

# Single studies using the CohortMethod package

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## 1 Introduction

This vignette describes how you can use the `CohortMethod` package to perform a single new-user cohort study. We will walk through all the steps needed to perform an exemplar study, and we have selected the well-studied topic of the effect of coxibs versus non-selective non-steroidal anti-inflammatory drugs (NSAIDs) on gastrointestinal (GI) bleeding-related hospitalization. For simplicity, we focus on one coxib – celecoxib – and one non-selective NSAID – diclofenac.

## 2 Installation instructions

Before installing the `CohortMethod` package make sure you have Java available. For Windows users, RTools is also necessary. See these instructions for properly configuring your R environment.

The `CohortMethod` package is currently maintained in a Github repository, and has dependencies on other packages in Github. All of these packages can be downloaded and installed from within R using the `drat` package:

```
install.packages("remotes")
remotes::install_github("ohdsi/CohortMethod")
```

Once installed, you can type `library(CohortMethod)` to load the package.

## 3 Data extraction

The first step in running the `CohortMethod` is extracting all necessary data from the database server holding the data in the Observational Medical Outcomes Partnership (OMOP) Common Data Model (CDM) format.

### 3.1 Configuring the connection to the server

We need to tell R how to connect to the server where the data are. `CohortMethod` uses the `DatabaseConnector` package, which provides the `createConnectionDetails` function. Type `?createConnectionDetails` for the specific settings required for the various database management systems (DBMS). For example, one might connect to a PostgreSQL database using this code:

```
connectionDetails <- createConnectionDetails(dbms = "postgresql",
                                             server = "localhost/ohdsi",
                                             user = "joe",
                                             password = "supersecret")

cdmDatabaseSchema <- "my_cdm_data"
cohortDatabaseSchema <- "my_results"
cohortTable <- "my_cohorts"
options(sqlRenderTempEmulationSchema = NULL)
```

The last few lines define the `cdmDatabaseSchema`, `cohortDatabaseSchema`, and `cohortTable` variables. We'll use these later to tell R where the data in CDM format live, and where we want to write intermediate tables. Note that for Microsoft SQL Server, databaseschemas need to specify both the database and the schema, so for example `cdmDatabaseSchema <- "my_cdm_data.dbo"`. For database platforms that do not support temp tables, such as Oracle, it is also necessary to provide a schema where the user has write access that can be used to emulate temp tables. PostgreSQL supports temp tables, so we can set `options(sqlRenderTempEmulationSchema = NULL)` (or not set the `sqlRenderTempEmulationSchema` at all.)

### 3.2 Preparing the exposures and outcome(s)

We need to define the exposures and outcomes for our study. Here, we will define our exposures using the `OHDSI Capr` package. We define two cohorts, one for celecoxib and one for diclofenac. For each cohort we require a prior diagnosis of 'osteoarthritis of knee', and 365 days of continuous prior observation. we restrict to the first exposure per person:

```
library(Capr)

osteoArthritisOfKneeConceptId <- 4079750
celecoxibConceptId <- 1118084
```

```

diclofenacConceptId <- 1124300
osteoArthritisOfKnee <- cs(
  descendants(osteoArthritisOfKneeConceptId),
  name = "Osteoarthritis of knee"
)
attrition = attrition(
  "prior osteoarthritis of knee" = withAll(
    atLeast(1, conditionOccurrence(osteoArthritisOfKnee), duringInterval(eventStarts(-Inf, 0)))
  )
)
celecoxib <- cs(
  descendants(celecoxibConceptId),
  name = "Celecoxib"
)
diclofenac <- cs(
  descendants(diclofenacConceptId),
  name = "Diclofenac"
)
celecoxibCohort <- cohort(
  entry = entry(
    drugExposure(celecoxib, firstOccurrence()),
    observationWindow = continuousObservation(priorDays = 365)
  ),
  attrition = attrition,
  exit = exit(endStrategy = drugExit(celecoxib,
                                     persistenceWindow = 30,
                                     surveillanceWindow = 0))
)
diclofenacCohort <- cohort(
  entry = entry(
    drugExposure(diclofenac, firstOccurrence()),
    observationWindow = continuousObservation(priorDays = 365)
  ),
  attrition = attrition,
  exit = exit(endStrategy = drugExit(diclofenac,
                                     persistenceWindow = 30,
                                     surveillanceWindow = 0))
)
# Note: this will automatically assign cohort IDs 1 and 2, respectively:
exposureCohorts <- makeCohortSet(celecoxibCohort, diclofenacCohort)

```

We'll pull the outcome definition from the OHDSI PhenotypeLibrary:

```

library(PhenotypeLibrary)
outcomeCohorts <- getPlCohortDefinitionSet(77) # GI bleed

```

We combine the exposure and outcome cohort definitions, and use CohortGenerator to generate the cohorts:

```

allCohorts <- bind_rows(outcomeCohorts,
                        exposureCohorts)

library(CohortGenerator)
cohortTableNames <- getCohortTableNames(cohortTable = cohortTable)
createCohortTables(connectionDetails = connectionDetails,
                   cohortDatabaseSchema = cohortDatabaseSchema,

```

```

        cohortTableNames = cohortTableNames)
generateCohortSet(connectionDetails = connectionDetails,
                  cdmDatabaseSchema = cdmDatabaseSchema,
                  cohortDatabaseSchema = cohortDatabaseSchema,
                  cohortTableNames = cohortTableNames,
                  cohortDefinitionSet = allCohorts)

```

If all went well, we now have a table with the cohorts of interest. We can see how many entries per cohort:

```

connection <- DatabaseConnector::connect(connectionDetails)
sql <- "SELECT cohort_definition_id, COUNT(*) AS count FROM @cohortDatabaseSchema.@cohortTable GROUP BY cohort_definition_id"
DatabaseConnector::renderTranslateQuerySql(connection, sql, cohortDatabaseSchema = cohortDatabaseSchema)
DatabaseConnector::disconnect(connection)

```

```

## cohort_concept_id count
## 1 109307
## 2 176675
## 3 77 733601

```

### 3.3 Extracting the data from the server

Now we can tell CohortMethod to extract the cohorts, construct covariates, and extract all necessary data for our analysis.

**Important:** The target and comparator drug must not be included in the covariates, including any descendant concepts. You will need to manually add the drugs and descendants to the `excludedCovariateConceptIds` of the covariate settings. In this example code we exclude the concepts for celecoxib and diclofenac and specify `addDescendantsToExclude = TRUE`:

```

# Define which types of covariates must be constructed:
covSettings <- createDefaultCovariateSettings(
  excludedCovariateConceptIds = c(diclofenacConceptId, celecoxibConceptId),
  addDescendantsToExclude = TRUE
)

#Load data:
cohortMethodData <- getDbCohortMethodData(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = cdmDatabaseSchema,
  targetId = 1,
  comparatorId = 2,
  outcomeIds = 77,
  exposureDatabaseSchema = cohortDatabaseSchema,
  exposureTable = cohortTable,
  outcomeDatabaseSchema = cohortDatabaseSchema,
  outcomeTable = cohortTable,
  covariateSettings = covSettings
)
cohortMethodData

## # CohortMethodData object
##
## Target cohort ID: 1
## Comparator cohort ID: 2
## Outcome cohort ID(s): 77
##
## Inherits from CovariateData:
## # CovariateData object

```

```
##
## All cohorts
##
## Inherits from Andromeda:
## # Andromeda object
## # Physical location: C:\Users\admin_mschuemi.EU\AppData\Local\Temp\2\RtmpsJCizU\file3d0c1e746f15.duckdb
##
## Tables:
## $analysisRef (analysisId, analysisName, domainId, startDay, endDay, isBinary, missingMeansZero)
## $cohorts (rowId, personSeqId, personId, treatment, cohortStartDate, daysFromObsStart, daysToCohortEnd, daysToObsEnd)
## $covariateRef (covariateId, covariateName, analysisId, conceptId, valueAsConceptId, collisions)
## $covariates (rowId, covariateId, covariateValue)
## $outcomes (rowId, outcomeId, daysToEvent)
```

There are many parameters, but they are all documented in the `CohortMethod` manual. The `createDefaultCovariateSettings` function is described in the `FeatureExtraction` package. In short, we are pointing the function to the table created earlier and indicating which concept IDs in that table identify the target, comparator and outcome. We instruct that the default set of covariates should be constructed, including covariates for all conditions, drug exposures, and procedures that were found on or before the index date. To customize the set of covariates, please refer to the `FeatureExtraction` package vignette by typing `vignette("UsingFeatureExtraction", package="FeatureExtraction")`.

