

# Package ‘CohortMethod’

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**Type** Package

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

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**Author** Martijn J. Schuemie [aut, cre],  
Marc A. Suchard [aut],  
Patrick B. Ryan [aut]

**Maintainer** Martijn J. Schuemie <schuemie@ohdsi.org>

**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.

**License** Apache License 2.0

**VignetteBuilder** knitr

**Depends** R (>= 3.2.2),  
DatabaseConnector (>= 1.3.0),  
Cyclops (>= 1.2.0),  
PatientLevelPrediction (>= 1.1.0)

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

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 knitr,  
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 EmpiricalCalibration

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## R topics documented:

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---

|              |                     |
|--------------|---------------------|
| CohortMethod | <i>CohortMethod</i> |
|--------------|---------------------|

---

## Description

CohortMethod

---

|                                   |                             |
|-----------------------------------|-----------------------------|
| cohortMethodDataSimulationProfile | <i>A simulation profile</i> |
|-----------------------------------|-----------------------------|

---

## 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(restrictedCohorts, cohortMethodData,
  excludePriorOutcome = TRUE, outcomeId = NULL)
```

**Arguments**

|                     |  |
|---------------------|--|
| restrictedCohorts   | A data frame containing the people that are remaining after matching and/or trimming.  |
| cohortMethodData    | An object of type cohortMethodData as generated using getDbCohortMethodData.   |
| excludePriorOutcome | Remove people that have the outcome prior to the index date?   |
| outcomeId           | The concept ID of the outcome. Persons marked for removal for the outcome will be removed when computing the balance before matching/trimming. |

**Details**

The restrictedCohorts 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 | (real)    | 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 | <i>Build eras</i> |
|---------------|-------------------|

---

### 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 <a href="#">getDbCohortMethodData</a> function.   |
| createPs                  | Should the <a href="#">createPs</a> function be used in this analysis?   |
| createPsArgs              | An object representing the arguments to be used when calling the <a href="#">createPs</a> function.  |
| trimByPs                  | Should the <a href="#">trimByPs</a> function be used in this analysis?   |
| trimByPsArgs              | An object representing the arguments to be used when calling the <a href="#">trimByPs</a> function.  |
| trimByPsToEquipoise       | Should the <a href="#">trimByPsToEquipoise</a> function be used in this analysis?  |
| trimByPsToEquipoiseArgs   | An object representing the arguments to be used when calling the <a href="#">trimByPsToEquipoise</a> function.   |
| matchOnPs                 | Should the <a href="#">matchOnPs</a> function be used in this analysis?  |

|                               |  |
|-------------------------------|--|
| matchOnPsArgs                 | An object representing the arguments to be used when calling the <a href="#">matchOnPs</a> function.                 |
| matchOnPsAndCovariates        | Should the <a href="#">matchOnPsAndCovariates</a> function be used in this analysis?                                 |
| matchOnPsAndCovariatesArgs    | An object representing the arguments to be used when calling the <a href="#">matchOnPsAndCovariates</a> function.    |
| stratifyByPs                  | Should the <a href="#">stratifyByPs</a> function be used in this analysis?   |
| stratifyByPsArgs              | An object representing the arguments to be used when calling the <a href="#">stratifyByPs</a> function.              |
| stratifyByPsAndCovariates     | Should the <a href="#">stratifyByPsAndCovariates</a> function be used in this analysis?                              |
| stratifyByPsAndCovariatesArgs | An object representing the arguments to be used when calling the <a href="#">stratifyByPsAndCovariates</a> function. |
| computeCovariateBalance       | Should the <a href="#">computeCovariateBalance</a> function be used in this analysis?                                |
| fitOutcomeModel               | Should the <a href="#">fitOutcomeModel</a> function be used in this analysis?  |
| fitOutcomeModelArgs           | An object representing the arguments to be used when calling the <a href="#">fitOutcomeModel</a> 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 `cohortMethodData` 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.

---

|                    |  |
|--------------------|--|
| createCreatePsArgs | <i>Create a parameter object for the function createPs</i> |
|--------------------|--|

---

**Description**

Create a parameter object for the function createPs

**Usage**

