

Package ‘CohortMethod’

April 4, 2016

Type Package

Title New-user cohort method with large scale propensity and outcome models

Version 1.1.3

Date 2015-11-18

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Description CohortMethod is an R package for performing new-user cohort studies in an observational database in the OMOP Common Data Model. It extracts the necessary data from a database in OMOP Common Data Model format, and uses a large set of covariates for both the propensity and outcome model, including for example all drugs, diagnoses, procedures, as well as age, comorbidity indexes, etc. Large scale regularized regression is used to fit the propensity and outcome models. Functions are included for trimming, stratifying and matching on propensity scores, as well as diagnostic functions, such as propensity score distribution plots and plots showing covariate balance before and after matching and/or trimming. Supported outcome models are (conditional) logistic regression, (conditional) Poisson regression, and (stratified) Cox regression.

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VignetteBuilder knitr

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

Imports bit,
ggplot2,
ff,
ffbase (>= 0.12.1),
plyr,
Rcpp (>= 0.11.2),
RJDBC,
SqlRender (>= 1.1.1),
survival,
jsonlite,
OhdsiRTools

Suggests testthat,
 pROC,
 gnm,
 knitr,
 rmarkdown,
 EmpiricalCalibration

LinkingTo Rcpp

NeedsCompilation yes

RoxygenNote 5.0.1

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CohortMethod	<i>CohortMethod</i>
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Description

CohortMethod

cohortMethodDataSimulationProfile	<i>A simulation profile</i>
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Description

A simulation profile

Usage

```
data(cohortMethodDataSimulationProfile)
```

computeCovariateBalance	<i>Compute covariate balance before and after matching and trimming</i>
-------------------------	---

Description

For every covariate, prevalence in treatment and comparator groups before and after matching/trimming are computed. When variable ratio matching was used the balance score will be corrected according the method described in Austin et al (2008).

Usage

```
computeCovariateBalance(population, cohortMethodData)
```

Arguments

population A data frame containing the people that are remaining after matching and/or trimming.

cohortMethodData An object of type cohortMethodData as generated using getDbCohortMethodData.

Details

The population data frame should have at least the following columns:

rowId	(integer)	A unique identifier for each row (e.g. the person ID)
treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group

Value

Returns a data frame describing the covariate balance before and after matching/trimming.

References

Austin, P.C. (2008) Assessing balance in measured baseline covariates when using many-to-one matching on the propensity-score. *Pharmacoepidemiology and Drug Safety*, 17: 1218-1225.

computePsAuc

Compute the area under the ROC curve

Description

computePsAuc computes the area under the ROC curve of the propensity score

Usage

```
computePsAuc(data, confidenceIntervals = FALSE)
```

Arguments

data A data frame with at least the two columns described below

confidenceIntervals Compute 95 percent confidence intervals (computationally expensive for large data sets)

Details

The data frame should have at least the following two columns:

treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
propensityScore	(numeric)	Propensity score

Value

A data frame holding the AUC and its 95 percent confidence interval

Examples

```
treatment <- rep(0:1, each = 100)
propensityScore <- c(rnorm(100, mean = 0.4, sd = 0.25), rnorm(100, mean = 0.6, sd = 0.25))
data <- data.frame(treatment = treatment, propensityScore = propensityScore)
data <- data[data$propensityScore > 0 & data$propensityScore < 1, ]
computePsAuc(data)
```

constructEras

*Build eras***Description**

Constructs eras (continuous periods of exposure or disease).

Usage

```
constructEras(connectionDetails, sourceDatabaseSchema,
  sourceTable = "drug_exposure",
  targetDatabaseSchema = sourceDatabaseSchema, targetTable = "drug_era",
  createTargetTable = FALSE, cdmDatabaseSchema = sourceDatabaseSchema,
  gracePeriod = 30, rollUp = TRUE, rollUpConceptClassId = "Ingredient",
  rollUpVocabularyId = "RxNorm", cdmVersion = "5")
```

Arguments

connectionDetails

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

sourceDatabaseSchema

The name of the database schema that contains the source table. Requires read permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.

sourceTable

The name of the source table.

targetDatabaseSchema

The name of the database schema that contains the target table. Requires write permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.

targetTable

The name of the target table.

createTargetTable

Should the target table be created? If not, the data is inserted in an existing table.

cdmDatabaseSchema

Only needed when rolling up concepts to ancestors: The name of the database schema that contains the vocabulary files. Requires read permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.

gracePeriod

The number of days allowed between periods for them to still be considered part of the same era.

rollUp

Should concepts be rolled up to their ancestors?

rollUpConceptClassId

The identifier of the concept class to which concepts should be rolled up.

rollUpVocabularyId

The identifier of the vocabulary to which concepts should be rolled up.

cdmVersion

The version of the CDM that is being used.

Details

This function creates eras from source data. For example, one could use this function to create drug eras based on drug exposures. The function allows drugs to be rolled up to ingredients, and prescriptions to the same ingredient that overlap in time are merged into a single ingredient. Note that stockpiling is not assumed to take place (ie. overlap is discarded), but a grace period can be specified allowing for a small gap between prescriptions when merging. The user can specify the source and target table. These tables are assumed to have the same structure as the cohort table in the Common Data Model (CDM), except when the table names are 'drug_exposure' or 'condition_occurrence' for the source table, or 'drug_era' or 'condition_era' for the target table, in which case the tables are assumed to have the structure defined for those tables in the CDM. If both the source and target table specify a field for type_concept_id, the era construction will partition by the type_concept_id, in other words periods with different type_concept_ids will be treated independently.