All data about the cohorts, outcomes, and covariates are extracted from the server and stored in the `cohortMethodData` object. This object uses the `Andromeda` package to store information in a way that ensures R does not run out of memory, even when the data are large. We can use the generic `summary()` function to view some more information of the data we extracted:

```
summary(cohortMethodData)
```

```
## CohortMethodData object summary
##
## Target cohort ID: 1
## Comparator cohort ID: 2
## Outcome cohort ID(s): 77
##
## Target persons: 120201
## Comparator persons: 182281
##
## Outcome counts:
##   Event count Person count
## 77      54231      29027
##
## Covariates:
## Number of covariates: 93004
## Number of non-zero covariate values: 157142848
```

### 3.3.1 Saving the data to file

Creating the `cohortMethodData` file can take considerable computing time, and it is probably a good idea to save it for future sessions. Because `cohortMethodData` uses `Andromeda`, we cannot use R's regular save function. Instead, we'll have to use the `saveCohortMethodData()` function:

```
saveCohortMethodData(cohortMethodData, "coxibVsNonselVsGiBleed.zip")
```

We can use the `loadCohortMethodData()` function to load the data in a future session.

### 3.3.2 Defining new users

Typically, a new user is defined as first time use of a drug (either target or comparator), and typically a washout period (a minimum number of days prior first use) is used to make sure it is truly first use. When using the `CohortMethod` package, you can enforce the necessary requirements for new use in three ways:

1. When creating the cohorts in the database, for example using `Capr`.
2. When loading the cohorts using the `getDbCohortMethodData` function, you can use the `firstExposureOnly`, `removeDuplicateSubjects`, `restrictToCommonPeriod`, and `washoutPeriod` arguments. (As shown in the example above).
3. When defining the study population using the `createStudyPopulation` function (see below) using the `firstExposureOnly`, `removeDuplicateSubjects`, `restrictToCommonPeriod`, and `washoutPeriod` arguments.

The advantage of option 1 is that the input cohorts are already fully defined outside of the `CohortMethod` package, and for example external cohort characterization tools can be used on the same cohorts used in this package. The advantage of options 2 and 3 is that it saves you the trouble of limiting to first use yourself, for example allowing you to directly use the `drug_era` table in the CDM. Option 2 is more efficient than 3, since only data for first use will be fetched, while option 3 is less efficient but allows you to compare the original cohorts to the study population.

## 4 Defining the study population

Typically, the exposure cohorts and outcome cohorts will be defined independently of each other. When we want to produce an effect size estimate, we need to further restrict these cohorts and put them together, for example by removing exposed subjects that had the outcome prior to exposure, and only keeping outcomes that fall within a defined risk window. For this we can use the `createStudyPopulation` function:

```
studyPop <- createStudyPopulation(  
  cohortMethodData = cohortMethodData,  
  outcomeId = 3,  
  firstExposureOnly = FALSE,  
  restrictToCommonPeriod = FALSE,  
  washoutPeriod = 0,  
  removeDuplicateSubjects = "keep all",  
  removeSubjectsWithPriorOutcome = TRUE,  
  minDaysAtRisk = 1,  
  riskWindowStart = 0,  
  startAnchor = "cohort start",  
  riskWindowEnd = 30,  
  endAnchor = "cohort end"  
)
```

Note that we've set `firstExposureOnly` and `removeDuplicateSubjects` to `FALSE`, and `washoutPeriod` to zero because we already filtered on these arguments when using the `getDbCohortMethodData` function. During loading we set `restrictToCommonPeriod` to `FALSE`, and we do the same here because we do not want to force the comparison to restrict only to time when both drugs are recorded. We specify the outcome ID we will use, and that people with outcomes prior to the risk window start date will be removed. The risk window is defined as starting at the cohort start date (the index date, `riskWindowStart = 0` and `startAnchor = "cohort start"`), and the risk windows ends 30 days after the cohort ends (`riskWindowEnd = 30` and `endAnchor = "cohort end"`). Note that the risk windows are truncated at the end of observation or the study end date. We also remove subjects who have no time at risk. To see how many people are left in the study population we can always use the `getAttritionTable` function:

```
getAttritionTable(studyPop)
```

```
## # A tibble: 4 x 5
```

##	description	targetPersons	comparatorPersons	targetExposures	comparatorExposures
##	<chr>	<int>	<int>	<int>	<int>
## 1	Original cohorts	120201	182281	120201	182281
## 2	Restricting duplicate subje ...	109596	169374	109596	169374
## 3	No prior outcome	105754	160964	105754	160964
## 4	Have at least 1 days at ris ...	105703	160883	105703	160883

One additional filtering step that is often used is matching or trimming on propensity scores, as will be discussed next.

## 5 Propensity scores

The `CohortMethod` can use propensity scores to adjust for potential confounders. Instead of the traditional approach of using a handful of predefined covariates, `CohortMethod` typically uses thousands to millions of covariates that are automatically constructed based on conditions, procedures and drugs in the records of the subjects.

### 5.1 Fitting a propensity model

We can fit a propensity model using the covariates constructed by the `getDbcohortMethodData()` function:

```
ps <- createPs(cohortMethodData = cohortMethodData, population = studyPop)
```

The `createPs()` function uses the `Cyclops` package to fit a large-scale regularized logistic regression.

To fit the propensity model, `Cyclops` needs to know the hyperparameter value which specifies the variance of the prior. By default `Cyclops` will use cross-validation to estimate the optimal hyperparameter. However, be aware that this can take a really long time. You can use the `prior` and `control` parameters of the `createPs()` to specify `Cyclops` behavior, including using multiple CPUs to speed-up the cross-validation.

