cohorts"]])

cohortAttrition(cdm[["drug_cohorts"]])
```

indicationToStrata	<i>Create new variables summarising the data of indication that can be used as stratification columns</i>
--------------------	---

Description

Create new variables summarising the data of indication that can be used as stratification columns

Usage

```
indicationToStrata(  
  cohort,  
  indicationVariables = indicationColumns(cohort),  
  keep = FALSE  
)
```

Arguments

cohort	A cohort in the cdm
indicationVariables	Indication variables that we want to join
keep	Whether to keep the prior indication variables or not

Value

description The cohort with the new variable

Examples

```
library(DrugUtilisation)  
  
cdm <- mockDrugUtilisation()  
cdm[["cohort1"]] <- cdm[["cohort1"]] %>%  
  addIndication(cdm, "cohort2") %>%  
  indicationToStrata()
```

mockDrugUtilisation *It creates a mock database for testing drugutilisation package*

Description

It creates a mock database for testing drugutilisation package

Usage

```

mockDrugUtilisation(
  connectionDetails = list(con = DBI::dbConnect(duckdb::duckdb(), ":memory:"),
    writeSchema = "main"),
  numberIndividuals = 10,
  seed = 1,
  concept = NULL,
  concept_ancestor = NULL,
  drug_strength = NULL,
  person = NULL,
  observation_period = NULL,
  drug_exposure = NULL,
  condition_occurrence = NULL,
  observation = NULL,
  concept_relationship = NULL,
  extraTables = list(),
  ...
)

```

Arguments

connectionDetails	Details of the connection
numberIndividuals	Number of individuals in the mock cdm
seed	Seed for the random numbers
concept	A concept tibble, if NULL a mock one is created
concept_ancestor	A concept_ancestor tibble, if NULL a mock one is created
drug_strength	A drug_strength tibble, if NULL a mock one is created
person	A person tibble, if NULL a mock one is created
observation_period	A observation_period tibble, if NULL a mock one is created
drug_exposure	A drug_exposure tibble, if NULL a mock one is created
condition_occurrence	A condition_occurrence tibble, if NULL a mock one is created
observation	A observation tibble, if NULL a mock one is created
concept_relationship	A concept_relationship tibble, if NULL a mock one is created.
extraTables	Extra tibbles to be instantiated that are not cohorts or cdm tables
...	Cohorts can be added to the cdm reference, cohort1 and cohort2 will be created if not provided

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 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)
```

readConceptList	<i>Get concept ids from a provided path to json files</i>
-----------------	---

Description

Get concept ids from a provided path to json files

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
)
```

stratifyByUnit	<i>Function to stratify a conceptSet by unit</i>
----------------	--

Description

Function to stratify a conceptSet by unit

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)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()

codelist <- getDrugIngredientCodes(cdm, "acetaminophen")

codelistStratified <- stratifyByUnit(codelist, cdm, 1125315)

codelistStratified
```

summariseCharacteristicsFromCodelist	<i>Summarise a cohort from multipl codelist and windows</i>
--------------------------------------	---

Description

Summarise a cohort from multipl codelist and windows

Usage

```
summariseCharacteristicsFromCodelist(
  cohort,
  cdm = lifecycle::deprecated(),
  conceptSet,
  strata = list(),
  window = list(c(-Inf, -366), c(-365, -31), c(-30, -1), c(0, 0), c(1, 30), c(31, 365),
    c(366, Inf)),
  overlap = TRUE,
  minCellCount = lifecycle::deprecated()
)
```

Arguments

cohort	Cohort to summarise
cdm	cdm_reference
conceptSet	A list of concept sets
strata	Stratification list
window	Windows to characterize
overlap	Whether we consider episodes (overlap = TRUE) or incident (overlap = FALSE)
minCellCount	Minimum cell counts

Value

A SummarisedResults object that contains the characterization

summariseDrugUse	<i>This function is used to summarise the dose table over multiple cohorts.</i>
------------------	---

Description

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

Usage

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


Arguments

cohort	Cohort with drug use variables and strata
cdm	cdm_reference generated by CDMConnector
strata	Stratification list
drugUseEstimates	Estimates that we want for the columns
minCellCount	Below this number counts will be suppressed