Examples

```
## Not run:
# Constructing drug eras in CDM v4:
constructEras(connectionDetails,
               sourceDatabaseSchema = cdmDatabaseSchema,
               sourceTable = "drug_exposure",
               targetTable = "drug_era",
               createTargetTable = FALSE,
               gracePeriod = 30,
               rollUpVocabularyId = 8,
               rollUpConceptClassId = "Ingredient",
               cdmVersion = "4")

# Constructing drug eras in CDM v5:
constructEras(connectionDetails,
               sourceDatabaseSchema = cdmDatabaseSchema,
               sourceTable = "drug_exposure",
               targetTable = "drug_era",
               createTargetTable = FALSE,
               gracePeriod = 30,
               rollUpVocabularyId = "RxNorm",
               rollUpConceptClassId = "Ingredient",
               cdmVersion = "5")

## End(Not run)
```

createCmAnalysis

Create a CohortMethod analysis specification

Description

Create a CohortMethod analysis specification

Usage

```
createCmAnalysis(analysisId = 1, description = "", targetType = NULL,
  comparatorType = NULL, indicationType = NULL, getDbCohortMethodDataArgs,
  createPs = FALSE, createPsArgs = NULL, trimByPs = FALSE,
  trimByPsArgs = NULL, trimByPsToEquipoise = FALSE,
  trimByPsToEquipoiseArgs = NULL, matchOnPs = FALSE, matchOnPsArgs = NULL,
  matchOnPsAndCovariates = FALSE, matchOnPsAndCovariatesArgs = NULL,
  stratifyByPs = FALSE, stratifyByPsArgs = NULL,
  stratifyByPsAndCovariates = FALSE, stratifyByPsAndCovariatesArgs = NULL,
  computeCovariateBalance = FALSE, fitOutcomeModel = FALSE,
  fitOutcomeModelArgs = NULL)
```

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.
targetType	If more than one target is provided for each drugComparatorOutcome, this field should be used to select the specific target to use in this analysis.
comparatorType	If more than one comparator is provided for each drugComparatorOutcome, this field should be used to select the specific comparator to use in this analysis.
indicationType	If more than one indication is provided for each drugComparatorOutcome, this field should be used to select the specific indication to use in this analysis.
getDbCohortMethodDataArgs	An object representing the arguments to be used when calling the getDbCohortMethodData function.
createPs	Should the createPs function be used in this analysis?
createPsArgs	An object representing the arguments to be used when calling the createPs function.
trimByPs	Should the trimByPs function be used in this analysis?
trimByPsArgs	An object representing the arguments to be used when calling the trimByPs function.
trimByPsToEquipoise	Should the trimByPsToEquipoise function be used in this analysis?
trimByPsToEquipoiseArgs	An object representing the arguments to be used when calling the trimByPsToEquipoise function.
matchOnPs	Should the matchOnPs function be used in this analysis?
matchOnPsArgs	An object representing the arguments to be used when calling the matchOnPs function.
matchOnPsAndCovariates	Should the matchOnPsAndCovariates function be used in this analysis?
matchOnPsAndCovariatesArgs	An object representing the arguments to be used when calling the matchOnPsAndCovariates function.
stratifyByPs	Should the stratifyByPs function be used in this analysis?
stratifyByPsArgs	An object representing the arguments to be used when calling the stratifyByPs function.

stratifyByPsAndCovariates

Should the [stratifyByPsAndCovariates](#) function be used in this analysis?

stratifyByPsAndCovariatesArgs

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

computeCovariateBalance

Should the [computeCovariateBalance](#) function be used in this analysis?

fitOutcomeModel

Should the [fitOutcomeModel](#) function be used in this analysis?

fitOutcomeModelArgs

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

Details

Create a set of analysis choices, to be used with the [runCmAnalyses](#) function.

createCohortMethodDataSimulationProfile
Create simulation profile

Description

createCohortMethodDataSimulationProfile creates a profile based on the provided cohort-MethodData object, which can be used to generate simulated data that has similar characteristics.

Usage

```
createCohortMethodDataSimulationProfile(cohortMethodData)
```

Arguments

cohortMethodData

An object of type cohortMethodData as generated using getDbCohortMethodData.

Details

The output of this function is an object that can be used by the simulateCohortMethodData function to generate a cohortMethodData object.

Value

An object of type cohortDataSimulationProfile.

createDrugComparatorOutcomes

Create drug-comparator-outcomes combinations.

Description

Create drug-comparator-outcomes combinations.

Usage

```
createDrugComparatorOutcomes(targetId, comparatorId, outcomeIds,
  indicationConceptIds = c(), exclusionConceptIds = c(),
  excludedCovariateConceptIds = c(), includedCovariateConceptIds = c())
```

Arguments

- | | |
|-----------------------------|---|
| targetId | A concept ID indentifying the target drug in the exposure table. If multiple strategies for picking the target 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 #' targetType parameter in the createCmAnalysis function. |
| comparatorId | A concept ID indentifying the comparator drug in the exposure table. If multiple strategies for picking the comparator 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 #' comparatorType parameter in the createCmAnalysis function. |
| outcomeIds | A vector of concept IDs indentifying the outcome(s) in the outcome table. |
| indicationConceptIds | A vector of concept IDs identifying conditions that are required to appear prior to or on the index date. If multiple strategies for picking the indication will be tested in the analysis, a named list of vectors can be provided instead. In the analysis, the name of the vector to be used can be specified using the indicationType parameter in the createCmAnalysis function. |
| exclusionConceptIds | A list of concept IDs that cannot appear on or before the index date. This argument is to be used only for exclusion criteria that are specific to the drug-comparator combination. |
| excludedCovariateConceptIds | A list of concept IDs that cannot be used to construct covariates. This argument is to be used only for exclusion concepts that are specific to the drug-comparator combination. |
| includedCovariateConceptIds | A list of concept IDs that must be used to construct covariates. This argument is to be used only for inclusion concepts that are specific to the drug-comparator combination. |

Details

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

createPs

*Create propensity scores***Description**

createPs creates propensity scores using a regularized logistic regression.

