

Package ‘CaseControl’

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Type Package

Title Case-Control

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Description CaseControl is an R package for performing (nested) matched case-control analyses in an observational database in the OMOP Common Data Model.

VignetteBuilder knitr

Depends R (>= 3.2.2),
Cyclops (>= 1.2.0),
DatabaseConnector (>= 1.3.0),
survival

Imports RJDBC,
SqlRender (>= 1.1.1),
bit,
ff,
ffbase (>= 0.12.1),
Rcpp (>= 0.11.2),
OhdsiRTools (>= 1.1.1),
plyr

Suggests testthat,
knitr,
rmarkdown

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CaseControl	<i>CaseControl</i>
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Description

CaseControl

createCaseControlData	<i>Create case-control data</i>
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Description

Create case-control data

Usage

```
createCaseControlData(caseControlsExposure, exposureId,
  firstExposureOnly = FALSE, riskWindowStart = 0, riskWindowEnd = 0)
```

Arguments

caseControlsExposure	An object of type caseControlsExposure as created using the getDbExposureData function.
exposureId	The identifier of the exposure.
firstExposureOnly	Should only the first exposure per subject be included?
riskWindowStart	The start of the risk window (in days) relative to the index date. This number should be non-positive.
riskWindowEnd	The end of the risk window (in days) relative to the index date. This number should be non-positive.

Details

For each case and control, assesses whether exposure takes place within the risk window. The output can be directly used in a conditional logistic regression.

Value

A data frame with these columns:

personId The person ID

indexDate The index date

isCase Is the person a case or a control?

stratumId The ID linking cases and controls in a matched set

exposed Was the subject exposed during the risk window?

createCcAnalysis	Create a case-control analysis specification
------------------	--

Description

Create a case-control analysis specification

Usage

```
createCcAnalysis(analysisId = 1, description = "", exposureType = NULL,
  outcomeType = NULL, getDbCaseDataArgs, selectControlsArgs,
  createCaseControlDataArgs)
```

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 exposureOutcomeNestingCohort, 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 exposureOutcomeNestingCohort, this field should be used to select the specific outcome to use in this analysis.

getDbCaseDataArgs

An object representing the arguments to be used when calling the [createGetDbCaseDataArgs](#) function.

selectControlsArgs

An object representing the arguments to be used when calling the [createSelectControlsArgs](#) function.

createCaseControlDataArgs

An object representing the arguments to be used when calling the [createCreateCaseControlDataArgs](#) function.

nestingCohortType

If more than one nesting cohort is provided for each exposureOutcomeNestingCohort, this field should be used to select the specific nesting cohort to use in this analysis.

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

Create a parameter object for the function `createCaseControlData`

Create a parameter object for the function `createCaseControlData`

```
createCreateCaseControlDataArgs(firstExposureOnly = FALSE,
  riskWindowStart = 0, riskWindowEnd = 0)
```

firstExposureOnly	Should only the first exposure per subject be included?
riskWindowStart	The start of the risk window (in days) relative to the index date. This number should be non-positive.
riskWindowEnd	The end of the risk window (in days) relative to the index date. This number should be non-positive.

Create an object defining the parameter values.

Create exposure-outcome-nesting-cohort combinations.

Create exposure-outcome-nesting-cohort combinations.

```
createExposureOutcomeNestingCohort(exposureId, outcomeId,
    nestingCohortId = NULL)
```

Arguments

exposureId	A concept ID indentifying the target drug 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 createCcAnalysis function.
outcomeId	A concept ID indentifying the outcome 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 createCcAnalysis function.
nestingCohortId	A concept ID indentifying the nesting cohort in the nesting cohort table. If multiple strategies for picking the nesting cohort 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 nestingCohortType parameter in the createCcAnalysis function.