### 5.2 Propensity score diagnostics

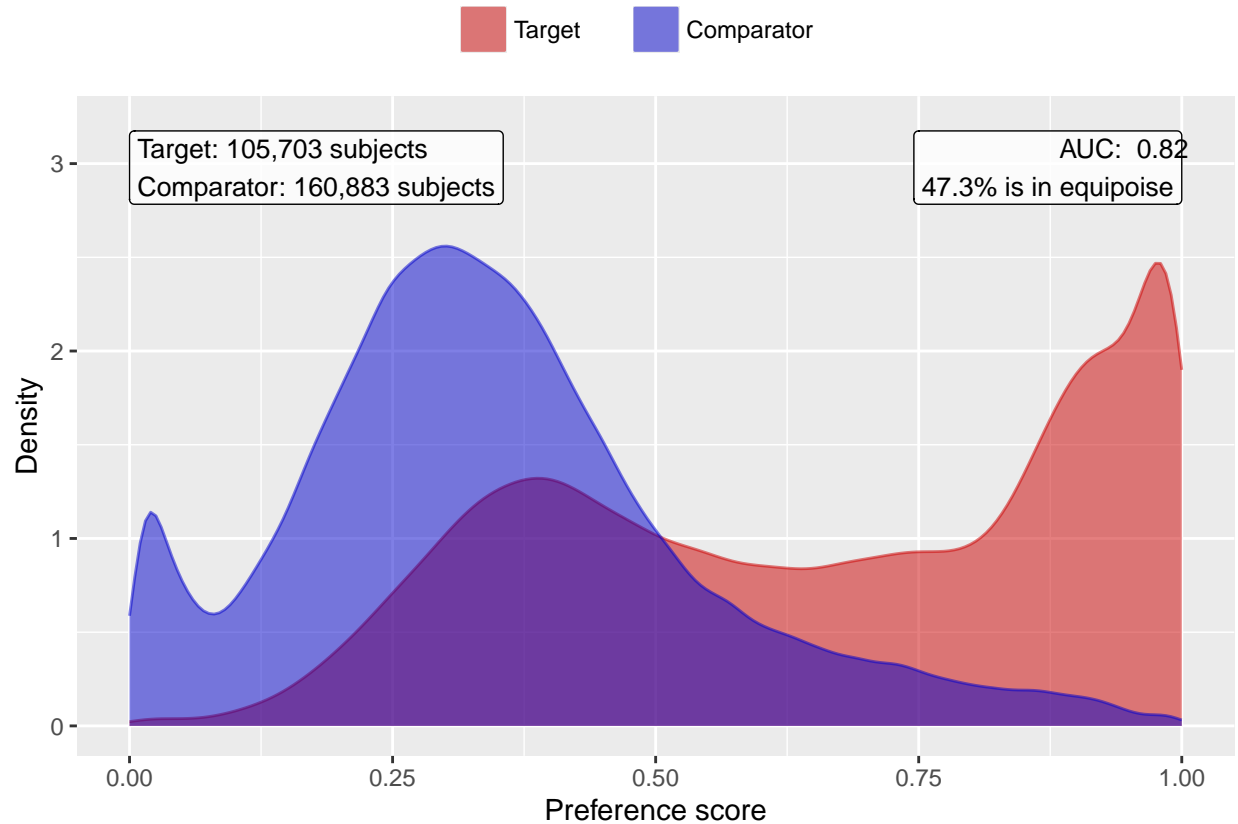
We can compute the area under the receiver-operator curve (AUC) for the propensity score model:

```
computePsAuc(ps)
```

```
## [1] 0.81
```

We can also plot the propensity score distribution, although we prefer the preference score distribution:

```
plotPs(ps,
  scale = "preference",
  showCountsLabel = TRUE,
  showAucLabel = TRUE,
  showEquiposeLabel = TRUE)
```



It is also possible to inspect the propensity model itself by showing the covariates that have non-zero coefficients:

```
getPsModel(ps, cohortMethodData)
```

```
## # A tibble: 6 x 3
##   coefficient covariateId covariateName
##   <dbl>      <dbl> <chr>
## 1    -3.52  1150871413 ...gh 0 days relative to index: misoprostol
## 2     2.96   2001006 index year: 2001
## 3     2.79   2002006 index year: 2002
## 4     2.39   2003006 index year: 2003
## 5     2.20   2004006 index year: 2004
## 6    -1.52  2211735504 ... with intraocular lens power calculation
```

One advantage of using the regularization when fitting the propensity model is that most coefficients will shrink to zero and fall out of the model. It is a good idea to inspect the remaining variables for anything that should not be there, for example variations of the drugs of interest that we forgot to exclude.

Finally, we can inspect the percent of the population in equipoise, meaning they have a preference score between 0.3 and 0.7:

```
CohortMethod::computeEquipoise(ps)
```

```
## [1] 0.4733744
```

A low equipoise indicates there is little overlap between the target and comparator populations.

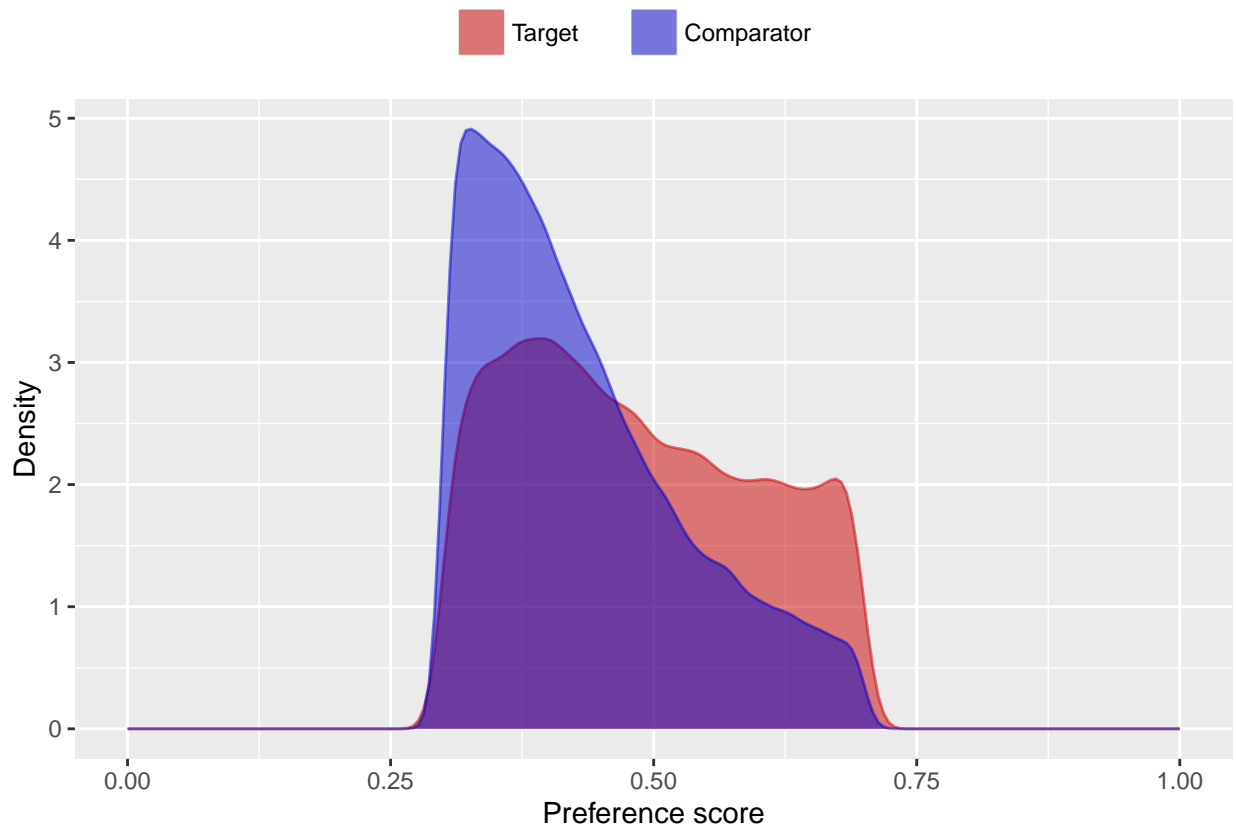


### 5.3 Using the propensity score

We can use the propensity scores to trim, stratify, match, or weigh our population. For example, one could trim to equipoise, meaning only subjects with a preference score between 0.25 and 0.75 are kept:

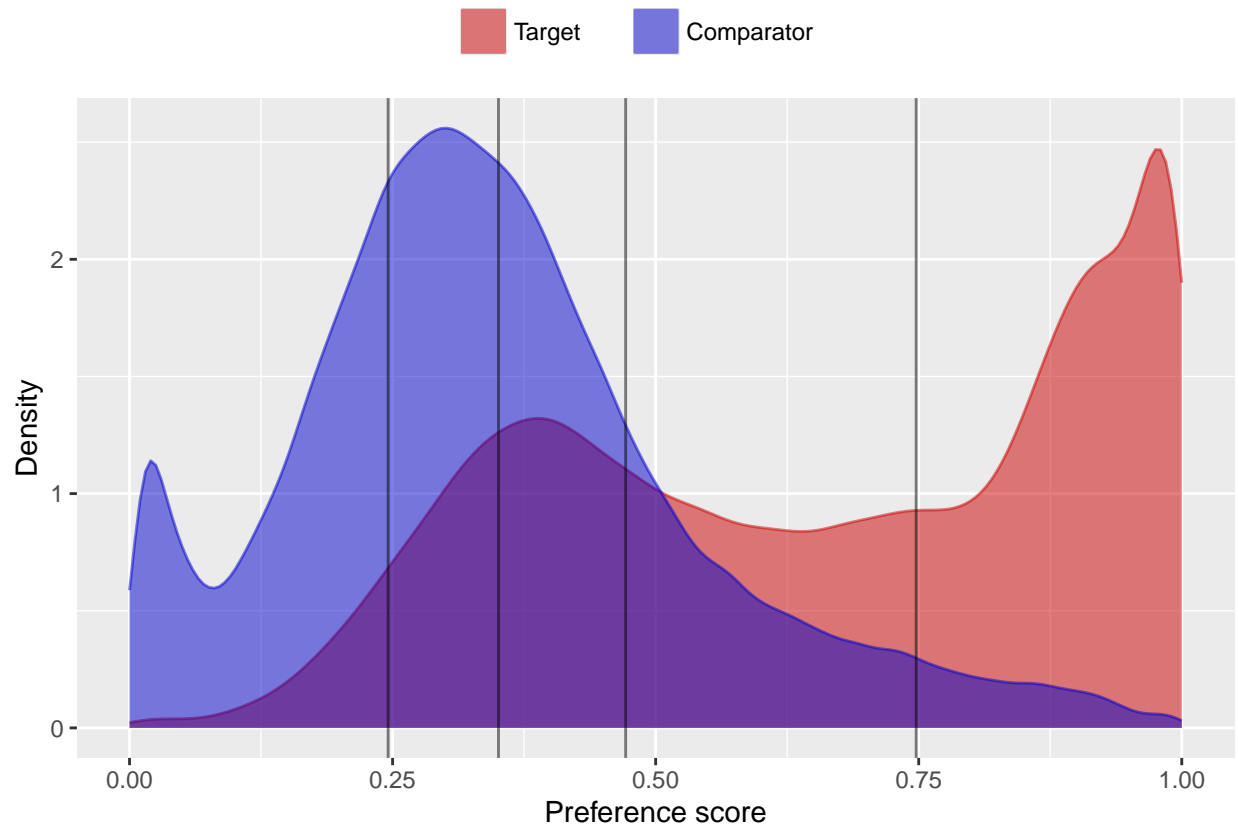
```
trimmedPop <- trimByPsToEquipoise(ps)
plotPs(trimmedPop, ps, scale = "preference")
```

```
## Population size after trimming is 126195
```



Instead (or additionally), we could stratify the population based on the propensity score:

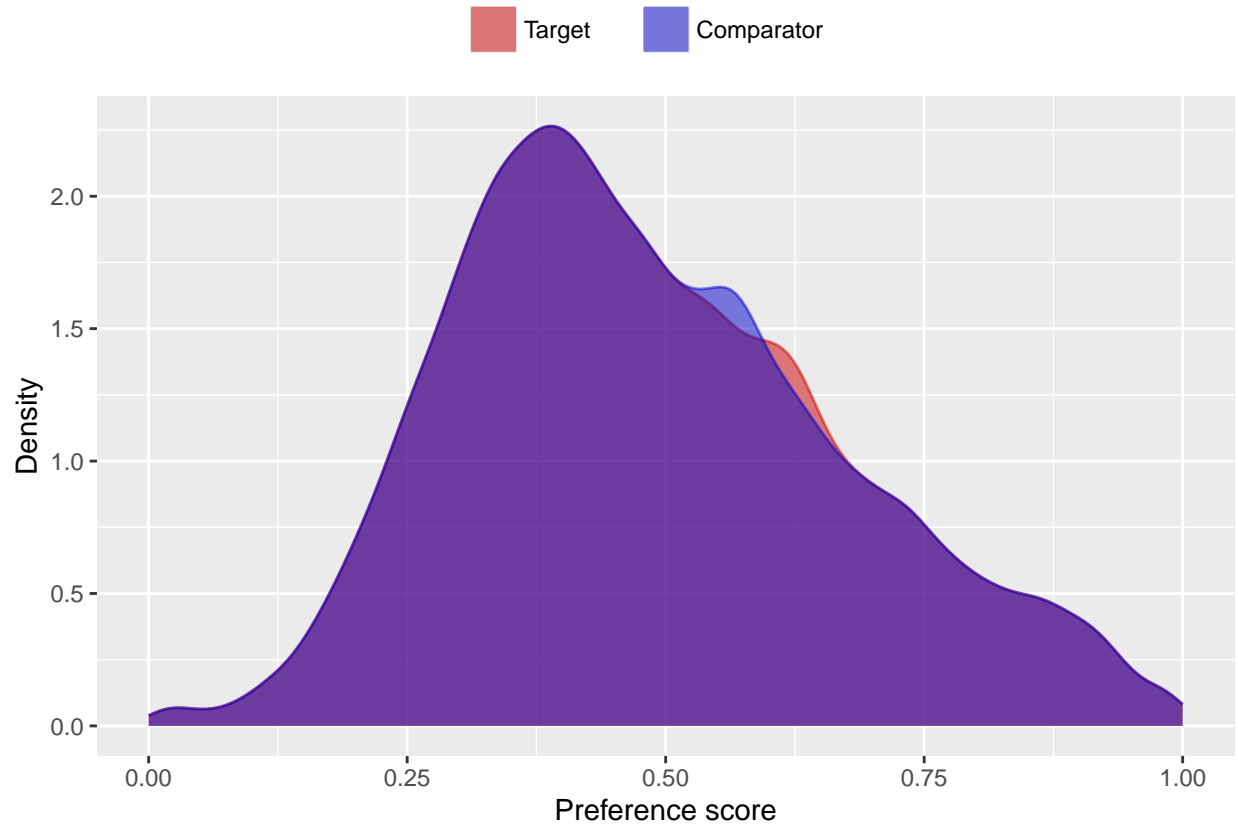
```
stratifiedPop <- stratifyByPs(ps, numberOfStrata = 5)
plotPs(stratifiedPop, ps, scale = "preference")
```



We can also match subjects based on propensity scores. In this example, we're using one-to-one matching:

```
matchedPop <- matchOnPs(ps, caliper = 0.2, caliperScale = "standardized logit", maxRatio = 1)
plotPs(matchedPop, ps)
```

```
## Population size after matching is 124148
```



Note that for both stratification and matching it is possible to specify additional matching criteria such as age and sex using the `stratifyByPsAndCovariates()` and `matchOnPsAndCovariates()` functions, respectively.