Usage

```
createPs(cohortMethodData, population, excludeCovariateIds = c(),
  includeCovariateIds = c(), stopOnHighCorrelation = TRUE,
  prior = createPrior("laplace", exclude = c(0), useCrossValidation = TRUE),
  control = createControl(noiseLevel = "silent", cvType = "auto", tolerance =
    2e-07, cvRepetitions = 10, startingVariance = 0.01))
```

Arguments

cohortMethodData	An object of type cohortMethodData as generated using getDbCohortMethodData.
population	A data frame describing the population. This should at least have a 'rowId' column corresponding to the rowId column in the cohortMethodData covariates object and a 'treatment' column. If population is not specified, the full population in the cohortMethodData will be used.
excludeCovariateIds	Exclude these covariates from the propensity model.
includeCovariateIds	Include only these covariates in the propensity model.
stopOnHighCorrelation	If true, the function will test each covariate for correlation with the treatment assignment. If any covariate has an unusually high correlation (either positive or negative), this will be reported and the function will stop.
prior	The prior used to fit the model. See createPrior for details.
control	The control object used to control the cross-validation used to determine the hyperparameters of the prior (if applicable). See createControl for details.

Details

createPs creates propensity scores using a regularized logistic regression.

Examples

```
data(cohortMethodDataSimulationProfile)
cohortMethodData <- simulateCohortMethodData(cohortMethodDataSimulationProfile, n = 1000)
ps <- createPs(cohortMethodData)
```

createStudyPopulation *Create a study population*

Description

Create a study population

Usage

```
createStudyPopulation(cohortMethodData, population = NULL, outcomeId,
  firstExposureOnly = FALSE, washoutPeriod = 0,
  removeDuplicateSubjects = FALSE, removeSubjectsWithPriorOutcome = TRUE,
  priorOutcomeLookback = 99999, requireTimeAtRisk = FALSE,
  riskWindowStart = 0, addExposureDaysToStart = FALSE, riskWindowEnd = 0,
  addExposureDaysToEnd = TRUE)
```

Arguments

cohortMethodData	An object of type cohortMethodData as generated using getDbCohortMethodData.
population	If specified, this population will be used as the starting point instead of the cohorts in the cohortMethodData object.
outcomeId	The ID of the outcome. If not specified, no outcome-specific transformations will be performed.
firstExposureOnly	Should only the first exposure per subject be included? Note that this is typically done in the createStudyPopulation function,
washoutPeriod	The minimum required continuous observation time prior to index date for a person to be included in the cohort.
removeDuplicateSubjects	Remove subjects that are in both the treated and comparator cohort?
removeSubjectsWithPriorOutcome	Remove subjects that have the outcome prior to the risk window start?
priorOutcomeLookback	How many days should we look back when identifying prior outcomes?
requireTimeAtRisk	Should subject without time at risk be removed?
riskWindowStart	The start of the risk window (in days) relative to the index date (+ days of exposure if the addExposureDaysToStart parameter is specified).
addExposureDaysToStart	Add the length of exposure the start of the risk window?
riskWindowEnd	The end of the risk window (in days) relative to the index data (+ days of exposure if the addExposureDaysToEnd parameter is specified).
addExposureDaysToEnd	Add the length of exposure the risk window?

Details

Create a study population by enforcing certain inclusion and exclusion criteria, defining a risk window, and determining which outcomes fall inside the risk window.

Value

A data frame specifying the study population. This data frame will have the following columns:

rowId A unique identifier for an exposure

subjectId The person ID of the subject

cohortStartDate The index date

outcomeCount The number of outcomes observed during the risk window

timeAtRisk The number of days in the risk window

survivalTime The number of days until either the outcome or the end of the risk window

drawAttritionDiagram	<i>Draw the attrition diagram</i>
----------------------	-----------------------------------

Description

drawAttritionDiagram draws the attrition diagram, showing how many people were excluded from the study population, and for what reasons.

Usage

```
drawAttritionDiagram(object, treatmentLabel = "Treated",
  comparatorLabel = "Comparator", fileName = NULL)
```

Arguments

object	Either an object of type cohortMethodData, a population object generated by functions like createStudyPopulation, or an object of type outcomeModel.
treatmentLabel	A label to us for the treated cohort.
comparatorLabel	A label to us for the comparator cohort.
fileName	Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats.

Value

A ggplot object. Use the [ggsave](#) function to save to file in a different format.

fitOutcomeModel	Create an outcome model, and compute the relative risk
-----------------	--

Description

fitOutcomeModel creates an outcome model, and computes the relative risk

Usage

```
fitOutcomeModel(population, cohortMethodData, modelType = "logistic",
  stratified = TRUE, useCovariates = TRUE, excludeCovariateIds = c(),
  includeCovariateIds = c(), prior = createPrior("laplace",
  useCrossValidation = TRUE), control = createControl(cvType = "auto",
  startingVariance = 0.01, tolerance = 2e-07, cvRepetitions = 10, selectorType =
  "byPid", noiseLevel = "quiet"))
```

Arguments

population	A population object generated by createStudyPopulation, potentially filtered by other functions.
cohortMethodData	An object of type cohortMethodData as generated using getDbCohortMethodData.
modelType	The type of outcome model that will be used. Possible values are "logistic", "poisson", or "cox".
stratified	Should the regression be conditioned on the strata defined in the population object (e.g. by matching or stratifying on propensity scores)?
useCovariates	Whether to use the covariate matrix in the cohortMethodData object in the outcome model.
excludeCovariateIds	Exclude these covariates from the outcome model.
includeCovariateIds	Include only these covariates in the outcome model.
prior	The prior used to fit the model. See createPrior for details.
control	The control object used to control the cross-validation used to determine the hyperparameters of the prior (if applicable). See createControl for details.

