

Package ‘PhenotypeR’

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Type Package

Title Assess Study Cohorts Using a Common Data Model

Version 0.5.0

Description Phenotype study cohorts in data mapped to the Observational Medical Outcomes Partnership Common Data Model. Diagnostics are run at the database, code list, cohort, and population level to assess whether study cohorts are ready for research.

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addCodelistAttribute *Adds the cohort_codelist attribute to a cohort*

Description

addCodelistAttribute() allows the users to add a codelist to a cohort in OMOP CDM.

This is particularly important for the use of codelistDiagnostics(), as the underlying assumption is that the cohort that is fed into codelistDiagnostics() has a cohort_codelist attribute attached to it.

Usage

```
addCodelistAttribute(cohort, codelist, cohortName = names(codelist))
```

Arguments

cohort	Cohort table in a cdm reference
codelist	Named list of concepts
cohortName	For each element of the codelist, the name of the cohort in cohort to which the codelist refers

Value

A cohort

Examples

```
library(omock)
library(CohortConstructor)
library(PhenotypeR)

cdm <- mockCdmFromDataset(source = "duckdb")
cdm$warfarin <- conceptCohort(cdm,
                             conceptSet = list(warfarin = c(1310149L,
                                                             40163554L)),
                             name = "warfarin")

cohort <- addCodelistAttribute(cohort = cdm$warfarin,
                              codelist = list("warfarin" = c(1310149L, 40163554L)))
attr(cohort, "cohort_codelist")

CDMConnector::cdmDisconnect(cdm)
```

clinicalDescriptionSpecification

Clinical description specification

Description

Clinical description specification

Usage

```
clinicalDescriptionSpecification(path = NULL)
```

Arguments

path	If NULL, specification will be returned as an R object. If a path to a directory is provided the specification will be exported.
------	--

Value

JSON specification for clinical descriptions

codelistDiagnostics *Run codelist-level diagnostics*

Description

codelistDiagnostics() runs phenotypeR diagnostics on the cohort_codelist attribute on the cohort. Thus codelist attribute of the cohort must be populated. If it is missing then it could be populated using addCodelistAttribute() function.

Furthermore codelistDiagnostics() requires achilles tables to be present in the cdm so that concept counts could be derived.

Usage

```
codelistDiagnostics(
  cohort,
  cohortId = NULL,
  achillesCodeUse = FALSE,
  orphanCodeUse = TRUE,
  cohortCodeUse = TRUE,
  drugDiagnostics = FALSE,
  drugDiagnosticsSample = 20000,
  measurementDiagnostics = FALSE,
  measurementDiagnosticsSample = 20000
)
```

Arguments

cohort	A cohort table in a cdm reference. The cohort_codelist attribute must be populated. The cdm reference must contain achilles tables as these will be used for deriving concept counts.
cohortId	Specific cohort definition ID for which to run codelist diagnostics.
achillesCodeUse	Whether to run CodelistGenerator::summariseAchillesCodeUse() (TRUE) or not (FALSE).
orphanCodeUse	Whether to run CodelistGenerator::summariseOrphanCodeUse() (TRUE) or not (FALSE).
cohortCodeUse	Whether to run CodelistGenerator::summariseCohortCodeUse() (TRUE) or not (FALSE).
drugDiagnostics	Whether to run drug diagnostics (TRUE) or not (FALSE). Note that, if set to TRUE, the diagnostics will only run if the cohort code list contains drug codes.

drugDiagnosticsSample

The number of people to take a random sample for drug diagnostics. If `drugDiagnosticsSample = NULL`, no sampling will be performed. If `drugDiagnosticsSample = 0` drug diagnostics will not be run.

measurementDiagnostics

Whether to run measurement diagnostics (TRUE) or not (FALSE). Note that, if set to TRUE, the diagnostics will only run if the cohort code list contains measurement codes.

measurementDiagnosticsSample

The number of people to take a random sample for measurement diagnostics. If `measurementDiagnosticsSample = NULL`, no sampling will be performed. If `measurementDiagnosticsSample = 0` measurement diagnostics will not be run.

Value

A summarised result

Examples

```
library(omock)
library(CohortConstructor)
library(PhenotypeR)

cdm <- mockCdmFromDataset(source = "duckdb")
cdm$warfarin <- conceptCohort(cdm,
                             conceptSet = list(warfarin = c(1310149L,
                                                             40163554L)),
                             name = "warfarin")
result <- codelistDiagnostics(cdm$warfarin)

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

cohortDiagnostics *Run cohort-level diagnostics*

Description

Runs phenotypeR diagnostics on the cohort. The diagnostics include:

- Age groups and sex summarised.
- A summary of visits of everyone in the cohort using `visit_occurrence` table.
- A summary of age and sex density of the cohort.
- Attrition of the cohorts.
- Overlap between cohorts (if more than one cohort is being used).

Usage