```
createCreatePsArgs(excludePriorOutcome = TRUE, excludeCovariateIds = NULL,
  stopOnHighCorrelation = TRUE, prior = createPrior("laplace", exclude =
  c(0), useCrossValidation = TRUE), control = createControl(noiseLevel =
  "silent", cvType = "auto", startingVariance = 0.1))
```

**Arguments**

|                       |   |
|-----------------------|---|
| excludePriorOutcome   | Remove people that have the outcome prior to the index date?  |
| excludeCovariateIds   | Exclude these covariates from 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**

Create an object defining the parameter values.

---

|                              |  |
|------------------------------|--|
| createDrugComparatorOutcomes | <i>Create drug-comparator-outcomes combinations.</i> |
|------------------------------|--|

---

**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 <a href="#">createCmAnalysis</a> 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 <a href="#">createCmAnalysis</a> 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 <a href="#">createCmAnalysis</a> 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.

---

createFitOutcomeModelArgs

*Create a parameter object for the function fitOutcomeModel*

---

## Description

Create a parameter object for the function fitOutcomeModel

## Usage

```
createFitOutcomeModelArgs(excludePriorOutcome = TRUE, stratifiedCox = TRUE,
  riskWindowStart = 0, riskWindowEnd = 9999, addExposureDaysToEnd = FALSE,
  useCovariates = TRUE, fitModel = TRUE, modelType = "cox",
  prior = createPrior("laplace", useCrossValidation = TRUE),
  control = createControl(cvType = "auto", startingVariance = 0.1,
    selectorType = "byPid", noiseLevel = "quiet"))
```

**Arguments**

|                      |   |
|----------------------|---|
| excludePriorOutcome  | Remove people that have the outcome prior to the risk window start date?  |
| stratifiedCox        | Specifically for Cox regressions: specify whether to use the stratadefined in subPopulation in the analysis. For Poissonregression and logistic regression, this is implied in 'clr' and 'cpr'. |
| riskWindowStart      | The start of the risk window (in days) relative to the index data.  |
| riskWindowEnd        | The end of the risk window (in days) relative to the index data (+days of exposure if the addExposureDaysToEnd parameter isspecified).  |
| addExposureDaysToEnd | Add the length of exposure the risk window?   |
| useCovariates        | Whether to use the covariate matrix in the cohortMethodData in theoutcome model.  |
| fitModel             | If false, the model will not be fit, and only summary statistics areavailable.  |
| modelType            | The type of model to be fitted. See details for options.  |
| prior                | The prior used to fit the model. SeecreatePrior for details.  |
| control              | The control object used to control the cross-validation used todetermine the hyperparameters of the prior (if applicable). SeecreateControl for details.  |

**Details**

Create an object defining the parameter values.

---

```
createGetDbCohortMethodDataArgs
```

*Create a parameter object for the function getDbCohortMethodData*

---

**Description**

Create a parameter object for the function getDbCohortMethodData

**Usage**

```
createGetDbCohortMethodDataArgs(washoutWindow = 183,
  indicationLookbackWindow = 183, studyStartDate = "", studyEndDate = "",
  exclusionConceptIds = c(), outcomeConditionTypeConceptIds = c(),
  excludeDrugsFromCovariates = TRUE, covariateSettings)
```

**Arguments**

|                          |  |
|--------------------------|--|
| washoutWindow            | The minimum required continuous observation time prior to indexdate for a person to be included in the cohort. |
| indicationLookbackWindow | NA   |
| studyStartDate           | A calendar date specifying the minimum date that a cohort indexdate can appear. Date format is 'yyyymmdd'.     |

|                                |   |
|--------------------------------|---|
| studyEndDate                   | A calendar date specifying the maximum date that a cohort indexdate can appear. Date format is 'yyyymmdd'.  |
| exclusionConceptIds            | A list of CONCEPT_IDs used to restrict the cohorts, based on anydescendant conditions/drugs/procedures occurring at least onceanytime prior to the cohort index date.                         |
| outcomeConditionTypeConceptIds | A list of TYPE_CONCEPT_ID values that will restrictcondition occurrences. Only applicable if outcomeTable =CONDITION_OCCURRENCE.  |
| excludeDrugsFromCovariates     | Should the target and comparator drugs (and their descendantconcepts) be excluded from the covariates? Note that this willwork if the drugs are actualy drug concept IDs (and not cohortIDs). |
| covariateSettings              | An object of type covariateSettings as created using thecreateCovariateSettings function in thePatientLevelPrediction package..   |

### Details

Create an object defining the parameter values.

---