Value

An object of class outcomeModel. Generic function summary, coef, and confint are available.

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

Description

Get the attrition table for a population

Usage

```
getAttritionTable(object)
```

Arguments

object	Either an object of type cohortMethodData, a population object generated by functions like createStudyPopulation, or an object of type outcomeModel.
--------	--

Value

A data frame specifying the number of people and exposures in the population after specific steps of filtering.

getDbCohortMethodData	<i>Get the cohort data from the server</i>
-----------------------	--

Description

This function executes a large set of SQL statements against the database in OMOP CDM format to extract the data needed to perform the analysis.

Usage

```
getDbCohortMethodData(connectionDetails, cdmDatabaseSchema,
  oracleTempSchema = cdmDatabaseSchema, targetId, comparatorId, outcomeIds,
  studyStartDate = "", studyEndDate = "",
  exposureDatabaseSchema = cdmDatabaseSchema, exposureTable = "drug_era",
  outcomeDatabaseSchema = cdmDatabaseSchema,
  outcomeTable = "condition_occurrence", cdmVersion = "5",
  excludeDrugsFromCovariates = TRUE, firstExposureOnly = FALSE,
  removeDuplicateSubjects = FALSE, washoutPeriod = 0, covariateSettings)
```

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	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.
targetId	A unique identifier to define the target cohort. If exposureTable = DRUG_ERA, targetId is a CONCEPT_ID and all descendant concepts within that CONCEPT_ID will be used to define the cohort. If exposureTable <> DRUG_ERA, targetId is used to select the cohort_concept_id in the cohort-like table.
comparatorId	A unique identifier to define the comparator cohort. If exposureTable = DRUG_ERA, comparatorId is a CONCEPT_ID and all descendant concepts within that CONCEPT_ID will be used to define the cohort. If exposureTable <> DRUG_ERA, comparatorId is used to select the cohort_concept_id in the cohort-like table.
outcomeIds	A list of cohort_definition_ids used to define outcomes.
studyStartDate	A calendar date specifying the minimum date that a cohort index date can appear. Date format is 'yyyymmdd'.
studyEndDate	A calendar date specifying the maximum date that a cohort index date can appear. Date format is 'yyyymmdd'. Important: the study end data is also used to truncate risk windows, meaning no outcomes beyond the study end date will be considered.
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.
cdmVersion	Define the OMOP CDM version used: currently support "4" and "5".
excludeDrugsFromCovariates	Should the target and comparator drugs (and their descendant concepts) be excluded from the covariates? Note that this will work if the drugs are actually drug concept IDs (and not cohort IDs).
firstExposureOnly	Should only the first exposure per subject be included? Note that this is typically done in the createStudyPopulation function, but can already be done here for efficiency reasons.
removeDuplicateSubjects	Remove subjects that are in both the treated and comparator cohort? Note that this is typically done in the createStudyPopulation function, but can already be done here for efficiency reasons.

washoutPeriod	The minimum required continuous observation time prior to index date for a person to be included in the cohort. Note that this is typically done in the createStudyPopulation function, but can already be done here for efficiency reasons.
covariateSettings	An object of type covariateSettings as created using the createCovariateSettings function in the FeatureExtraction package.

Details

Based on the arguments, the treatment and comparator cohorts are retrieved, as well as outcomes occurring in exposed subjects. The treatment and comparator cohorts can be identified using the drug_era table, or through user-defined cohorts in a cohort table either inside the CDM instance or in a separate schema. Similarly, outcomes are identified using the condition_era table or through user-defined cohorts in a cohort table either inside the CDM instance or in a separate schema. Covariates are automatically extracted from the appropriate tables within the CDM. Important: The target and comparator drug must not be included in the covariates, including any descendant concepts. If the targetId and comparatorId arguments represent real concept IDs, you can set the excludeDrugsFromCovariates argument to TRUE and automatically the drugs and their descendants will be excluded from the covariates. However, if the targetId and comparatorId arguments do not represent concept IDs, you will need to manually add the drugs and descendants to the excludedCovariateConceptIds of the covariateSettings argument.

getOutcomeModel	<i>Get the outcome model</i>
-----------------	------------------------------

Description

getOutcomeModel shows the full outcome model, so showing the betas of all variables included in the outcome model, not just the treatment variable.

Usage

```
getOutcomeModel(outcomeModel, cohortMethodData)
```

Arguments

outcomeModel	An object of type outcomeModel as generated using the createOutcomeModel function.
cohortMethodData	An object of type cohortMethodData as generated using getDbCohortMethodData.

Details

Shows the coefficients and names of the covariates with non-zero coefficients.

Examples

```
# todo
```

getPsModel	<i>Get the propensity model</i>
------------	---------------------------------

Description

getPsModel shows the propensity score model

Usage

```
getPsModel(propensityScore, cohortMethodData)
```

Arguments

propensityScore

The propensity scores as generated using the createPs function.

cohortMethodData

An object of type cohortMethodData as generated using getDbCohortMethodData.

Details

Shows the coefficients and names of the covariates with non-zero coefficients.

Examples

```
# todo
```

grepCovariateNames	<i>Extract covariate names</i>
--------------------	--------------------------------

Description

Extracts covariate names using a regular-expression.

Usage

```
grepCovariateNames(pattern, object)
```

Arguments

pattern

A regular expression with which to name covariate names

object

An R object of type cohortMethodData or covariateData.

Details

This function extracts covariate names that match a regular-expression for a cohortMethodData or covariateData object.

