Package 'SelfControlledCohort'

April 1, 2021

Type Package

Title Population-level estimation method that estimates incidence rate comparison of exposed/unexposed time within an exposed cohort

Version 1.5.1

Date 2021-29-03

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Description This package provides a method to estimate risk by comparing time exposed with time unexposed among the exposed cohort.

URL https://github.com/OHDSI/SelfControlledCohort

BugReports https://github.com/OHDSI/SelfControlledCohort/issues

Depends DatabaseConnector (¿= 2.0.0)

Imports SqlRender (¿= 1.4.3), ParallelLogger, rateratio.test

Suggests withr, testthat, knitr, rmarkdown, Eunomia, DiagrammeR, dplyr

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RoxygenNote 7.1.1

VignetteBuilder knitr

R topics documented:

`createExposureOutcome` *Create exposure-outcome combinations.*

Description

Create exposure-outcome combinations.

Usage

```
createExposureOutcome(exposureId, outcomeId)
```

Arguments

`exposureId`	A concept ID indentifying the drug of interest in the exposure table. If multiple strategies for picking the exposure will be tested in the analysis, a named list of numbers can be provided instead. In the analysis, the name of the number to be used can be specified using the `exposureType` parameter in the `createSccAnalysis` function.
`outcomeId`	A concept ID indentifying the outcome of interest in the outcome table. If multiple strategies for picking the outcome will be tested in the analysis, a named list of numbers can be provided instead. In the analysis, the name of the number to be used can be specified using the #' `outcomeType` parameter in the `createSccAnalysis` function.

Details

Create a hypothesis of interest, to be used with the `runSccAnalyses` function.

`createRunSelfControlledCohortArgs`
Create a parameter object for the function runSelfControlledCohort

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Description

Create a parameter object for the function runSelfControlledCohort

Usage

```
createRunSelfControlledCohortArgs(
  firstExposureOnly = TRUE,
  firstOutcomeOnly = TRUE,
  minAge = "",
  maxAge = "",
  studyStartDate = "",
  studyEndDate = "",
  addLengthOfExposureExposed = TRUE,
  riskWindowStartExposed = 1,
  riskWindowEndExposed = 30,
  addLengthOfExposureUnexposed = TRUE,
  riskWindowEndUnexposed = -1,
  riskWindowStartUnexposed = -30,
  hasFullTimeAtRisk = FALSE,
  washoutPeriod = 0,
  followupPeriod = 0,
  computeTarDistribution = FALSE
)
```

Arguments

`firstExposureOnly`	If TRUE, only use first occurrence of each drug concept idfor each person
`firstOutcomeOnly`	If TRUE, only use first occurrence of each condition conceptid for each person.
`minAge`	Integer for minimum allowable age.
`maxAge`	Integer for maximum allowable age.
`studyStartDate`	Date for minimum allowable data for index exposure. Dateformat is 'yyyymmdd'.
`studyEndDate`	Date for maximum allowable data for index exposure. Dateformat is 'yyyymmdd'.
`addLengthOfExposureExposed`	If TRUE, use the duration from drugEraStart -¿ drugEraEnd aspart of timeAtRisk.
`riskWindowStartExposed`	Integer of days to add to drugEraStart for start oftimeAtRisk (0 to include index date, 1 to start the dayafter).
`riskWindowEndExposed`	Additional window to add to end of exposure period (ifaddLengthOf-ExposureExposed = TRUE, then add to exposure enddate, else add to exposure start date).
`addLengthOfExposureUnexposed`	If TRUE, use the duration from exposure start -¿ exposureend as part of timeAtRisk looking back before exposurestart.
`riskWindowEndUnexposed`	Integer of days to add to exposure start for end oftimeAtRisk (0 to include index date, -1 to end the daybefore).

`riskWindowStartUnexposed`
: Additional window to add to start of exposure period (ifaddLengthOfExposureUnexposed = TRUE, then add to exposureend date, else add to exposure start date).