```
createMatchOnPsAndCovariatesArgs
```

*Create a parameter object for the function matchOnPsAndCovariates*

---

### Description

Create a parameter object for the function matchOnPsAndCovariates

### Usage

```
createMatchOnPsAndCovariatesArgs(caliper = 0.25,
  caliperScale = "standardized", maxRatio = 1, covariateIds)
```

### Arguments

|              |  |
|--------------|--|
| caliper      | The caliper for matching. A caliper is the distance which is acceptablefor 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 aresupported:caliperScale = 'propensity score' orcaliperScale = 'standardized'. On the standardized scale, thecaliper is interpreted in standard deviations of the propensity scoredistribution. |
| maxRatio     | The maximum number of persons int the comparator arm to be matched to each-person in the treatment arm. A maxRatio of 0 means no maximum: allcomparators will be assigned to a treated person.   |
| covariateIds | One or more covariate IDs in the cohortMethodData object on whichsubjects should be also matched.  |

### Details

Create an object defining the parameter values.

---

|                     |   |
|---------------------|---|
| createMatchOnPsArgs | <i>Create a parameter object for the function matchOnPs</i> |
|---------------------|---|

---

## Description

Create a parameter object for the function matchOnPs

## Usage

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

## Arguments

|                       |   |
|-----------------------|---|
| 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

Create an object defining the parameter values.

---

|          |                                 |
|----------|---------------------------------|
| createPs | <i>Create propensity scores</i> |
|----------|---------------------------------|

---

## Description

createPs creates propensity scores using a regularized logistic regression.

## Usage

```
createPs(cohortMethodData, excludePriorOutcome = TRUE, outcomeId = NULL,
  excludeCovariateIds = NULL, stopOnHighCorrelation = TRUE,
  prior = createPrior("laplace", exclude = c(0), useCrossValidation = TRUE),
  control = createControl(noiseLevel = "silent", cvType = "auto",
    startingVariance = 0.1))
```

**Arguments**

|                       |   |
|-----------------------|---|
| cohortMethodData      | An object of type cohortMethodData as generated using getDbCohortMethodData.  |
| excludePriorOutcome   | Remove people that have the outcome prior to the index date?  |
| outcomeId             | The concept ID of the outcome. Persons marked for removal for the outcome will be removed prior to creating the propensity score model.   |
| excludeCovariateIds   | Exclude these covariates from 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 <a href="#">createPrior</a> for details.   |
| control               | The control object used to control the cross-validation used to determine the hyperparameters of the prior (if applicable). See <a href="#">createControl</a> for details.  |

**Details**

createPs creates propensity scores using a regularized logistic regression.

**Examples**

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

---

createStratifyByPsAndCovariatesArgs

*Create a parameter object for the function stratifyByPsAndCovariates*

---

**Description**

Create a parameter object for the function stratifyByPsAndCovariates

**Usage**

```
createStratifyByPsAndCovariatesArgs(numberOfStrata = 5, covariateIds)
```

**Arguments**

|                |  |
|----------------|--|
| numberOfStrata | 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. |
| covariateIds   | One or more covariate IDs in the cohortMethodData object on which subjects should also be stratified.  |

**Details**

Create an object defining the parameter values.

---

```
createStratifyByPsArgs
```

*Create a parameter object for the function stratifyByPs*

---

### Description

Create a parameter object for the function stratifyByPs

### Usage