Value

Returns a `data.frame` containing information about covariates that match a regular expression. This `data.frame` has the following columns:

covariateId Numerical identifier for use in model fitting using these covariates

covariateName Text identifier

analysisId Analysis identifier

conceptId OMOP common data model concept identifier, or 0

insertDbPopulation	<i>Insert a population into a database</i>
--------------------	--

Description

Insert a population into a database

Usage

```
insertDbPopulation(population, cohortIds = c(1, 0), connectionDetails,
  cohortDatabaseSchema, cohortTable = "cohort", createTable = FALSE,
  dropTableIfExists = TRUE, cdmVersion = "5")
```

Arguments

population	Either an object of type <code>cohortMethodData</code> or a population object generated by functions like <code>createStudyPopulation</code> .
cohortIds	The IDs to be used for the treated and comparator cohort, respectively.
connectionDetails	An R object of type <code>connectionDetails</code> created using the function <code>createConnectionDetails</code> in the <code>DatabaseConnector</code> 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 <code>'cdm_instance.dbo'</code> .
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 <code>createTable = TRUE</code> and the table already exists it will be overwritten.
cdmVersion	Define the OMOP CDM version used: currently support "4" and "5".

Details

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

loadCmAnalysisList	<i>Load a list of cmAnalysis from file</i>
--------------------	--

Description

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

Usage

```
loadCmAnalysisList(file)
```

Arguments

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

Value

A list of objects of type cmAnalysis.

loadCohortMethodData	<i>Load the cohort data from a folder</i>
----------------------	---

Description

loadCohortMethodData loads an object of type cohortMethodData from a folder in the file system.

Usage

```
loadCohortMethodData(file, readOnly = TRUE)
```

Arguments

file	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 cohortMethodData.

Examples

```
# todo
```

```
loadDrugComparatorOutcomesList
```

Load a list of drugComparatorOutcomes from file

Description

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

Usage

```
loadDrugComparatorOutcomesList(file)
```

Arguments

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

Value

A list of objects of type drugComparatorOutcome.

```
matchOnPs
```

Match persons by propensity score

Description

matchOnPs uses the provided propensity scores to match treated to comparator persons.

Usage

```
matchOnPs(population, caliper = 0.25, caliperScale = "standardized",
  maxRatio = 1, stratificationColumns = c())
```

Arguments

population	A data frame with the three columns described below.
caliper	The caliper for matching. A caliper is the distance which is acceptable for any match. Observations which are outside of the caliper are dropped. A caliper of 0 means no caliper is used.
caliperScale	The scale on which the caliper is defined. Two scales are supported: caliperScale = 'propensity score' or caliperScale = 'standardized'. On the standardized scale, the caliper is interpreted in standard deviations of the propensity score distribution.
maxRatio	The maximum number of persons in the comparator arm to be matched to each person in the treatment arm. A maxRatio of 0 means no maximum: all comparators will be assigned to a treated person.
stratificationColumns	Names or numbers of one or more columns in the data data.frame on which subjects should be stratified prior to matching. No persons will be matched with persons outside of the strata identified by the values in these columns.

Details

The data frame should have at least the following three columns:

rowId	(numeric)	A unique identifier for each row (e.g. the person ID)
treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
propensityScore	(numeric)	Propensity score

This function implements the greedy variable-ratio matching algorithm described in Rassen et al (2012).

Value

Returns a data frame with the same columns as the input data plus one extra column: stratumId. Any rows that could not be matched are removed

References

Rassen JA, Shelat AA, Myers J, Glynn RJ, Rothman KJ, Schneeweiss S. (2012) One-to-many propensity score matching in cohort studies, *Pharmacoepidemiology and Drug Safety*, May, 21 Suppl 2:69-80.

Examples

```
rowId <- 1:5
treatment <- c(1, 0, 1, 0, 1)
propensityScore <- c(0, 0.1, 0.3, 0.4, 1)
age_group <- c(1, 1, 1, 1, 1)
data <- data.frame(rowId = rowId,
                  treatment = treatment,
                  propensityScore = propensityScore,
                  age_group = age_group)
result <- matchOnPs(data, caliper = 0, maxRatio = 1, stratificationColumns = "age_group")
```

matchOnPsAndCovariates

Match by propensity score as well as other covariates

Description

matchOnPsAndCovariates uses the provided propensity scores and a set of covariates to match treated to comparator persons.

Usage

```
matchOnPsAndCovariates(population, caliper = 0.25,
                       caliperScale = "standardized", maxRatio = 1, cohortMethodpopulation,
                       covariateIds)
```

Arguments

population	A data frame with the three columns described below.
caliper	The caliper for matching. A caliper is the distance which is acceptable for any match. Observations which are outside of the caliper are dropped. A caliper of 0 means no caliper is used.
caliperScale	The scale on which the caliper is defined. Two scales are supported: caliperScale = 'propensity score' or caliperScale = 'standardized'. On the standardized scale, the caliper is interpreted in standard deviations of the propensity score distribution.
maxRatio	The maximum number of persons in the comparator arm to be matched to each person in the treatment arm. A maxRatio of 0 means no maximum: all comparators will be assigned to a treated person.
covariateIds	One or more covariate IDs in the cohortMethodData object on which subjects should be also matched.
cohortMethodData	An object of type cohortMethodData as generated using getDbCohortMethodData.

Details

The data frame should have at least the following three columns:

rowId	(numeric)	A unique identifier for each row (e.g. the person ID)
treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
propensityScore	(numeric)	Propensity score

This function implements the greedy variable-ratio matching algorithm described in Rassen et al (2012).

Value

Returns a data frame with the same columns as the input data plus one extra column: stratumId. Any rows that could not be matched are removed

References

Rassen JA, Shelat AA, Myers J, Glynn RJ, Rothman KJ, Schneeweiss S. (2012) One-to-many propensity score matching in cohort studies, *Pharmacoepidemiology and Drug Safety*, May, 21 Suppl 2:69-80.