`hasFullTimeAtRisk`
: If TRUE, restrict to people who have full time-at-riskexposed and unexposed.

`washoutPeriod`
: Integer to define required time observed before exposurestart.

`followupPeriod`
: Integer to define required time observed after exposurestart.

`computeTarDistribution`
: If TRUE, computer the distribution of time-at-risk and average absolute time between treatment and outcome. Note, may add significant computation time on some database engines. If set true in one analysis will default to true for all others.

Details

Create an object defining the parameter values.

`createSccAnalysis` *Create a SelfControlledCohort analysis specification*

Description

Create a SelfControlledCohort analysis specification

Usage

```
createSccAnalysis(
  analysisId = 1,
  description = "",
  exposureType = NULL,
  outcomeType = NULL,
  runSelfControlledCohortArgs
)
```

Arguments

`analysisId`
: An integer that will be used later to refer to this specific set of analysis choices.

`description`
: A short description of the analysis.

`exposureType`
: If more than one exposure is provided for each exposureOutcome, this field should be used to select the specific exposure to use in this analysis.

`outcomeType`
: If more than one outcome is provided for each exposureOutcome, this field should be used to select the specific outcome to use in this analysis.

`runSelfControlledCohortArgs`
: An object representing the arguments to be used when calling the `runSelfControlledCohort` function.

Details

Create a set of analysis choices, to be used with the `runSccAnalyses` function.

`loadExposureOutcomeList` *Load a list of exposureOutcome from file*

Description

Load a list of objects of type `exposureOutcome` from file. The file is in JSON format.

Usage

```
loadExposureOutcomeList(file)
```

Arguments

`file`	The name of the file

Value

A list of objects of type `exposureOutcome`.

`loadSccAnalysisList` *Load a list of sccAnalysis from file*

Description

Load a list of objects of type `sccAnalysis` from file. The file is in JSON format.

Usage

```
loadSccAnalysisList(file)
```

Arguments

`file`	The name of the file

Value

A list of objects of type `sccAnalysis`.

`runSccAnalyses` *Run a list of analyses*

Description

Run a list of analyses

Usage

```
runSccAnalyses(
  connectionDetails,
  cdmDatabaseSchema,
  oracleTempSchema = cdmDatabaseSchema,
  exposureDatabaseSchema = cdmDatabaseSchema,
  exposureTable = "drug_era",
  outcomeDatabaseSchema = cdmDatabaseSchema,
  outcomeTable = "condition_occurrence",
  cdmVersion = 5,
  outputFolder = "./SelfControlledCohortOutput",
  sccAnalysisList,
  exposureOutcomeList,
  analysisThreads = 1,
  computeThreads = 1
)
```

Arguments

`connectionDetails`
: An R object of type `connectionDetails` created using the function `createConnectionDetails` in the `DatabaseConnector` package.

`cdmDatabaseSchema`
: The name of the database schema that contains the OMOP CDM instance. Requires read permissions to this database. On SQL Server, this should specifiy both the database and the schema, so for example 'cdm_instance.dbo'.

`oracleTempSchema`
: For Oracle only: the name of the database schema where you want all temporary tables to be managed. Requires create/insert permissions to this database.

`exposureDatabaseSchema`
: The name of the database schema that is the location where the exposure data used to define the exposure cohorts is available. If exposureTable = DRUG_ERA, exposureDatabaseSchema is not used by assumed to be cdmSchema. Requires read permissions to this database.

`exposureTable`
: The tablename that contains the exposure cohorts. If exposureTable ¡¿ DRUG_ERA, then expectation is exposureTable has format of COHORT table: COHORT_DEFINITION_ID, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.

`outcomeDatabaseSchema`
: The name of the database schema that is the location where the data used to define the outcome cohorts is available. If exposureTable = CONDITION_ERA, exposureDatabaseSchema is not used by assumed to be cdmSchema. Requires read permissions to this database.