Details

Create a set of hypotheses of interest, to be used with the [runCcAnalyses](#) function.

createGetDbCaseDataArgs

Create a parameter object for the function getDbCaseData

Description

Create a parameter object for the function getDbCaseData

Usage

```
createGetDbCaseDataArgs(useNestingCohort = FALSE,
  useObservationEndAsNestingEndDate = TRUE, getVisits = TRUE,
  studyStartDate = "", studyEndDate = "")
```

Arguments

useNestingCohort	Should the study be nested in a cohort (e.g. people with a specific indication)? If not, the study will be nested in the general population.
useObservationEndAsNestingEndDate	When using a nesting cohort, should the observation period end date be used instead of the cohort end date?
getVisits	Get data on visits? This is needed when matching on visit date is requested later on.
studyStartDate	A calendar date specifying the minimum date where data is used. Date format is 'yyyymmdd'.
studyEndDate	A calendar date specifying the maximum date where data is used. Date format is 'yyyymmdd'.

Details

Create an object defining the parameter values.

```
createSelectControlsArgs
```

Create a parameter object for the function selectControls

Description

Create a parameter object for the function selectControls

Usage

```
createSelectControlsArgs(outcomeId, firstOutcomeOnly = TRUE,
  washoutPeriod = 180, controlsPerCase = 2, matchOnAge = TRUE,
  ageCaliper = 2, matchOnGender = TRUE, matchOnProvider = FALSE,
  matchOnVisitDate = FALSE, visitDateCaliper = 30,
  removedUnmatchedCases = TRUE)
```

Arguments

outcomeId	The outcome ID of the cases for which we need to pick controls.
firstOutcomeOnly	Use the first outcome per person?
washoutPeriod	Minimum required numbers of days of observation for inclusion as either case or control.
controlsPerCase	Maximum number of controls to select per case.
matchOnAge	Match on age?
ageCaliper	Maximum difference (in years) in age when matching on age.
matchOnGender	Match on gender?
matchOnProvider	Match on provider (as specified in the person table)?
matchOnVisitDate	Should the index date of the control be changed to the nearest visit date?
visitDateCaliper	Maximum difference (in days) between the index date and the visit date when matching on visit date.
removedUnmatchedCases	Should cases with no matched controls be removed?

Details

Create an object defining the parameter values.

fitCaseControlModel	<i>Fit the case-control model</i>
---------------------	-----------------------------------

Description

Fit the case-control model

Usage

```
fitCaseControlModel(caseControlData)
```

Arguments

caseControlData

A data frame as generated by the [createCaseControlData](#) function.

Details

Fits the model using a conditional logistic regression.

Value

An object of type outcomeModel.

getAttritionTable	<i>Get the attrition table for a population</i>
-------------------	---

Description

Get the attrition table for a population

Usage

```
getAttritionTable(caseControls)
```

Arguments

caseControls

A data frame of cases and controls as generated by the function [selectControls](#).

Value

A data frame specifying the number of cases and events after various steps of filtering.

getDbCaseData	<i>Load case data from the database</i>
---------------	---

Description

Load all data about the cases and nesting cohort from the database.

Usage

```
getDbCaseData(connectionDetails, cdmDatabaseSchema,
  oracleTempSchema = cdmDatabaseSchema,
  outcomeDatabaseSchema = cdmDatabaseSchema, outcomeTable = "condition_era",
  outcomeIds = c(), useNestingCohort = FALSE,
  nestingCohortDatabaseSchema = cdmDatabaseSchema,
  nestingCohortTable = "cohort", nestingCohortId,
  useObservationEndAsNestingEndDate = TRUE, getVisits = TRUE,
  studyStartDate = "", studyEndDate = "")
```