Examples

```
# todo
```

`plotCovariateBalanceOfTopVariables`*Plot variables with largest imbalance*

Description

Create a plot showing those variables having the largest imbalance before matching, and those variables having the largest imbalance after matching. Requires running `computeCovariateBalance` first.

Usage

```
plotCovariateBalanceOfTopVariables(balance, n = 20, maxNameWidth = 100,  
  fileName = NULL)
```

Arguments

<code>balance</code>	A data frame created by the <code>computeCovariateBalance</code> function.
<code>n</code>	Count of variates to plot.
<code>maxNameWidth</code>	Covariate names longer than this number of characters are truncated to create a nicer plot.
<code>fileName</code>	Name of the file where the plot should be saved, for example 'plot.png'. See the function <code>ggsave</code> in the <code>ggplot2</code> package for supported file formats.

Value

A ggplot object. Use the [ggsave](#) function to save to file in a different format.

`plotCovariateBalanceScatterPlot`*Create a scatterplot of the covariate balance*

Description

Create a scatterplot of the covariate balance, showing all variables with balance before and after matching on the x and y axis respectively. Requires running `computeCovariateBalance` first.

Usage

```
plotCovariateBalanceScatterPlot(balance, fileName = NULL)
```

Arguments

<code>balance</code>	A data frame created by the <code>computeCovariateBalance</code> function.
<code>fileName</code>	Name of the file where the plot should be saved, for example 'plot.png'. See the function <code>ggsave</code> in the <code>ggplot2</code> package for supported file formats.

Value

A ggplot object. Use the [ggsave](#) function to save to file in a different format.

plotKaplanMeier	<i>Plot the Kaplan-Meier curve</i>
-----------------	------------------------------------

Description

plotKaplanMeier creates the Kaplan-Meier survival plot

Usage

```
plotKaplanMeier(population, censorMarks = FALSE, confidenceIntervals = TRUE,  
  includeZero = TRUE, dataCutoff = 0.99, treatmentLabel = "Treated",  
  comparatorLabel = "Comparator", title = "Kaplan-Meier Plot",  
  fileName = NULL)
```

Arguments

population	A population object generated by createStudyPopulation, potentially filtered by other functions.
censorMarks	Whether or not to include censor marks in the plot.
confidenceIntervals	Plot 95 percent confidence intervals?
includeZero	Should the y axis include zero, or only go down to the lowest observed survival?
dataCutoff	Fraction of the data (number censored) after which the graph will not be shown.
treatmentLabel	A label to us for the treated cohort.
comparatorLabel	A label to us for the comparator cohort.
title	The main title of the plot.
fileName	Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats.

Value

A ggplot object. Use the [ggsave](#) function to save to file in a different format.

Examples

```
# todo
```

plotPs	<i>Plot the propensity score distribution</i>
--------	---

Description

plotPs shows the propensity (or preference) score distribution

Usage

```
plotPs(data, unfilteredData = NULL, scale = "preference",
        type = "density", binWidth = 0.05, fileName = NULL)
```

Arguments

data	A data frame with at least the two columns described below
unfilteredData	To be used when computing preference scores on data from which subjects have already been removed, e.g. through trimming and/or matching. This data frame should have the same structure as data.
scale	The scale of the graph. Two scales are supported: scale = 'propensity' or scale = 'preference'. The preference score scale is defined by Walker et al (2013).
type	Type of plot. Two possible values: type = 'density' or type = 'histogram'
binWidth	For histograms, the width of the bins
fileName	Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats.

Details

The data frame should have a least the following two columns:

treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
propensityScore	(numeric)	Propensity score

Value

A ggplot object. Use the [ggsave](#) function to save to file in a different format.

References

Walker AM, Patrick AR, Lauer MS, Hornbrook MC, Marin MG, Platt R, Roger VL, Stang P, and Schneeweiss S. (2013) A tool for assessing the feasibility of comparative effectiveness research, Comparative Effective Research, 3, 11-20

Examples

```
treatment <- rep(0:1, each = 100)
propensityScore <- c(rnorm(100, mean = 0.4, sd = 0.25), rnorm(100, mean = 0.6, sd = 0.25))
data <- data.frame(treatment = treatment, propensityScore = propensityScore)
```

```
data <- data[data$propensityScore > 0 & data$propensityScore < 1, ]
plotPs(data)
```

```
recomputePsForFullData
```

Recompute the PS for the full data set

Description

Recompute the PS for the full data set

Usage

```
recomputePsForFullData(psSample, cohortMethodDataSample, cohortMethodData)
```

Arguments

psSample The propensity scores as created on the sample data.
 cohortMethodDataSample The sample data on which the PS model was fitted.
 cohortMethodData The full data.

Details

After using the [sampleCohorts](#) or [sampleComparator](#) to reduce the population size, this function can be used to apply a propensity model fitted on the sample to the full data.