```
createStratifyByPsArgs(numberOfStrata = 5, stratificationColumns = c())
```

### Arguments

`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

Create an object defining the parameter values.

---

```
createTrimByPsArgs
```

*Create a parameter object for the function trimByPs*

---

### Description

Create a parameter object for the function trimByPs

### Usage

```
createTrimByPsArgs(trimFraction = 0.05)
```

### Arguments

`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

Create an object defining the parameter values.

---

```
createTrimByPsToEquipoiseArgs
```

*Create a parameter object for the function trimByPsToEquipoise*

---

### Description

Create a parameter object for the function trimByPsToEquipoise

### Usage

```
createTrimByPsToEquipoiseArgs(bounds = c(0.25, 0.75))
```

### Arguments

bounds                      The upper and lower bound on the preference score for keeping persons

### Details

Create an object defining the parameter values.

---

```
drawAttritionDiagram    Draw the attrition diagram
```

---

### Description

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

### Usage

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

### Arguments

outcomeModel    An object of type outcomeModel as generated using the createOutcomeMode function.

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(outcomeId, cohortMethodData, excludePriorOutcome = TRUE,
  subPopulation = NULL, stratifiedCox = TRUE, riskWindowStart = 0,
  riskWindowEnd = 9999, addExposureDaysToEnd = FALSE,
  useCovariates = TRUE, fitModel = TRUE, modelType = "cox",
  prior = createPrior("laplace", useCrossValidation = TRUE),
  control = createControl(cvType = "auto", startingVariance = 0.1,
  selectorType = "byPid", noiseLevel = "quiet"))
```

## Arguments

|                      |  |
|----------------------|--|
| outcomeId            | The concept ID of the outcome. Persons marked for removal for the outcome will be removed prior to creating the outcome model.   |
| cohortMethodData     | An object of type cohortMethodData as generated using getDbCohortMethodData.   |
| excludePriorOutcome  | Remove people that have the outcome prior to the risk window start date?   |
| subPopulation        | A data frame specifying the (matched and/or trimmed) subpopulation to be used in the study, as well as their strata (for conditional models). This data frame should have at least a RowId, and a StratumId when including stratification. |
| stratifiedCox        | Specifically for Cox regressions: specify whether to use the strata defined in subPopulation in the analysis. For Poisson regression and logistic regression, this is implied in 'clr' and 'cpr'.  |
| riskWindowStart      | The start of the risk window (in days) relative to the index data.   |
| 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?  |
| useCovariates        | Whether to use the covariate matrix in the cohortMethodData in the outcome model.  |
| fitModel             | If false, the model will not be fit, and only summary statistics are available.  |
| modelType            | The type of model to be fitted. See details for options.   |
| prior                | The prior used to fit the model. See <a href="#">createPrior</a> for details.  |
| control              | The control object used to control the cross-validation used to determine the hyperparameters of the prior (if applicable). See <a href="#">createControl</a> for details.   |

## Details

The model type can be one of these:

|     |   |
|-----|---|
| lr  | Logistic regression   |
| clr | Conditional logistic regression   |
| cox | Cox regression (stratified or not, depending on whether stata is specified) |
| pr  | Poisson regression  |
| cpr | Conditional Poisson regression  |