Value

A summary of the drug use stratified by cohort_name and strata_name

Examples

```
library(DrugUtilisation)
library(PatientProfiles)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()
cdm <- generateDrugUtilisationCohortSet(
  cdm, "dus_cohort", getDrugIngredientCodes(cdm, "acetaminophen")
)
cdm[["dus_cohort"]] <- cdm[["dus_cohort"]] %>%
  addDrugUse(cdm, 1125315)
result <- summariseDrugUse(cdm[["dus_cohort"]], cdm)
print(result)

cdm[["dus_cohort"]] <- cdm[["dus_cohort"]] %>%
  addSex(cdm) %>%
  addAge(cdm, ageGroup = list("<40" = c(0, 30), ">40" = c(40, 150)))

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

summariseIndication	<i>This function is used to summarise the indication table over multiple cohorts.</i>
---------------------	---

Description

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

Usage

```
summariseIndication(
  cohort,
  cdm = lifecycle::deprecated(),
  strata = list(),
  minCellCount = lifecycle::deprecated()
)
```

Arguments

cohort	Cohort with indications and strata
cdm	cdm_reference created by CDMConnector
strata	Stratification list
minCellCount	Minimum counts that a group can have. Cohorts with less counts than this value are obscured.

Value

A Tibble with 4 columns: cohort_definition_id, variable, estimate and value. There will be one row for each cohort, variable and cohort combination.

Examples

```
library(DrugUtilisation)
library(PatientProfiles)
library(CodelistGenerator)

cdm <- mockDrugUtilisation()
indications <- list("headache" = 378253, "asthma" = 317009)
cdm <- generateConceptCohortSet(cdm, indications, "indication_cohorts")
acetaminophen <- getDrugIngredientCodes(cdm, "acetaminophen")
cdm <- generateDrugUtilisationCohortSet(cdm, "drug_cohort", acetaminophen)
cdm[["drug_cohort"]] <- cdm[["drug_cohort"]] %>%
  addIndication(cdm, "indication_cohorts", indicationGap = c(0, 30, 365))

summariseIndication(cdm[["drug_cohort"]], cdm)

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

summariseIndication(
  cdm[["drug_cohort"]], cdm, strata = list(
    "age_group" = "age_group", "age_group and sex" = c("age_group", "sex")
  )
)
```

```
summariseTreatmentFromCohort
```

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

Description

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

Usage

```
summariseTreatmentFromCohort(  
  cohort,  
  strata = list(),  
  window,  
  treatmentCohortName,  
  treatmentCohortId = NULL,  
  combination = FALSE,  
  minCellCount = 5  
)
```

Arguments

cohort	Cohort with drug use variables and strata.
strata	Stratification list.
window	Window where to summarise the treatments.
treatmentCohortName	Name of a cohort in the cdm that contains the interest treatments.
treatmentCohortId	Cohort definition id of interest from treatmentCohortName.
combination	Whether to include combination treatments.
minCellCount	Below this number counts will be suppressed.

Value

A summary of the drug use stratified by cohort_name and strata_name

Examples

```
library(DrugUtilisation)  
library(PatientProfiles)  
library(CodeListGenerator)  
  
cdm <- mockDrugUtilisation()  
cdm <- generateDrugUtilisationCohortSet(  
  cdm, "dus_cohort", getDrugIngredientCodes(cdm, "acetaminophen")
```

```

)
cdm[["dus_cohort"]] <- cdm[["dus_cohort"]] %>%
  addDrugUse(cdm, 1125315)
result <- summariseDrugUse(cdm[["dus_cohort"]], cdm)
print(result)

cdm[["dus_cohort"]] <- cdm[["dus_cohort"]] %>%
  addSex(cdm) %>%
  addAge(cdm, ageGroup = list("<40" = c(0, 30), ">40" = c(40, 150)))

summariseDrugUse(
  cdm[["dus_cohort"]], cdm, strata = list(
    "age_group" = "age_group", "sex" = "sex",
    "age_group and sex" = c("age_group", "sex")
  )
)

```

```
summariseTreatmentFromConceptSet
```

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

Description

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

Usage

```

summariseTreatmentFromConceptSet(
  cohort,
  strata = list(),
  window,
  treatmentConceptSet,
  combination = FALSE,
  minCellCount = 5
)

```

Arguments

cohort	Cohort with drug use variables and strata.
strata	Stratification list.
window	Window where to summarise the treatments.
treatmentConceptSet	Concept set list to summarise.
combination	Whether to include combination treatments.
minCellCount	Below this number counts will be suppressed.

Value

A summary of the drug use stratified by cohort_name and strata_name

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