Value

A new propensity score object.

```
runCmAnalyses
```

Run a list of analyses

Description

Run a list of analyses

Usage

```
runCmAnalyses(connectionDetails, cdmDatabaseSchema,
  oracleTempSchema = cdmDatabaseSchema,
  exposureDatabaseSchema = cdmDatabaseSchema, exposureTable = "drug_era",
  outcomeDatabaseSchema = cdmDatabaseSchema,
  outcomeTable = "condition_occurrence", cdmVersion = 4,
  outputFolder = "../CohortMethodOutput", cmAnalysisList,
  drugComparatorOutcomesList, refitPsForEveryOutcome = FALSE,
  underSampleComparatorToTreatedRatio = 0, getDbCohortMethodDataThreads = 1,
  createPsThreads = 1, psCvThreads = 1, trimMatchStratifyThreads = 1,
  computeCovarBalThreads = 1, fitOutcomeModelThreads = 1,
  outcomeCvThreads = 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 specify 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.

cmAnalysisList

A list of objects of type `cmAnalysis` as created using the [createCmAnalysis](#) function.

drugComparatorOutcomesList

A list of objects of type `drugComparatorOutcomes` as created using the [createDrugComparatorOutcomes](#) function.

refitPsForEveryOutcome

Should the propensity model be fitted for every outcome (i.e. after people who already had the outcome are removed)? If false, a single propensity model will be fitted, and people who had the outcome previously will be removed afterwards.

underSampleComparatorToTreatedRatio

If the comparator group size exceeds the treated group size by this factor, the comparator group will be down-sampled before fitting the PS model. This can be useful when the comparator group is extremely large.

getDbCohortMethodDataThreads

The number of parallel threads to use for building the `cohortMethod` data objects.

createPsThreads

The number of parallel threads to use for fitting the propensity models.

psCvThreads	The number of parallel threads to use for the cross- validation when estimating the hyperparameter for the propensity model. Note that the total number of CV threads at one time could be 'createPsThreads * psCvThreads'.
trimMatchStratifyThreads	The number of parallel threads to use for trimming, matching and stratifying.
computeCovariateBalanceThreads	The number of parallel threads to use for computing the covariate balance.
fitOutcomeModelThreads	The number of parallel threads to use for fitting the outcome models.
outcomeCvThreads	The number of parallel threads to use for the cross- validation when estimating the hyperparameter for the outcome model. Note that the total number of CV threads at one time could be 'fitOutcomeModelThreads * outcomeCvThreads'.

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)' (if all analyses specify an outcome model should be fitted). When you provide several analyses it will determine whether any of the analyses have anything in common, and will take advantage of this fact. For example, if we specify several analyses that only differ in the way the outcome model is fitted, then this function will extract the data and fit the propensity model only once, and re-use this in all the analysis.

Value

A data frame with the following columns:

analysisId	The unique identifier for a set of analysis choices.
targetId	The ID of the target drug.
comparatorId	The ID of the comparator group.
indicationConceptIds	The ID(s) of indications in which to nest to study.
exclusionConceptIds	The ID(s) of concepts used to exclude subjects.
excludedCovariateConceptIds	The ID(s) of concepts that cannot be used to construct covariates.
includedCovariateConceptIds	The ID(s) of concepts that should be used to construct covariates.
cohortMethodDataFolder	The ID of the outcome.
sharedPsFile	The name of the file containing the propensity scores of the shared propensity model. This model is used to create the outcome-specific propensity scores by removing people with prior outcomes.
psFile	The name of file containing the propensity scores for a specific outcomes (ie after people with prior outcomes have been removed).
subPopFile	The name of the file containing the identifiers of the population after any trimming, matching or stratifying, including their strata.
covariateBalanceFile	The name of the file containing the covariate balance (ie. the output of the computeCovariateBalance function).
outcomeModelFile	The name of the file containing the outcome model.

sampleCohorts

Sample the target or comparator group down

Description

Sample the target or comparator group down

Usage

```
sampleCohorts(cohortMethodData, treatedSampleSize = 10000,
               comparatorSampleSize = 20000)
```

Arguments

`cohortMethodData`
The original cohortMethodData.

`treatedSampleSize`
The sampe size for the treated cohort.

`comparatorSampleSize`
The sample size for the comparator cohort.

Details

When the target and/or comparator cohorts are extremely large, it may be more efficient to only use a sample to fit the propensity model. This function creates a new cohortMethodData object with sampled populations.

Value

An object of type cohortMethodData with the sampled populations.

sampleComparator	<i>Sample the comparator group down</i>
------------------	---

Description

Sample the comparator group down

Usage

```
sampleComparator(cohortMethodData, comparatorToTreatedRatio = 2)
```

Arguments

`cohortMethodData`
The original cohortMethodData.

`comparatorToTreatedRatio`
The ratio between comparator and treated group.

Details

When the comparator group is extremely large, it may be more efficient to only use a sample to fit the propensity model. This function creates a new cohortMethodData object where to comparator group is sampled down to a size relative to the treated group.

Value

An object of type cohortMethodData with the sampled populations.

saveCmAnalysisList	<i>Save a list of cmAnalysis to file</i>
--------------------	--

Description

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

Usage

```
saveCmAnalysisList(cmAnalysisList, file)
```

Arguments

cmAnalysisList	The cmAnalysis list to be written to file
file	The name of the file where the results will be written

saveCohortMethodData	<i>Save the cohort data to folder</i>
----------------------	---------------------------------------

Description

saveCohortMethodData saves an object of type cohortMethodData to folder.

Usage

```
saveCohortMethodData(cohortMethodData, file)
```

Arguments

cohortMethodData	An object of type cohortMethodData as generated using getDbCohortMethodData.
file	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 folder specified by the user.

Examples

```
# todo
```

`saveDrugComparatorOutcomesList`*Save a list of drugComparatorOutcome to file*

Description

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

Usage

```
saveDrugComparatorOutcomesList(drugComparatorOutcomesList, file)
```

Arguments

drugComparatorOutcomesList

The drugComparatorOutcomes list to be written to file

file

The name of the file where the results will be written

`simulateCohortMethodData`*Generate simulated data*

Description

simulateCohortMethodData creates a cohortMethodData object with simulated data.

Usage

```
simulateCohortMethodData(cohortDataSimulationProfile, n = 10000)
```

Arguments

cohortDataSimulationProfile

An object of type cohortDataSimulationProfile as generated using the createCohortMethodDataSimulationProfile function.

n

The size of the population to be generated.

Details

This function generates simulated data that is in many ways similar to the original data on which the simulation profile is based. The contains same outcome, comparator, and outcome concept IDs, and the covariates and their 1st order statistics should be comparable.

Value

An object of type cohortMethodData.

stratifyByPs	<i>Stratify persons by propensity score</i>
--------------	---

Description

stratifyByPs uses the provided propensity scores to stratify persons. Additional stratification variables for stratifications can also be used.

Usage