```

cohortDiagnostics(
  cohort,
  cohortId = NULL,
  cohortCount = TRUE,
  cohortCharacteristics = TRUE,
  largeScaleCharacteristics = TRUE,
  compareCohorts = FALSE,
  cohortSurvival = FALSE,
  cohortSample = 20000,
  matchedSample = 1000
)

```

Arguments

cohort	Cohort table in a cdm reference
cohortId	Specific cohort definition ID for which to run cohort diagnostics.
cohortCount	Whether to run CohortCharacteristics::summariseCohortCount() and CohortCharacteristics::summariseCohortCount() (TRUE) or not (FALSE).
cohortCharacteristics	Whether to run CohortCharacteristics::summariseCharacteristics() and summarise age density (TRUE) or not (FALSE).
largeScaleCharacteristics	Whether to run CohortCharacteristics::summariseLargeScaleCharacteristics() (TRUE) or not (FALSE).
compareCohorts	Whether to run CohortCharacteristics::summariseCohortOverlap() and CohortCharacteristics::summariseCohortTiming() (TRUE) or not (FALSE). Notice that, if set to TRUE, the diagnostics will only be run when there are more than one cohort.
cohortSurvival	Whether to run CohortSurvival::estimateSingleEventSurvival() (TRUE) or not (FALSE).
cohortSample	The number of people to take a random sample for cohortDiagnostics. If cohortSample = NULL, no sampling will be performed.
matchedSample	The number of people to take a random sample for matching. If matchedSample = NULL, no sampling will be performed. If matchedSample = 0, no matched cohorts will be created.

Value

A summarised result

Examples

```

library(omock)
library(CohortConstructor)
library(PhenotypeR)

```

```
library(omock)
library(CDMConnector)

cdm <- mockCdmFromDataset(source = "duckdb")
cdm$warfarin <- conceptCohort(cdm,
                             conceptSet = list(warfarin = c(1310149L,
                                                             40163554L)),
                             name = "warfarin")

result <- cohortDiagnostics(cdm$warfarin)

cdmDisconnect(cdm)
```

databaseDiagnostics *Database diagnostics*

Description

PhenotypeR diagnostics on the cdm object.

Diagnostics include:

- Summarise a cdm_reference object, creating a snapshot with the metadata of the cdm_reference object
- Summarise the observation period table getting some overall statistics in a summarised_result object.
- Summarise the person table including demographics (sex, race, ethnicity, year of birth) and related statistics.
- Summarise the OMOP clinical tables where the codes associated with your cohort are found.

Usage

```
databaseDiagnostics(
  cohort,
  cohortId = NULL,
  snapshot = TRUE,
  personTableSummary = TRUE,
  observationPeriodsSummary = TRUE,
  clinicalRecordsSummary = FALSE
)
```

Arguments

cohort	Cohort table in a cdm reference
cohortId	Specific cohort definition ID for which to run database diagnostics. This will only affect the clinical tables summary results.
snapshot	Whether to run <code>OmopSketch::summariseOmopSnapshot()</code> (TRUE) or not (FALSE).

personTableSummary
Whether to run `OmopSketch::summarisePerson()` (TRUE) or not (FALSE).

observationPeriodsSummary
Whether to run `OmopSketch::summariseObservationPeriod()` (TRUE) or not (FALSE).

clinicalRecordsSummary
Whether to run `OmopSketch::summariseClinicalRecords()` on those clinical tables where the codes associated with your cohort are found (TRUE) or not (FALSE).

Value

A summarised result

Examples

```
library(omock)
library(PhenotypeR)
library(CohortConstructor)
library(CDMConnector)

cdm <- mockCdmFromDataset(source = "duckdb")

cdm$new_cohort <- conceptCohort(cdm,
                              conceptSet = list("codes" = c(40213201L, 4336464L)),
                              name = "new_cohort")

result <- databaseDiagnostics(cohort = cdm$new_cohort)

cdmDisconnect(cdm = cdm)
```

dataSourceDescriptionSpecification

Data source description specification

Description

Data source description specification

Usage

```
dataSourceDescriptionSpecification(path = NULL)
```

Arguments

path If NULL, specification will be returned as an R object. If a path to a directory is provided the specification will be exported.

Value

JSON specification for data source descriptions

`downloadClinicalDescriptionTemplate`

Download a Clinical Description Template

Description

Download a Clinical Description Template

Usage

```
downloadClinicalDescriptionTemplate(  
  directory,  
  name = "clinical_description_template"  
)
```

Arguments

<code>directory</code>	Directory where to download the clinical description.
<code>name</code>	Name of the Word file. Note that the file must match the cohort names used in PhenotypeR Diagnostics if you want to integrate the clinical description into the PhenotypeR Shiny app.

Value

A Word document with the template of the clinical description.

Examples