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 specify both the database and the schema, so for example 'cdm_instance.dbo'.
oracleTempSchema	A schema where temp tables can be created in Oracle.
outcomeDatabaseSchema	The name of the database schema that is the location where the data used to define the outcome cohorts is available. If outcomeTable = CONDITION_ERA, outcomeDatabaseSchema is not used. Requires read permissions to this database.
outcomeTable	The tablename that contains the outcome cohorts. If outcomeTable is not CONDITION_OCCURRENCE or CONDITION_ERA, then expectation is outcomeTable has format of COHORT table: COHORT_DEFINITION_ID, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.
outcomeIds	A list of ids used to define outcomes. If outcomeTable = CONDITION_OCCURRENCE, the list is a set of ancestor CONCEPT_IDS, and all occurrences of all descendant concepts will be selected. If outcomeTable <> CONDITION_OCCURRENCE, the list contains records found in COHORT_DEFINITION_ID field.
useNestingCohort	Should the study be nested in a cohort (e.g. people with a specific indication)? If not, the study will be nested in the general population.
nestingCohortDatabaseSchema	The name of the database schema that is the location where the nesting cohort is defined.
nestingCohortTable	Name of the table holding the nesting cohort. This table should have the same structure as the cohort table.

nestingCohortId	A cohort definition ID identifying the records in the nestingCohortTable to use as nesting cohort
useObservationEndAsNestingEndDate	When using a nesting cohort, should the observation period end date be used instead of the cohort end date?
getVisits	Get data on visits? This is needed when matching on visit date is requested later on.
studyStartDate	A calendar date specifying the minimum date where data is used. Date format is 'yyyymmdd'.
studyEndDate	A calendar date specifying the maximum date where data is used. Date format is 'yyyymmdd'.

Value

Returns an object of type `caseData`, containing information on the cases, the nesting cohort, and optionally visits. Information about multiple outcomes can be captured at once for efficiency reasons. The generic `summary()` function has been implemented for this object.

<code>getDbExposureData</code>	<i>Get exposure data for cases and controls from a database</i>
--------------------------------	---

Description

Get exposure data for cases and controls from a database

Usage

```
getDbExposureData(caseControls, connectionDetails, oracleTempSchema = NULL,
  exposureDatabaseSchema, exposureTable = "drug_era", exposureIds = c())
```

Arguments

<code>caseControls</code>	A data frame as generated by the <code>selectControls</code> function.
<code>connectionDetails</code>	An R object of type <code>connectionDetails</code> created using the function <code>createConnectionDetails</code> in the <code>DatabaseConnector</code> package.
<code>oracleTempSchema</code>	A schema where temp tables can be created in Oracle.
<code>exposureDatabaseSchema</code>	The name of the database schema that is the location where the exposure data used to define the exposure cohorts is available. If <code>exposureTable = DRUG_ERA</code> , <code>exposureDatabaseSchema</code> is not used but assumed to be <code>cdmSchema</code> . Requires read permissions to this database.
<code>exposureTable</code>	The tablename that contains the exposure cohorts. If <code>exposureTable <> drug_era</code> , then expectation is <code>exposureTable</code> has format of COHORT table: <code>cohort_definition_id</code> , <code>subject_id</code> , <code>cohort_start_date</code> , <code>cohort_end_date</code> .

exposureIds A list of identifiers to define the exposures of interest. If `exposureTable = drug_era`, `exposureIds` should be `concept_id`. If `exposureTable <> drug_era`, `exposureIds` is used to select the `cohort_definition_id` in the cohort-like table. If no `exposureIds` are provided, all drugs or cohorts in the `exposureTable` are included as exposures.

<code>insertDbPopulation</code>	<i>Insert cases and controls into a database</i>
---------------------------------	--

Description

Insert cases and controls into a database

Usage

```
insertDbPopulation(caseControls, cohortIds = c(1, 0), connectionDetails,
  cohortDatabaseSchema, cohortTable = "cohort", createTable = FALSE,
  dropTableIfExists = TRUE)
```

Arguments

caseControls A data frame as generated by the [selectControls](#) function.

cohortIds The IDs to be used for the cohorts of cases and controls, respectively.