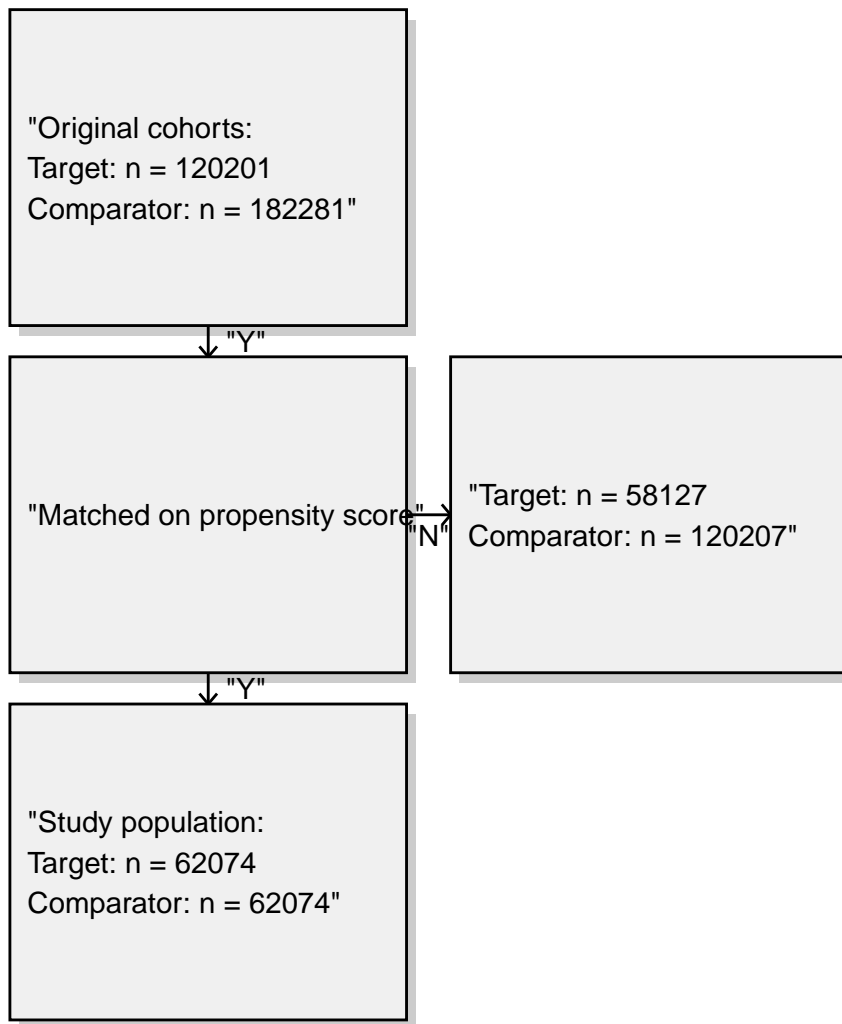
We can see the effect of trimming and/or matching on the population using the `getAttritionTable` function:

```
getAttritionTable(matchedPop)
```

```
## # A tibble: 2 x 5
##   description          targetPersons comparatorPersons targetExposures comparatorExposures
##   <chr>                <int>          <int>          <int>          <int>
## 1 Original cohorts      120201        182281        120201        182281
## 2 Matched on propensity 62074         62074         62074         62074
```

Or, if we like, we can plot an attrition diagram:

```
drawAttritionDiagram(matchedPop)
```



## 5.4 Evaluating covariate balance

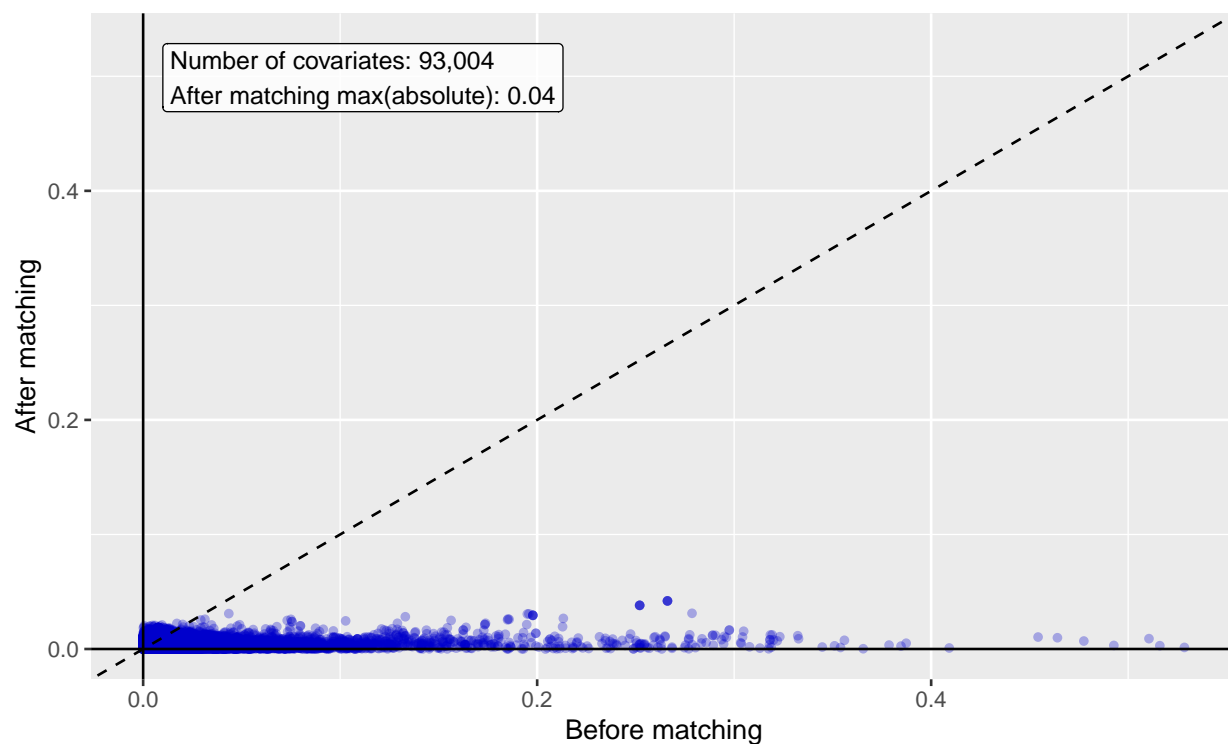
To evaluate whether our use of the propensity score is indeed making the two cohorts more comparable, we can compute the covariate balance before and after trimming, matching, and/or stratifying:

```
balance <- computeCovariateBalance(matchedPop, cohortMethodData)
```