`outcomeTable`
: The tablename that contains the outcome cohorts. If outcomeTable ¡¿ CONDITION_OCCURRENCE, then expectation is outcomeTable has format of COHORT table: COHORT_DEFINITION_ID, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.

`cdmVersion`
: Define the OMOP CDM version used: currently support "4" and "5".

`outputFolder`
: Name of the folder where all the outputs will written to.

`sccAnalysisList`
: A list of objects of type `sccAnalysis` as created using the `createSccAnalysis` function.

`exposureOutcomeList`
: A list of objects of type `exposureOutcome` as created using the `createExposureOutcome` function.

`analysisThreads`
: The number of parallel threads to use to execute the analyses.

`computeThreads`
: Number of parallel threads per analysis thread for computing IRRs with exact confidence intervals.

Details

Run a list of analyses for the drug-comparator-outcomes of interest. This function will run all specified analyses against all hypotheses of interest, meaning that the total number of outcome models is 'length(cmAnalysisList) * length(drugComparatorOutcomesList)'.

`runSelfControlledCohort` *Run self-controlled cohort*

Description

`runSelfControlledCohort` generates population-level estimation by comparing exposed and unexposed time among exposed cohort.

Usage

```
runSelfControlledCohort(
  connectionDetails,
  cdmDatabaseSchema,
  cdmVersion = 5,
  oracleTempSchema = NULL,
  exposureIds,
  outcomeIds,
  exposureDatabaseSchema = cdmDatabaseSchema,
  exposureTable = "drug_era",
  outcomeDatabaseSchema = cdmDatabaseSchema,
  outcomeTable = "condition_era",
```

```
  firstExposureOnly = TRUE,
  firstOutcomeOnly = TRUE,
  minAge = "",
  maxAge = "",
  studyStartDate = "",
  studyEndDate = "",
  addLengthOfExposureExposed = TRUE,
  riskWindowStartExposed = 1,
  riskWindowEndExposed = 30,
  addLengthOfExposureUnexposed = TRUE,
  riskWindowEndUnexposed = -1,
  riskWindowStartUnexposed = -30,
  hasFullTimeAtRisk = FALSE,
  washoutPeriod = 0,
  followupPeriod = 0,
  computeTarDistribution = FALSE,
  computeThreads = 1
)
```

Arguments

connectionDetails	An R object of type connectionDetails created using the function createConnectionDetails in the DatabaseConnector package.
cdmDatabaseSchema	Name of database schema that contains the OMOP CDM and vocabulary.
cdmVersion	Define the OMOP CDM version used: currently support "4" and "5".
oracleTempSchema	For Oracle only: the name of the database schema where you want all temporary tables to be managed. Requires create/insert permissions to this database.
exposureIds	A vector containing the drug_concept_ids or cohort_definition_ids of the exposures of interest. If empty, all exposures in the exposure table will be included.
outcomeIds	The condition_concept_ids or cohort_definition_ids of the outcomes of interest. If empty, all the outcomes in the outcome table will be included.
exposureDatabaseSchema	The name of the database schema that is the location where the exposure data used to define the exposure cohorts is available. If exposureTable = DRUG_ERA, exposureDatabaseSchema is not used by assumed to be cdmSchema. Requires read permissions to this database.
exposureTable	The tablename that contains the exposure cohorts. If exposureTable ¡¿ DRUG_ERA, then expectation is exposureTable has format of COHORT table: cohort_concept_id, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.
outcomeDatabaseSchema	The name of the database schema that is the location where the data used to define the outcome cohorts is available. If exposureTable = CONDITION_ERA, exposureDatabaseSchema is not used by assumed to be cdmSchema. Requires read permissions to this database.

`outcomeTable` The tablename that contains the outcome cohorts. If outcomeTable ¡¿ CONDITION_OCCURRENCE, then expectation is outcomeTable has format of COHORT table: COHORT_DEFINITION_ID, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.