```
library(PhenotypeR)  
library(here)  
  
downloadClinicalDescriptionTemplate(directory = here(),  
                                   name = "metformin")
```

downloadDatabaseDescriptionTemplate

Download a Clinical Description Template

Description

Download a Clinical Description Template

Usage

```
downloadDatabaseDescriptionTemplate(  
  directory,  
  name = "database_description_template"  
)
```

Arguments

directory	Directory where to download the database description template.
name	Name of the Word file. Note that the file must match the database names used in PhenotypeR Diagnostics if you want to integrate the database description into the PhenotypeR Shiny app.

Value

A Word document with the template of the clinical description.

Examples

```
library(PhenotypeR)  
  
downloadDatabaseDescriptionTemplate(directory = tempdir(),  
  name = "GiBleed")
```

draftClinicalDescription

Draft clinical descriptions using an LLM

Description

Draft clinical descriptions using an LLM

Usage

```
draftClinicalDescription(chat, name, outputDir)
```

Arguments

chat	An ellmer chat
name	Clinical event of interest
outputDir	Folder to save clinical descriptions.

Value

Creates a draft clinical description for each event of interest.

`getCohortExpectations` *Get cohort expectations using an LLM*

Description

Get cohort expectations using an LLM

Usage

```
getCohortExpectations(chat, phenotypes, outputDir)
```

Arguments

chat	An ellmer chat
phenotypes	Either a vector of phenotype names or results from PhenotypeR.
outputDir	Folder to save expectations.

Value

A tibble with expectations about the cohort.

`importClinicalDescription`
Import clinical descriptions

Description

Import clinical descriptions

Usage

```
importClinicalDescription(path)
```

Arguments

path Either a directory containing clinical descriptions or a path to a specific clinical description

Value

A list of clinical descriptions

```
importDatabaseDescription
      Import database descriptions
```

Description

Import database descriptions

Usage

```
importDatabaseDescription(path)
```

Arguments

path Either a directory containing database descriptions or a path to a specific database description

Value

A list of database descriptions

```
phenotypeDiagnostics    Phenotype a cohort
```

Description

This comprises all the diagnostics that are being offered in this package, this includes:

- A diagnostic on the OMOP CDM dataset as a whole via `databaseDiagnostics`.
- A diagnostic on the codelists associated with cohorts via `codelistDiagnostics`.
- A diagnostic on the cohort itself via `cohortDiagnostics`.
- A diagnostic on the frequency of the cohort in the dataset population via `populationDiagnostics`.

Usage

```
phenotypeDiagnostics(
  cohort,
  databaseDiagnostics = list(),
  codelistDiagnostics = list(),
  cohortDiagnostics = list(),
  populationDiagnostics = list(),
  stagingDirectory = NULL
)
```

Arguments

cohort Cohort table in a cdm reference

databaseDiagnostics A list of arguments that uses databaseDiagnostics. If the list is empty, the default values will be used. Example: In the following example, all diagnostics will be run except *person table summary* from databaseDiagnostics: *databaseDiagnostics = list("personTableSummary" = FALSE)

codelistDiagnostics A list of arguments that uses codelistDiagnostics. If the list is empty, the default values will be used. Example: In the below example, all diagnostics will be run, and a subsample of 1,000 participants will be used to run measurement diagnostics and another independent subsample of 500 participants will be used to run drug diagnostics: *codelistDiagnostics = list("measurementDiagnosticsSample" = 1000, "drugDiagnosticsSample" = 500)

cohortDiagnostics A list of arguments that uses cohortDiagnostics. If the list is empty, the default values will be used. Example: *cohortDiagnostics = list("cohortSurvival" = TRUE)

populationDiagnostics A list of arguments that uses populationDiagnostics. If the list is empty, the default values will be used. Example: In the below example, all diagnostics will be run and a subsample of 100,000 participants will be used to run populationDiagnostics. *populationDiagnostics = list("populationSample" = 100000)

stagingDirectory Path to folder to save incremental results and log file

Value

A summarised result

Examples

```
library(omock)
library(CohortConstructor)
library(PhenotypeR)
```

```

cdm <- mockCdmFromDataset(source = "duckdb")
cdm$warfarin <- conceptCohort(cdm,
                             conceptSet = list(warfarin = c(1310149L,
                                                             40163554L)),
                             name = "warfarin")
result <- phenotypeDiagnostics(cdm$warfarin)

```

populationDiagnostics *Population-level diagnostics*

Description

PhenotypeR diagnostics on the cohort of input with relation to a denomination population. Diagnostics include:

- Incidence
- Period Prevalence

Usage