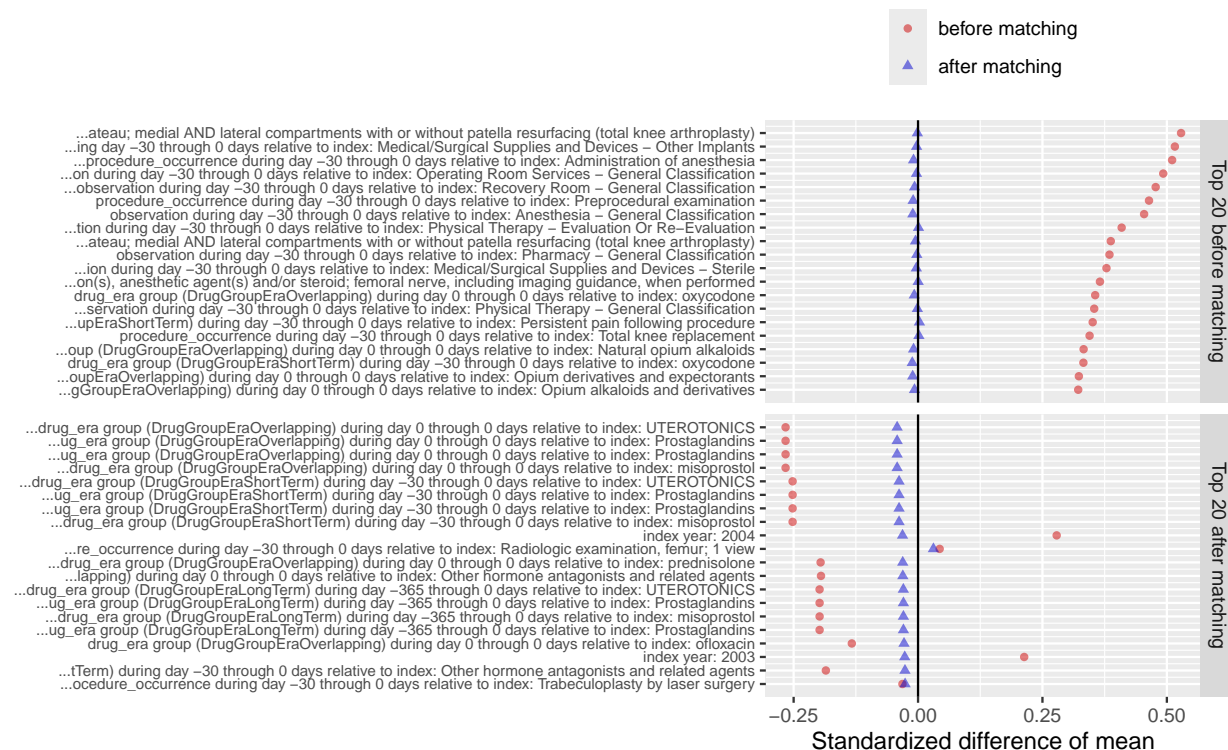
```
plotCovariateBalanceScatterPlot(balance, showCovariateCountLabel = TRUE, showMaxLabel = TRUE)
```

```
## Warning: Removed 34407 rows containing missing values or values outside the scale range (`geom_point`)
```

## Standardized difference of mean



```
plotCovariateBalanceOfTopVariables(balance)
```



The 'before matching' population is the population as extracted by the `getDbCohortMethodData` function,

so before any further filtering steps.

## 5.5 Inspecting select population characteristics

It is customary to include a table in your paper that lists some select population characteristics before and after matching/stratification/trimming. This is usually the first table, and so will be referred to as ‘table 1’. To generate this table, you can use the `createCmTable1` function:

```
createCmTable1(balance)
```

Characteristic	Before matching			After matching		
	Target %	Comparator %	Std. diff	Target %	Comparator %	Std. diff
Age group						
40 - 44	0.0	0.0	0.00	0.0	0.0	0.00
45 - 49	0.0	0.0	0.00	0.0	0.0	0.00
50 - 54	0.1	0.2	0.00	0.1	0.2	-0.01
55 - 59	0.4	0.5	-0.02	0.5	0.5	-0.01
60 - 64	1.0	1.2	-0.03	1.1	1.1	0.00
65 - 69	21.9	19.0	0.07	22.1	22.0	0.00
70 - 74	28.6	26.0	0.06	27.6	27.5	0.00
75 - 79	22.6	21.8	0.02	21.7	21.8	0.00
80 - 84	15.0	16.3	-0.04	15.3	15.2	0.00
85 - 89	7.4	9.9	-0.09	8.0	8.0	0.00
90 - 94	2.5	4.0	-0.08	2.8	2.9	0.00
95 - 99	0.4	0.9	-0.06	0.5	0.6	0.00
100 - 104	0.0	0.1	-0.02	0.0	0.1	-0.01
105 - 109	0.0	0.0	0.00		0.0	
Gender: female	64.1	67.6	-0.07	66.2	66.1	0.00
Medical history: General						
Acute respiratory disease	22.8	25.7	-0.07	24.1	24.0	0.00
Attention deficit hyperactivity disorder	0.2	0.2	0.00	0.2	0.2	0.00
Chronic liver disease	1.1	1.4	-0.03	1.1	1.2	0.00
Chronic obstructive pulmonary disease	10.0	11.6	-0.05	10.0	10.0	0.00
Crohn's disease	0.4	0.4	-0.01	0.4	0.4	0.00
Dementia	2.6	4.2	-0.09	2.9	2.9	0.00
Depressive disorder	10.2	12.1	-0.06	10.6	10.5	0.00
Diabetes mellitus	23.5	28.2	-0.11	24.6	24.6	0.00
Gastroesophageal reflux disease	18.1	19.9	-0.05	18.0	17.7	0.01
Gastrointestinal hemorrhage	3.6	3.9	-0.02	2.3	2.3	0.00
Human immunodeficiency virus infection	0.1	0.1	-0.01	0.1	0.1	0.00
Hyperlipidemia	48.5	54.1	-0.11	49.9	49.4	0.01
Hypertensive disorder	65.2	69.7	-0.10	65.5	65.4	0.00
Lesion of liver	0.5	0.7	-0.02	0.5	0.5	0.00
Obesity	11.4	11.3	0.00	10.2	10.1	0.01
Osteoarthritis	88.0	82.4	0.15	85.1	85.2	0.00
Pneumonia	4.4	5.4	-0.05	4.3	4.3	0.00
Psoriasis	1.4	1.5	-0.01	1.4	1.4	0.00
Renal impairment	7.8	13.4	-0.18	8.3	8.2	0.00
Rheumatoid arthritis	3.5	4.3	-0.04	3.7	3.7	0.00
Schizophrenia	0.1	0.1	-0.01	0.1	0.1	0.00
Ulcerative colitis	0.6	0.6	-0.01	0.5	0.5	0.00
Urinary tract infectious disease	11.6	13.9	-0.07	12.0	12.1	0.00
Viral hepatitis C	0.2	0.3	-0.02	0.2	0.2	0.00
Medical history: Cardiovascular disease						
Atrial fibrillation	9.8	12.2	-0.07	9.8	9.8	0.00
Cerebrovascular disease	11.1	12.7	-0.05	11.2	11.2	0.00
Coronary arteriosclerosis	19.4	21.6	-0.05	18.6	18.9	-0.01
Heart disease	44.0	45.8	-0.04	41.6	42.0	-0.01
Heart failure	8.0	10.7	-0.09	7.7	7.8	0.00
Ischemic heart disease	9.1	9.8	-0.03	8.4	8.5	-0.01
Peripheral vascular disease	9.4	12.8	-0.11	9.9	9.9	0.00
Pulmonary embolism	1.1	1.3	-0.02	1.1	1.1	0.00
Venous thrombosis	3.3	4.0	-0.03	3.4	3.5	0.00
Medical history: Neoplasms						
Malignant lymphoma	0.8	0.8	-0.01	0.7	0.8	-0.01
Malignant neoplasm of anorectum	0.3	0.3	0.01	0.3	0.3	0.00
Malignant neoplastic disease	18.8	19.6	-0.02	18.7	18.8	0.00
Malignant tumor of breast	3.8	4.2	-0.02	4.0	3.9	0.00
Malignant tumor of colon	0.7	0.7	0.00	0.6	0.6	0.00
Malignant tumor of lung	0.3	0.4	-0.02	0.4	0.4	-0.01
Malignant neoplasm of urinary bladder	0.8	0.9	-0.01	0.8	0.8	0.00
Primary malignant neoplasm of prostate	3.7	3.4	0.02	3.5	3.5	0.00
Medication use						
Agents acting on the renin-angiotensin system	50.7	53.9	-0.07	52.1	51.9	0.00
Antibacterials for systemic use	70.4	71.8	-0.03	69.5	69.6	0.00
Antidepressants	29.7	31.9	-0.05	31.0	31.0	0.00
Antiepileptics	22.4	23.3	-0.02	21.8	21.8	0.00
Antiinflammatory and antirheumatic products	38.3	36.0	0.05	37.8	37.8	0.00
Antineoplastic agents	5.2	5.9	-0.03	5.4	5.4	0.00
Antipsoriaties	0.9	1.3	-0.04	0.9	1.0	0.00
Antithrombotic agents	29.3	25.6	0.08	24.0	24.3	-0.01
Beta blocking agents	37.1	41.7	-0.09	38.0	38.0	0.00
Calcium channel blockers	28.8	31.9	-0.07	29.4	29.4	0.00
Diuretics	45.1	47.7	-0.05	45.4	45.6	0.00
Drugs for acid related disorders	43.6	45.6	-0.04	41.4	41.7	-0.01
Drugs for obstructive airway diseases	53.4	55.6	-0.04	54.4	54.2	0.00
Drugs used in diabetes	18.7	22.0	-0.08	19.5	19.6	0.00
Immunosuppressants	4.7	6.0	-0.06	5.1	5.1	0.00
Lipid modifying agents	56.4	59.8	-0.07	58.1	58.0	0.00
Opioids	66.4	58.3	0.17	59.8	60.2	-0.01
Psycholeptics	35.5	34.6	0.02	34.7	34.8	0.00
Psychostimulants, agents used for adhd and nootropics	1.9	2.1	-0.01	2.0	2.1	-0.01

