

Package ‘CohortPrevalence’

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Title Standardized Prevalence Calculator for OMOP/OHDSI Ecosystem

Version 0.0.2

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

License Apache License

Encoding UTF-8

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:

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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).

`createDenominatorType`

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`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.

`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.

```
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.

```
createSpanPrevalence
```

Create a PeriodOfInterest object

Description

Constructs an PeriodOfInterest object for span prevalence analyses.

Usage

```
createSpanPrevalence(startDates, endDates)
```

Arguments

startYears	A numeric vector of start years of interest.
endYears	A numeric vector of end years of interest.

Value

A PeriodOfInterest R6 object.

`createYearlyPrevalence`

Create a PeriodOfInterest object

Description

Constructs an PeriodOfInterest object for yearly prevalence analyses.

Usage

```
createYearlyPrevalence(range)
```

Arguments

<code>range</code>	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,
  executionSettings,
  outputFolder = NULL
)
```

Arguments

<code>prevalenceAnalysisClass</code>	
--------------------------------------	--

A CohortPrevalenceAnalysis R6 object with analysis settings (required).

<code>outputFolder</code>	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).
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`exportPrevalenceResults`

Export Prevalence Query

Description

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

Usage

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

Arguments

<code>results</code>	Dataframe: Result of a generateSinglePrevalence analysis.
<code>outputFolder</code>	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).

`generateMultiplePrevalence`

Run Multiple Prevalence Analyses

Description

Runs multiple prevalence analysis with a list of specified CohortPrevalenceAnalysis settings

Usage

```
generateMultiplePrevalence(prevalenceAnalysisList, executionSettings)
```

Arguments

<code>prevalenceAnalysisList</code>	A list CohortPrevalenceAnalysis R6 object with analysis settings.
<code>executionSettings</code>	An executionSettings R6 object with connection and schema details.

Value

A results dataframe with prevalence rates and strata per analysis id.

`generateSinglePrevalence`

Run Single Prevalence Analysis

Description

Runs a single 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 data frame with prevalence rates and strata.

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