```
stratifyByPs(population, numberOfStrata = 5, stratificationColumns = c())
```

Arguments

population	A data frame with the three columns described below
numberOfStrata	How many strata? The boundaries of the strata are automatically defined to contain equal numbers of treated persons.
stratificationColumns	Names of one or more columns in the data data.frame on which subjects should also be stratified in addition to stratification on propensity score.

Details

The data frame should have the following three columns:

rowId	(numeric)	A unique identifier for each row (e.g. the person ID)
treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
propensityScore	(numeric)	Propensity score

Value

Returns a data frame with the same columns as the input data plus one extra column: stratumId.

Examples

```
rowId <- 1:200
treatment <- rep(0:1, each = 100)
propensityScore <- c(runif(100, min = 0, max = 1), runif(100, min = 0, max = 1))
data <- data.frame(rowId = rowId, treatment = treatment, propensityScore = propensityScore)
result <- stratifyByPs(data, 5)
```

stratifyByPsAndCovariates	<i>Stratify persons by propensity score and other covariates</i>
---------------------------	--

Description

`stratifyByPsAndCovariates` uses the provided propensity scores and covariates to stratify persons.

Usage

```
stratifyByPsAndCovariates(data, numberOfStrata = 5, cohortMethodData,
  covariateIds)
```

Arguments

<code>data</code>	A data frame with the three columns described below
<code>numberOfStrata</code>	Into how many strata should the propensity score be divided? The boundaries of the strata are automatically defined to contain equal numbers of treated persons.
<code>cohortMethodData</code>	An object of type <code>cohortMethodData</code> as generated using <code>getDbCohortMethodData</code> .
<code>covariateIds</code>	One or more covariate IDs in the <code>cohortMethodData</code> object on which subjects should also be stratified.

Details

The data frame should have the following three columns:

<code>rowId</code>	(integer)	A unique identifier for each row (e.g. the person ID)
<code>treatment</code>	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
<code>propensityScore</code>	(numeric)	Propensity score

Value

Returns a data frame with the same columns as the input data plus one extra column: `stratumId`.

Examples

```
# todo
```

<code>summarizeAnalyses</code>	<i>Create a summary report of the analyses</i>
--------------------------------	--

Description

Create a summary report of the analyses

Usage

```
summarizeAnalyses(outcomeReference)
```

Arguments

outcomeReference

A data.frame as created by the `runCmAnalyses` function.**Value**

A data frame with the following columns:

analysisId	The unique identifier for a set of analysis choices.
targetId	The ID of the target drug.
comparatorId	The ID of the comparator group.
indicationConceptIds	The ID(s) of indications in which to nest to study.
outcomeId	The ID of the outcome.
rr	The estimated effect size.
ci95lb	The lower bound of the 95 percent confidence interval.
ci95ub	The upper bound of the 95 percent confidence interval.
treated	The number of subjects in the treated group (after any trimming and matching).
comparator	The number of subjects in the comparator group (after any trimming and matching).
eventsTreated	The number of outcomes in the treated group (after any trimming and matching).
eventsComparator	The number of outcomes in the comparator group (after any trimming and matching).
logRr	The log of the estimated relative risk.
seLogRr	The standard error of the log of the estimated relative risk.

trimByPs

*Trim persons by propensity score***Description**

trimByPs uses the provided propensity scores to trim subjects with extreme scores.

Usage

trimByPs(population, trimFraction = 0.05)

Arguments

population A data frame with the three columns described below

trimFraction This fraction will be removed from each treatment group. In the treatment group, persons with the highest propensity scores will be removed, in the comparator group person with the lowest scores will be removed.

Details

The data frame should have the following three columns:

rowId	(numeric)	A unique identifier for each row (e.g. the person ID)
treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
propensityScore	(numeric)	Propensity score

Value

Returns a data frame with the same three columns as the input.

Examples

```
rowId <- 1:2000
treatment <- rep(0:1, each = 1000)
propensityScore <- c(runif(1000, min = 0, max = 1), runif(1000, min = 0, max = 1))
data <- data.frame(rowId = rowId, treatment = treatment, propensityScore = propensityScore)
result <- trimByPs(data, 0.05)
```

trimByPsToEquipoise	<i>Keep only persons in clinical equipoise</i>
---------------------	--

Description

trimByPsToEquipoise uses the preference score to trim subjects that are not in clinical equipoise

Usage

```
trimByPsToEquipoise(population, bounds = c(0.25, 0.75))
```

Arguments

population	A data frame with at least the three columns described below
bounds	The upper and lower bound on the preference score for keeping persons

Details

The data frame should have the following three columns:

rowId	(numeric)	A unique identifier for each row (e.g. the person ID)
treatment	(integer)	Column indicating whether the person is in the treated (1) or comparator (0) group
propensityScore	(numeric)	Propensity score

Value

Returns a data frame with the same three columns as the input.

References

Walker AM, Patrick AR, Lauer MS, Hornbrook MC, Marin MG, Platt R, Roger VL, Stang P, and Schneeweiss S. (2013) A tool for assessing the feasibility of comparative effectiveness research, Comparative Effective Research, 3, 11-20

Examples

```
rowId <- 1:2000
treatment <- rep(0:1, each = 1000)
```

```
propensityScore <- c(runif(1000, min = 0, max = 1), runif(1000, min = 0, max = 1))  
data <- data.frame(rowId = rowId, treatment = treatment, propensityScore = propensityScore)  
result <- trimByPsToEquipoise(data)
```

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