## Value

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

## Examples

```
# todo
```

---

```
getDbCohortMethodData  Get the cohort data from the server
```

---

## 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,
  indicationConceptIds = c(), washoutWindow = 183,
  indicationLookbackWindow = 183, studyStartDate = "", studyEndDate = "",
  exclusionConceptIds = c(), outcomeIds,
  outcomeConditionTypeConceptIds = c(),
  exposureDatabaseSchema = cdmDatabaseSchema, exposureTable = "drug_era",
  outcomeDatabaseSchema = cdmDatabaseSchema,
  outcomeTable = "condition_occurrence", cdmVersion = "4",
  excludeDrugsFromCovariates = TRUE, 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. |
| indicationConceptIds           | A list of CONCEPT_IDs used to restrict the target and comparator cohorts, based on any descendant condition of this list occurring at least once within the indicationLookbackWindow prior to the cohort index date. If no concept IDs are specified, the cohorts are not restricted to any indication.           |
| washoutWindow                  | The minimum required continuous observation time prior to index date for a person to be included in the cohort.   |
| indicationLookbackWindow       | The window to look back prior to cohort index date to identify records of a indication condition. Only applicable if indicationConceptIds != ''.  |
| 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'.   |
| exclusionConceptIds            | A list of CONCEPT_IDs used to restrict the cohorts, based on any descendant conditions/drugs/procedures occurring at least once anytime prior to the cohort index date.   |
| outcomeIds                     | A list of CONCEPT_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.        |
| outcomeConditionTypeConceptIds | A list of TYPE_CONCEPT_ID values that will restrict condition occurrences. Only applicable if outcomeTable = CONDITION_OCCURRENCE.  |
| 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.  |

|   |   |
|---|---|
| <code>cdmVersion</code>                 | Define the OMOP CDM version used: currently support "4" and "5".  |
| <code>excludeDrugsFromCovariates</code> | 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). |
| <code>covariateSettings</code>          | An object of type <code>covariateSettings</code> as created using the <code>createCovariateSettings</code> function in the <code>PatientLevelPrediction</code> package..                          |

## Details

Based on the parameters, the treatment and comparator cohorts are constructed. Baseline covariates at or before the index date are extracted, as well as outcomes occurring on or after the index date. 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_occurrence` or `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. This function calls the `getDbCovariates` and `getDbOutcomes` functions. 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.

## Value

Returns an object of type `cohortMethodData`, containing information on the cohorts, their outcomes, and baseline covariates. Information about multiple outcomes can be captured at once for efficiency reasons. This object is a list with the following components:

**outcomes** An `ffdf` object listing the outcomes per person, including the time to event, and the outcome concept ID. Outcomes are not yet filtered based on risk window, since this is done at a later stage.

**cohorts** An `ffdf` object listing the persons in each cohort, listing their exposure status as well as the time to the end of the observation period and time to the end of the cohort (usually the end of the exposure era).

**covariates** An `ffdf` object listing the baseline covariates per person in the two cohorts. This is done using a sparse representation: covariates with a value of 0 are omitted to save space.

**exclude** An `ffdf` object listing for each outcome concept ID the persons that need to be excluded from the analysis because of prior outcomes.

**covariateRef** An `ffdf` object describing the covariates that have been extracted.

**metaData** A list of objects with information on how the `cohortMethodData` object was constructed.

The generic `summary()` function has been implemented for this object.

---

|               |  |
|---------------|--|
| getDbOutcomes | <i>Get outcomes for persons in the cohorts</i> |
|---------------|--|

---

## Description

Gets the outcomes for the cohorts in the cohortMethodData object.

## Usage

```
getDbOutcomes(connectionDetails = NULL, connection = NULL,
  cdmDatabaseSchema, oracleTempSchema = cdmDatabaseSchema, cohortMethodData,
  outcomeDatabaseSchema = cdmDatabaseSchema,
  outcomeTable = "condition_occurrence", outcomeIds = "",
  outcomeConditionTypeConceptIds = "", cdmVersion = "4")
```

## Arguments

|                                |  |
|--------------------------------|--|
| connectionDetails              | An R object of type ConnectionDetails created using the function createConnectionDetails in the DatabaseConnector package.   |
| connection                     | A connection to the server containing the schema as created using the connect function 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               | Schema where temp tables can be created in Oracle.   |
| cohortMethodData               | An object of type cohortMethodData as generated using getDbCohortMethodData.   |
| 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.   |
| outcomeIds                     | A list of CONCEPT_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. |
| outcomeConditionTypeConceptIds | A list of TYPE_CONCEPT_ID values that will restrict condition occurrences. Only applicable if outcomeTable = CONDITION_OCCURRENCE.   |
| cdmVersion                     | Define the OMOP CDM version used: currently support "4" and "5".   |

**Details**

If the connection parameter is specified, the cohorts are already assumed to be on the server in the appropriate temp table. Else, the temp table will be created by loading the cohorts from the cohortMethodData object to the server. This function can be used to add additional outcomes to an existing cohortMethodData object.