## 5.6 Generalizability

The goal of any propensity score adjustments is typically to make the target and comparator cohorts comparably, to allow proper causal inference. However, in doing so, we often need to modify our population, for example dropping subjects that have no counterpart in the other exposure cohort. The population we end up estimating an effect for may end up being very different from the population we started with. An important question is: how different? And in what ways? If the populations before and after adjustment are very different, our estimated effect may not generalize to the original population (if effect modification is present). The `getGeneralizabilityTable()` function informs on these differences:

```
getGeneralizabilityTable(balance)
```

```
# A tibble: 93,004 x 5
  covariateId covariateName beforeMatchingMean afterMatchingMean stdDiff
  <dbl> <chr> <dbl> <dbl> <dbl>
1 4160439504 ...: Administration of anesthesia 0.161 0.0296 0.358
2 2105103504 ...cing (total knee arthroplasty) 0.119 0.00975 0.336
3 38003162804 ...s and Devices - Other Implants 0.129 0.0175 0.333
4 38003208804 ...vices - General Classification 0.145 0.0298 0.327
5 38003390804 ... Room - General Classification 0.138 0.0279 0.318
6 38003213804 ...hesia - General Classification 0.125 0.0249 0.303
7 764608504 ...dex: Preprocedural examination 0.107 0.0149 0.297
8 38003138804 ...rmacy - General Classification 0.179 0.0680 0.290
9 38003245804 ... - Evaluation Or Re-Evaluation 0.124 0.0305 0.284
10 2105103502 ...cing (total knee arthroplasty) 0.171 0.0685 0.272
# i 92,994 more rows
```

In this case, because we used PS matching, we are likely aiming to estimate the average treatment effect in the treated (ATT). For this reason, the `getGeneralizabilityTable()` function automatically selected the target cohort as the basis for evaluating generalizability: it shows, for each covariate, the mean value before and PS adjustment in the target cohort. Also shown is the standardized difference of mean, and the table is reverse sorted by the absolute standard difference of mean (ASDM).

## 6 Follow-up and power

Before we start fitting an outcome model, we might be interested to know whether we have sufficient power to detect a particular effect size. It makes sense to perform these power calculations once the study population has been fully defined, so taking into account loss to the various inclusion and exclusion criteria (such as no prior outcomes), and loss due to matching and/or trimming. Since the sample size is fixed in retrospective studies (the data has already been collected), and the true effect size is unknown, the CohortMethod package provides a function to compute the minimum detectable relative risk (MDRR) instead:

```
computeMdr(
  population = studyPop,
  modelType = "cox",
  alpha = 0.05,
  power = 0.8,
  twoSided = TRUE
)
```

```
## targetPersons comparatorPersons targetExposures comparatorExposures targetDays comparatorDays totalOutcomes mdr se
## 1 105703 160883 105703 160883 14398133 12594077 1435 1.163215 0.05396506
```

In this example we used the `studyPop` object, so the population before any matching or trimming. If we want to know the MDRR after matching, we use the `matchedPop` object we created earlier instead:

```
computeMdr(
  population = matchedPop,
```

```

modelType = "cox",
alpha = 0.05,
power = 0.8,
twoSided = TRUE
)

```

```

## targetPersons comparatorPersons targetExposures comparatorExposures targetDays comparatorDays totalOutcomes mdrr se
## 1 62074 62074 62074 62074 8924422 5208859 670 1.241685 0.07726674

```

Even though the MDRR in the matched population is higher, meaning we have less power, we should of course not be fooled: matching most likely eliminates confounding, and is therefore preferred to not matching.

To gain a better understanding of the amount of follow-up available we can also inspect the distribution of follow-up time. We defined follow-up time as time at risk, so not censored by the occurrence of the outcome. The `getFollowUpDistribution` can provide a simple overview:

```

getFollowUpDistribution(population = matchedPop)

```

```

## 100% 75% 50% 25% 0% Treatment
## 1 2 60 60 134 4232 1
## 2 2 45 60 75 3833 0

```

The output is telling us number of days of follow-up each quantile of the study population has. We can also plot the distribution:

```

plotFollowUpDistribution(population = matchedPop)

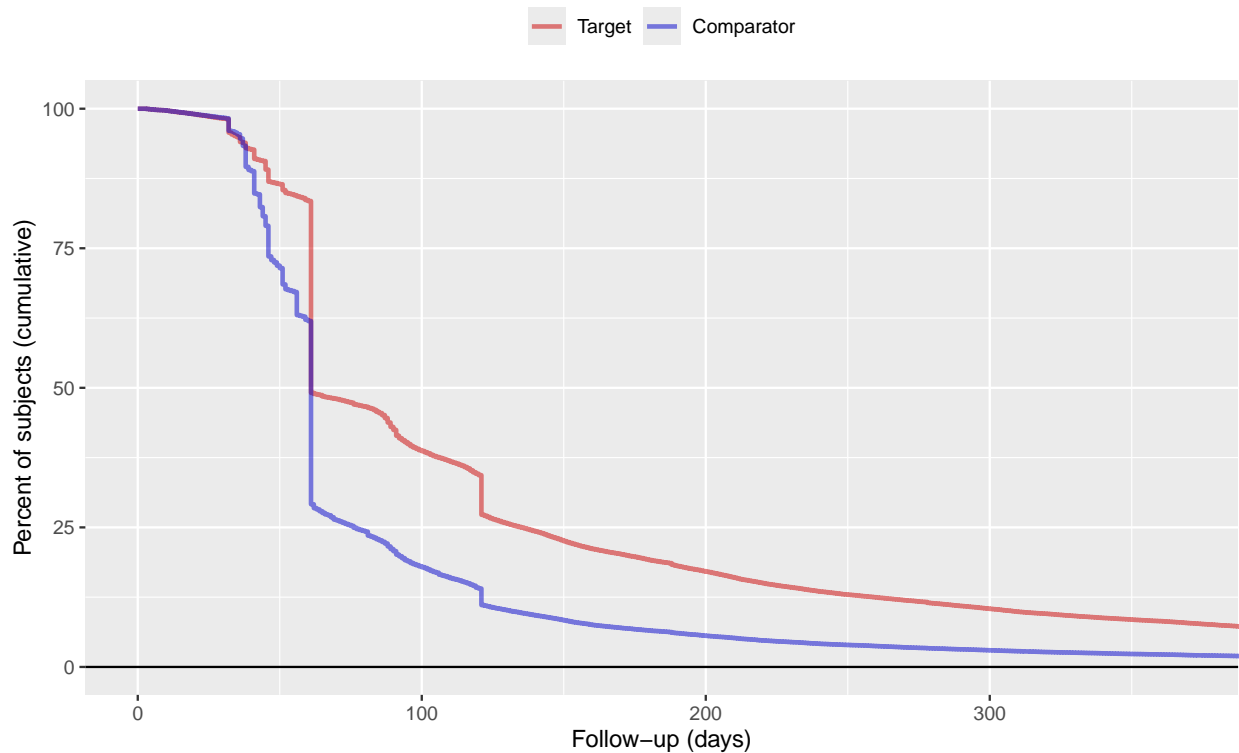
```

```

## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## i The deprecated feature was likely used in the CohortMethod package.
## Please report the issue at <https://github.com/OHDSI/CohortMethod/issues>.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was generated.