`firstExposureOnly`
If TRUE, only use first occurrence of each drug concept id for each person

`firstOutcomeOnly`
If TRUE, only use first occurrence of each condition concept id for each person.

`minAge` Integer for minimum allowable age.

`maxAge` Integer for maximum allowable age.

`studyStartDate` Date for minimum allowable data for index exposure. Date format is 'yyyymmdd'.

`studyEndDate` Date for maximum allowable data for index exposure. Date format is 'yyyymmdd'.

`addLengthOfExposureExposed`
If TRUE, use the duration from drugEraStart -¿ drugEraEnd as part of timeAtRisk.

`riskWindowStartExposed`
Integer of days to add to drugEraStart for start of timeAtRisk (0 to include index date, 1 to start the day after).

`riskWindowEndExposed`
Additional window to add to end of exposure period (if addLengthOfExposureExposed = TRUE, then add to exposure end date, else add to exposure start date).

`addLengthOfExposureUnexposed`
If TRUE, use the duration from exposure start -¿ exposure end as part of timeAtRisk looking back before exposure start.

`riskWindowEndUnexposed`
Integer of days to add to exposure start for end of timeAtRisk (0 to include index date, -1 to end the day before).

`riskWindowStartUnexposed`
Additional window to add to start of exposure period (if addLengthOfExposureUnexposed = TRUE, then add to exposure end date, else add to exposure start date).

`hasFullTimeAtRisk`
If TRUE, restrict to people who have full time-at-risk exposed and unexposed.

`washoutPeriod` Integer to define required time observed before exposure start.

`followupPeriod` Integer to define required time observed after exposure start.

`computeTarDistribution`
If TRUE, computer the distribution of time-at-risk and average absolute time between treatment and outcome. Note, may add significant computation time on some database engines.

`computeThreads` Number of parallel threads for computing IRRs with exact confidence intervals.

Details

Population-level estimation method that estimates incidence rate comparison of exposed/unexposed time within an exposed cohort. If multiple exposureIds and outcomeIds are provided, estimates will be generated for every combination of exposure and outcome.

Value

An object of type `sccResults` containing the results of the analysis.

References

Ryan PB, Schuemie MJ, Madigan D.Empirical performance of a self-controlled cohort method: lessons for developing a risk identification and analysis system. Drug Safety 36 Suppl1:S95-106, 2013

Examples

```
## Not run:
connectionDetails <- createConnectionDetails(dbms = "sql server",
                                             server = "RNDUSRDHIT07.jnj.com")
sccResult <- runSelfControlledCohort(connectionDetails,
                                     cdmDatabaseSchema = "cdm_truven_mdcr.dbo",
                                     exposureIds = c(767410, 1314924, 907879),
                                     outcomeIds = 444382,
                                     outcomeTable = "condition_era")

## End(Not run)
```

---

saveExposureOutcomeList

Save a list of exposureOutcome to file

Description

Write a list of objects of type `exposureOutcome` to file. The file is in JSON format.

Usage

```
saveExposureOutcomeList(exposureOutcomeList, file)
```

Arguments

`exposureOutcomeList`	The exposureOutcome list to be written to file
`file`	The name of the file where the results will be written

saveSccAnalysisList *Save a list of sccAnalysis to file*

Description

Write a list of objects of type `sccAnalysis` to file. The file is in JSON format.

Usage

```
saveSccAnalysisList(sccAnalysisList, file)
```

Arguments

`sccAnalysisList`	The sccAnalysis list to be written to file
`file`	The name of the file where the results will be written

summarizeAnalyses *Create a summary report of the analyses*

Description

Create a summary report of the analyses

Usage

```
summarizeAnalyses(resultsReference, outputFolder)
```

Arguments

`resultsReference`	A data.frame as created by the `runSccAnalyses` function.
`outputFolder`	Name of the folder where all the outputs have been written to.