

Package ‘CohortPrevalence’

February 23, 2026

Title Standardized Prevalence Calculator for OMOP/OHDSI Ecosystem

Version 0.0.4

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:

createCohortPrevalenceAnalysis	2
createDemographicConstraints	3
createDenominatorType	4
createLookBackOptions	4
createPopulationCohort	5
createPrevalenceCohort	5
createRassenIncidenceAnalysis	6
createSpan	7

createTargetCohort	7
createYearlyRange	8
exportPrevalenceQuery	8
exportPrevalenceResults	9
generateMultiplePrevalence	9
generateMultipleRassenIncidence	10
generateSinglePrevalence	10
generateSingleRassenIncidence	11

Index**12**

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,
  demographicConstraints = createDemographicConstraints(),
  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).

demographicConstraints
    a DemoConstraint object specifying the constraints of the population.

populationCohort
    A CohortPopulation object specifying the population of interest on which to
    compute prevalence.

lookbackOptions
    A LookBackOption object (required).

minimumObservationLength:
    Integer specifying minimum observation length (optional).

```

Value

A CohortPrevalenceAnalysis R6 object.

`createDemographicConstraints`

Create a DemoConstraint object

Description

Constructs an DemoConstraint object for prevalence analyses.

Usage

```

createDemographicConstraints(
  ageMin = 0,
  ageMax = 150,
  genderIds = c(8507, 8532)
)

```

Arguments

ageMin	The minimum age allowed for the population. Default is 0
ageMax	the maximum age allowed for the population. Default is 150
genderIds	the genderIds allowed. Default is 8507 - M, and 8532 - F

Value

A DemoConstraint R6 object.

`createDenominatorType` *Create a DenominatorType object*

Description

Constructs an DenominatorType object for denominator choice.

Usage

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

Arguments

- | | |
|-----------------------------|---|
| <code>denomType</code> | Character string specifying denominator type. Must be one of: |
| | <ul style="list-style-type: none"> • "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. |
| <code>sufficientDays</code> | 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

- | | |
|----------------------------------|---|
| <code>lookBackDays</code> | An integer number of days for the lookback period. |
| <code>useObservedTimeOnly</code> | 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.

createRassenIncidenceAnalysis*Create a IncidenceAnalysis object for Rassen Incidence***Description**

Constructs an IncidenceAnalysis object with the specified settings.

Usage

```
createRassenIncidenceAnalysis(
  analysisId,
  targetCohort,
  periodOfInterest,
  minimumObservationLength = 0L,
  useOnlyFirstObservationPeriod = FALSE,
  multiplier = 100000L,
  strata = NULL,
  demographicConstraints = createDemographicConstraints(),
  populationCohort = NULL
)
```

Arguments

<code>analysisId</code>	Unique integer analysisId to identify the analysis (required).
<code>targetCohort</code>	A TargetCohort object specifying the cohort of interest (required).
<code>periodOfInterest</code>	A PeriodOfInterest object (required).
<code>useOnlyFirstObservationPeriod</code>	Logical: TRUE to restrict analysis to the first observation period (optional).
<code>multiplier</code>	Integer specifying prevalence multiplier (optional).
<code>strata</code>	Character string. Must be one, or some of: "age", "gender", "race" (optional).
<code>demographicConstraints</code>	a DemoConstraint object specifying the constraints of the population.
<code>populationCohort</code>	A CohortPopulation object specifying the population of interest on which to compute prevalence.
<code>minimumObservationLength:</code>	Integer specifying minimum observation length (optional).

Value

A IncidenceAnalysis R6 object.

`createSpan`

Create a PeriodOfInterest object

Description

Constructs an PeriodOfInterest object for span prevalence analyses.

Usage

```
createSpan(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.

`createTargetCohort`

Create a target cohort CohortInfo object

Description

Constructs an CohortInfo object for target cohort of interest

Usage

```
createTargetCohort(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.

`createYearlyRange` *Create a PeriodOfInterest object*

Description

Constructs an PeriodOfInterest object for yearly prevalence analyses.

Usage

```
createYearlyRange(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,
  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).

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). |
-

generateMultiplePrevalence

Run Multiple Prevalence Analyses

Description

Runs multiple prevalence analysis with a list of specified CohortPrevalenceAnalysis settings

Usage

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

Arguments

- | | |
|------------------------|--|
| prevalenceAnalysisList | A list 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 per analysis id.

```
generateMultipleRassenIncidence  
Run Multiple Rassen Incidence Analyses
```

Description

Runs multiple incidence analysis with a list of specified `IncidenceAnalysis` settings

Usage

```
generateMultipleRassenIncidence(incidenceAnalysisList, executionSettings)
```

Arguments

`incidenceAnalysisList`

A list `IncidenceAnalysis` R6 object with analysis settings.

`executionSettings`

An `executionSettings` R6 object with connection and schema details.

Value

A results dataframe with incidence 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 dataframe with prevalence rates and strata.

```
generateSingleRassenIncidence  
Run Single Incidence Analysis
```

Description

Runs a single incidence analysis with specified `IncidenceAnalysis` settings

Usage

```
generateSingleRassenIncidence(incidenceAnalysisClass, executionSettings)
```

Arguments

`incidenceAnalysisClass`

A `IncidenceAnalysis` R6 object with analysis settings.

`executionSettings`

An `executionSettings` R6 object with connection and schema details.

Value

A results data frame with incidence rates and strata.

Index

createCohortPrevalenceAnalysis, 2
createDemographicConstraints, 3
createDenominatorType, 4
createLookBackOptions, 4
createPopulationCohort, 5
createPrevalenceCohort, 5
createRassenIncidenceAnalysis, 6
createSpan, 7
createTargetCohort, 7
createYearlyRange, 8

exportPrevalenceQuery, 8
exportPrevalenceResults, 9

generateMultiplePrevalence, 9
generateMultipleRassenIncidence, 10
generateSinglePrevalence, 10
generateSingleRassenIncidence, 11