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

cohortDatabaseSchema
The name of the database schema where the data will be written. Requires write permissions to this database. On SQL Server, this should specify both the database and the schema, so for example `'cdm_instance.dbo'`.

cohortTable The name of the table in the database schema where the data will be written.

createTable Should a new table be created? If not, the data will be inserted into an existing table.

dropTableIfExists
If `createTable = TRUE` and the table already exists it will be overwritten.

Details

Inserts cases and controls into a database. The table in the database will have the same structure as the `'cohort'` table in the Common Data Model.

loadCaseData	<i>Load the case data from a folder</i>
--------------	---

Description

loadCaseData loads an object of type caseData from a folder in the file system.

Usage

```
loadCaseData(folder, readOnly = TRUE)
```

Arguments

folder	The name of the folder containing the data.
readOnly	If true, the data is opened read only.

Details

The data will be written to a set of files in the folder specified by the user.

Value

An object of class caseData.

loadExposureOutcomeNestingCohortList
<i>Load a list of exposureOutcomeNestingCohort from file</i>

Description

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

Usage

```
loadExposureOutcomeNestingCohortList(file)
```

Arguments

file	The name of the file
------	----------------------

Value

A list of objects of type drugComparatorOutcome.

saveCaseData	<i>Save the case data to folder</i>
--------------	-------------------------------------

Description

saveCaseData saves an object of type caseData to folder.

Usage

```
saveCaseData(caseData, folder)
```

Arguments

caseData	An object of type caseData as generated using getDbCaseData .
folder	The name of the folder where the data will be written. The folder should not yet exist.

Details

The data will be written to a set of files in the specified folder.

saveCcAnalysisList	<i>Save a list of ccAnalysis to file</i>
--------------------	--

Description

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

Usage

```
saveCcAnalysisList(ccAnalysisList, file)
```

Arguments

ccAnalysisList	The ccAnalysis list to be written to file
file	The name of the file where the results will be written

```
saveExposureOutcomeNestingCohortList
    Save a list of drugComparatorOutcome to file
```

Description

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

Usage

```
saveExposureOutcomeNestingCohortList(exposureOutcomeNestingCohortList, file)
```

Arguments

exposureOutcomeNestingCohortList	The exposureOutcomeNestingCohort list to be written to file
file	The name of the file where the results will be written

selectControls	Select matched controls per case
----------------	----------------------------------

Description

Select matched controls per case

Usage

```
selectControls(caseData, outcomeId, firstOutcomeOnly = TRUE,
  washoutPeriod = 180, controlsPerCase = 2, matchOnAge = TRUE,
  ageCaliper = 2, matchOnGender = TRUE, matchOnProvider = FALSE,
  matchOnVisitDate = FALSE, visitDateCaliper = 30,
  removedUnmatchedCases = TRUE)
```

Arguments

caseData	An object of type caseData as generated using the getDbCaseData function.
outcomeId	The outcome ID of the cases for which we need to pick controls.
firstOutcomeOnly	Use the first outcome per person?
washoutPeriod	Minimum required numbers of days of observation for inclusion as either case or control.
controlsPerCase	Maximum number of controls to select per case.
matchOnAge	Match on age?
ageCaliper	Maximum difference (in years) in age when matching on age.
matchOnGender	Match on gender?
matchOnProvider	Match on provider (as specified in the person table)?

`matchOnVisitDate`

Should the index date of the control be changed to the nearest visit date?

`visitDateCaliper`

Maximum difference (in days) between the index date and the visit date when matching on visit date.

`removedUnmatchedCases`

Should cases with no matched controls be removed?

Details

Select controls per case. Controls are matched on calendar time and the criteria defined in the arguments. Controls are randomly sampled to the required number.

Value

A data frame with these columns:

personId The person ID

indexDate The index date

isCase Is the person a case or a control?

stratumId The ID linking cases and controls in a matched set

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