```

populationDiagnostics(
  cohort,
  cohortId = NULL,
  incidence = TRUE,
  periodPrevalence = TRUE,
  populationSample = 1e+05,
  populationDateRange = as.Date(c(NA, NA))
)

```

Arguments

cohort	Cohort table in a cdm reference
cohortId	Specific cohort definition ID for which to run population diagnostics.
incidence	Whether to run <code>IncidencePrevalence::estimateIncidence()</code> (TRUE) or not (FALSE).
periodPrevalence	Whether to run <code>IncidencePrevalence::estimatePeriodPrevalence()</code> (TRUE) or not (FALSE).
populationSample	Number of people from the cdm to sample. If NULL no sampling will be performed. Sample will be within <code>populationDateRange</code> if specified.
populationDateRange	Two dates. The first indicating the earliest cohort start date and the second indicating the latest possible cohort end date. If NULL or the first date is set as missing, the earliest <code>observation_start_date</code> in the <code>observation_period</code> table will be used for the former. If NULL or the second date is set as missing, the latest <code>observation_end_date</code> in the <code>observation_period</code> table will be used for the latter.

Value

A summarised result

Examples

```
library(omock)
library(CohortConstructor)
library(PhenotypeR)
library(CDMConnector)

cdm <- mockCdmFromDataset(source = "duckdb")
cdm$warfarin <- conceptCohort(cdm,
                             conceptSet = list(warfarin = c(1310149L,
                                                             40163554L)),
                             name = "warfarin")

result <- cdm$warfarin |>
  populationDiagnostics(populationSample = 100000)

cdmDisconnect(cdm = cdm)
```

shinyClinicalDescriptions

Shiny app to create clinical descriptions for contextualising diagnostic results

Description

Shiny app to create clinical descriptions for contextualising diagnostic results

Usage

```
shinyClinicalDescriptions(directory, open = rlang::is_interactive())
```

Arguments

directory	Directory where to save shiny app
open	If TRUE, the shiny app will be launched in a new session. If FALSE, the shiny app will be created but not launched.

Value

Shiny app

Examples

```
shinyClinicalDescriptions(tempdir())
```

shinyDataSourceDescriptions

Shiny app to create data source descriptions for contextualising diagnostic results

Description

Shiny app to create data source descriptions for contextualising diagnostic results

Usage

```
shinyDataSourceDescriptions(directory, open = rlang::is_interactive())
```

Arguments

directory	Directory where to save shiny app
open	If TRUE, the shiny app will be launched in a new session. If FALSE, the shiny app will be created but not launched.

Value

Shiny app

Examples

```
shinyDataSourceDescriptions(tempdir())
```

shinyDiagnostics

Create a shiny app summarising your phenotyping results

Description

A shiny app that is designed for any diagnostics results from phenotypeR, this includes:

- A diagnostics on the database via databaseDiagnostics.
- A diagnostics on the cohort_codelist attribute of the cohort via codelistDiagnostics.
- A diagnostics on the cohort via cohortDiagnostics.
- A diagnostics on the population via populationDiagnostics.
- A diagnostics on the matched cohort via matchedDiagnostics.

Usage

```
shinyDiagnostics(
  result,
  directory,
  minCellCount = 5,
  open = rlang::is_interactive(),
  expectationsDir = NULL,
  clinicalDescriptionsDir = NULL,
  databaseDescriptionsDir = NULL,
  removeEmptyTabs = TRUE
)
```

Arguments

result	A summarised result
directory	Directory where to save report
minCellCount	Minimum cell count for suppression when exporting results.
open	If TRUE, the shiny app will be launched in a new session. If FALSE, the shiny app will be created but not launched.
expectationsDir	Directory where to find the expectations CSV.
clinicalDescriptionsDir	Directory where to find the clinical descriptions word documents.
databaseDescriptionsDir	Directory where to find the database descriptions word documents.
removeEmptyTabs	Whether to remove tabs of those diagnostics that have not been performed or that were insufficient counts to produce a result (TRUE) or not (FALSE)

Value

A shiny app

Examples

```
library(omock)
library(CohortConstructor)
library(PhenotypeR)

cdm <- mockCdmFromDataset(source = "duckdb")
cdm$warfarin <- conceptCohort(cdm,
  conceptSet = list(warfarin = c(1310149L,
                                40163554L)),
  name = "warfarin")

result <- phenotypeDiagnostics(cdm$warfarin,
  populationDiagnostics = list("populationSample" = 100000))
```

```
shinyDiagnostics(result,  
                 tempdir())  
  
CDMConnector::cdmDisconnect(cdm = cdm)
```

tableCohortExpectations

Create a table summarising cohort expectations

Description

Create a table summarising cohort expectations

Usage

```
tableCohortExpectations(expectations, type = "reactable")
```

Arguments

expectations	Data frame or tibble with cohort expectations. It must contain the following columns: cohort_name, estimate, value, and source.
type	Table type to view results. See visOmopResults::tableType() for supported tables.

Value

Summary of cohort expectations

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