**Value**

The original cohortMethodData object with the new outcome data added.

---

|                 |                              |
|-----------------|------------------------------|
| 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

---

|                    |  |
|--------------------|--|
| 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 = FALSE)
```

**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(data, caliper = 0.25, caliperScale = "standardized",
  maxRatio = 1, stratificationColumns = c())
```

**Arguments**

|                       |   |
|-----------------------|---|
| data                  | 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:<br>caliperScale = 'propensity score' or caliperScale = 'standardized'.<br>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           | (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 |
| propensityScore | (real)    | 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(data, caliper = 0.25, caliperScale = "standardized",
                        maxRatio = 1, cohortMethodData, covariateIds)
```

**Arguments**

|                               |  |
|-------------------------------|--|
| <code>data</code>             | A data frame with the three columns described below.   |
| <code>caliper</code>          | 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.   |
| <code>caliperScale</code>     | The scale on which the caliper is defined. Two scales are supported: <code>caliperScale = 'propensity score'</code> or <code>caliperScale = 'standardized'</code> . On the standardized scale, the caliper is interpreted in standard deviations of the propensity score distribution. |
| <code>maxRatio</code>         | The maximum number of persons in the comparator arm to be matched to each person in the treatment arm. A <code>maxRatio</code> of 0 means no maximum: all comparators will be assigned to a treated person.  |
| <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 be also matched.  |

**Details**

The data frame should have at least 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> | (real)    | 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(outcomeModel, censorMarks = FALSE,  
  confidenceIntervals = TRUE, includeZero = TRUE, dataCutoff = 0.99,  
  treatmentLabel = "Treated", comparatorLabel = "Comparator",  
  title = "Kaplan-Meier Plot", fileName = NULL)
```

## Arguments

|                     |   |
|---------------------|---|
| outcomeModel        | An object of type outcomeModel as generated using the fitOutcomeModel function.   |
| 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 use for the treated cohort.  |
| comparatorLabel     | A label to use 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: <code>scale = 'propensity'</code> or <code>scale = 'preference'</code> . The preference score scale is defined by Walker et al (2013).          |
| type           | Type of plot. Two possible values: <code>type = 'density'</code> or <code>type = 'histogram'</code>   |
| 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 <code>ggsave</code> in the <code>ggplot2</code> package for supported file formats.                     |

## 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 | (real)    | 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.  |
| computeCovarBalThreads   | 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(data, numberOfStrata = 5, stratificationColumns = c())
```

### Arguments

|                       |  |
|-----------------------|--|
| data                  | 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           | (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 |
| propensityScore | (real)    | 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 covariatesto stratify persons.

**Usage**

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

**Arguments**

- data                    A data frame with the three columns described below
- numberOfStrata       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.
- cohortMethodData     An object of type cohortMethodData as generated using getDbCohortMethodData.
- covariateIds         One or more covariate IDs in the cohortMethodData object on which subjects should also be stratified.

**Details**

The data frame should have the following three 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
- propensityScore     (real)       Propensity score

**Value**

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

**Examples**

```
# todo
```

---

|                   |   |
|-------------------|---|
| summarizeAnalyses | Create a summary report of the analyses |
|-------------------|---|

---

**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 | <i>Trim persons by propensity score</i> |
|----------|---|

---

**Description**

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

**Usage**

```
trimByPs(data, trimFraction = 0.05)
```

**Arguments**

|              |   |
|--------------|---|
| data         | 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           | (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 |
| propensityScore | (real)    | 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(data, bounds = c(0.25, 0.75))
```

**Arguments**

|        |   |
|--------|---|
| data   | 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           | (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 |
| propensityScore | (real)    | 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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