Package 'CohortPrevalence'

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Title Standardized Prevalence Calculator for OMOP/OHDSI Ecosystem

Version 0.0.1

Description This package calculates prevalence of a condition in a population.

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Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Imports cli,
crayon,
fs,
purrr,
SqlRender,
snakecase,
DatabaseConnector,
dplyr,
glue,
readr,
tibble,
tidyr,
here,
methods

Additional_repositories https://OHDSI.github.io/drat

Suggests knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

`createCohortPrevalenceAnalysis` *Create a* `CohortPrevalenceAnalysis` *object*

Description

Constructs an `CohortPrevalenceAnalysis` object with the specified settings.

Usage

```
createCohortPrevalenceAnalysis(
  analysisId,
  prevalentCohort,
  periodOfInterest,
  lookBackOptions,
  numeratorType,
  denominatorType,
  minimumObservationLength = 0L,
  useOnlyFirstObservationPeriod = FALSE,
  multiplier = 100000L,
  strata = NULL,
  populationCohort = NULL
)
```

Arguments

`analysisId`	Unique integer analysisId to identify the analysis (required).
`prevalentCohort`	A `PrevalenceCohort` object specifying the cohort of interest (required).
`periodOfInterest`	A `PeriodOfInterest` object (required).
`numeratorType`	Character string specifying numerator type. Must be one of: • `"pn1"`: Patients who have been observed to have the condition of interest on the first day of the period of interest or within the lookback time • `"pn2"`: patients who have been observed to have the condition of interest at any time in the period of interest or within the lookback time
`denominatorType`	A `DenominatorType` object (required).
`useOnlyFirstObservationPeriod`	Logical: `TRUE` to restrict analysis to the first observation period (optional).
`multiplier`	Integer specifying prevalence multiplier (optional).
`strata`	Character string. Must be one, or some of: `"age"`, `"gender"`, `"race"` (optional).
`populationCohort`	A `CohortPopulation` object specifying the population of interest on which to compute prevalence.
`lookBackDays`	Integer used for specifying length of lookback (required).

`minimumObservationLength`:
Integer specifying minimum observation length (optional).

`lookbackOptions`
A `LookBackOption` object (required).

Value

A `CohortPrevalenceAnalysis` R6 object.

`createDenominatorType` *Create a* `DenominatorType` *object*

Description

Constructs an `DenominatorType` object for denominator choice.

Usage

```
createDenominatorType(denomType, sufficientDays = NULL)
```

Arguments

`denomType`	Character string specifying denominator type. Must be one of: • `"pd1"`: Patients who have been observed on the first day of the period of interest • `"pd2"`: Patients who contribute all observable person-days in the period of interest. • `"pd3"`: Patients who contribute at least 1 day in the period of interest. • `"pd4"`: Patients who contribute sufficient time in the period of interest based on at least n observable person-days in the period of interest.
`sufficientDays`	Integer: For denominator choice `"pd4"`, the number of minimum observable days patients must be observed.

Value

A `DenominatorType` R6 object.

`createLookBackOptions` *Create a* `LookBackOptions` *object*

Description

Constructs an `LookBackOptions` object with the specified settings.

Usage

```
createLookBackOptions(lookBackDays = 99999L, useObservedTimeOnly = FALSE)
```

Arguments

lookBackDays	An integer number of days for the lookback period.
useObservedTimeOnly	Logical: TRUE restricts the lookback period to only using observed periods.

Value

A LookBackOptions R6 object.

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createPopulationCohort

Create a population cohort CohortInfo *object*

Description

Constructs an CohortInfo object for population of interest.

Usage

```
createPopulationCohort(cohortId, cohortName)
```

Arguments

cohortId	Integer: the cohort ID within the database results schema of interest.
cohortName	Character string specifying a name for the cohort.

Value

A CohortInfo R6 object.

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createPrevalenceCohort

Create a prevalence cohort CohortInfo *object*

Description

Constructs an CohortInfo object for target cohort of interest

Usage

```
createPrevalenceCohort(cohortId, cohortName)
```

Arguments

cohortId	Integer: the cohort ID within the database results schema of interest.
cohortName	Character string specifying a name for the cohort.

Value

A CohortInfo R6 object.

createYearlyPrevalence *Create a* PeriodOfInterest *object*

Description

Constructs an PeriodOfInterest object for yearly prevalence analyses.

Usage

```
createYearlyPrevalence(range)
```

Arguments

range	A numeric vector of years of interest.

Value

A PeriodOfInterest R6 object.

exportPrevalenceQuery *Export Prevalence Query*

Description

Exports the full SQL query of a CohortPrevalenceAnalysis analysis.

Usage

```
exportPrevalenceQuery(prevalenceAnalysisClass, outputFolder = NULL)
```

Arguments

prevalenceAnalysisClass	A CohortPrevalenceAnalysis R6 object with analysis settings (required).
outputFolder	Character string specifying the path to the folder where the output files will be saved. If left NULL, will default to current working directory (optional).

exportPrevalenceResults *Export Prevalence Query*

Description

Saves the results of a CohortPrevalenceAnalysis analysis as a .csv.

Usage

```
exportPrevalenceResults(results, outputFolder = NULL)
```

Arguments

results	Dataframe: Result of a generateSinglePrevalence analysis.
outputFolder	Character string specifying the path to the folder where the output files will be saved. If left NULL, will default to current working directory (optional).

generateSinglePrevalence *Run Prevalence Analysis*

Description

Runs a prevalence analysis with specified CohortPrevalenceAnalysis settings

Usage

```
generateSinglePrevalence(prevalenceAnalysisClass, executionSettings)
```

Arguments

prevalenceAnalysisClass	A CohortPrevalenceAnalysis R6 object with analysis settings.
executionSettings	An executionSettings R6 object with connection and schema details.

Value

A results dataframe with prevalence rates and strata.

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