```





## 7 Outcome models

The outcome model is a model describing which variables are associated with the outcome.

### 7.1 Fitting a simple outcome model

In theory we could fit an outcome model without using the propensity scores. In this example we are fitting an outcome model using a Cox regression:

```
outcomeModel <- fitOutcomeModel(population = studyPop,
                                modelType = "cox")
outcomeModel
```

```
## Model type: cox
## Stratified: FALSE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Target estimand: ate
## Status: OK
##
##           Estimate lower .95 upper .95      logRr seLogRr
## treatment  0.907988  0.814872  1.011628 -0.096524  0.0552
```

But of course we want to make use of the matching done on the propensity score:

```
outcomeModel <- fitOutcomeModel(population = matchedPop,
                                modelType = "cox",
                                stratified = TRUE)
outcomeModel
```

```
## Model type: cox
## Stratified: TRUE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Target estimand: att
## Status: OK
##
##           Estimate lower .95 upper .95      logRr seLogRr
## treatment  0.963813  0.812047  1.140642 -0.036858  0.0867
```

Note that we define the sub-population to be only those in the `matchedPop` object, which we created earlier by matching on the propensity score. We also now use a stratified Cox model, conditioning on the propensity score match sets.

Instead of matching or stratifying we can also perform Inverse Probability of Treatment Weighting (IPTW):

```
outcomeModel <- fitOutcomeModel(population = ps,
                                modelType = "cox",
                                inversePtWeighting = TRUE)

outcomeModel

## Model type: cox
## Stratified: FALSE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: TRUE
## Target estimand: att
## Status: OK
##
##           Estimate lower .95 upper .95      logRr seLogRr
## treatment  1.001179  0.812604  1.237797  0.001178  0.1074
```

## 7.2 Adding interaction terms

We may be interested whether the effect is different across different groups in the population. To explore this, we may include interaction terms in the model. In this example we include three interaction terms:

```
interactionCovariateIds <- c(8532001, 201826210, 21600960413)
# 8532001 = Female
# 201826210 = Type 2 Diabetes
# 21600960413 = Concurrent use of antithrombotic agents
outcomeModel <- fitOutcomeModel(population = matchedPop,
                                modelType = "cox",
                                stratified = TRUE,
                                interactionCovariateIds = interactionCovariateIds)

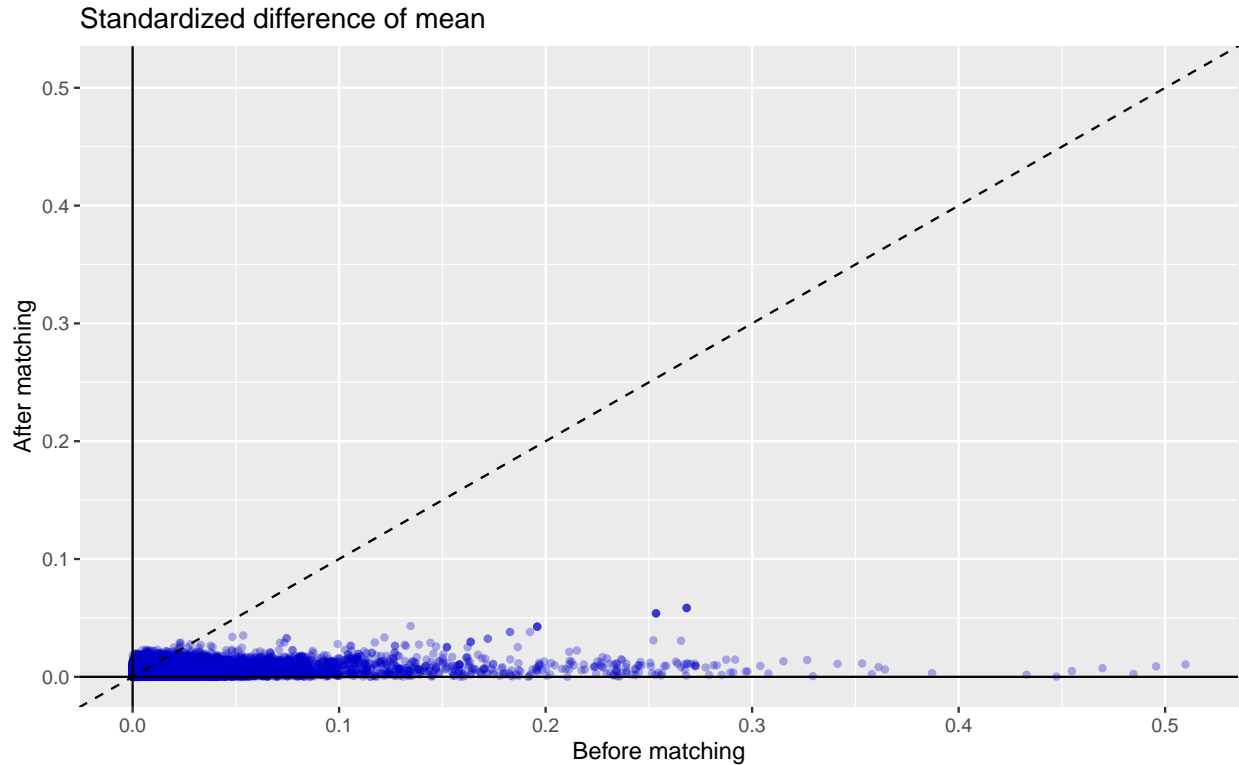
outcomeModel

## Model type: cox
## Stratified: TRUE
## Use covariates: FALSE
## Use inverse probability of treatment weighting: FALSE
## Target estimand: ate
## Status: OK
##
##           Estimate lower .95 upper .95      logRr seLogRr
## treatment  0.887549  0.715867  1.100420 -0.119291  0.1097
## treatment * drug_era group (DrugGroupEraOverlapping) during day 0 through 0 days relative to index: ANTITHROMBOTIC AGENTS 0.794772  0.630198  1.002414 -0.229700  0.1184
## treatment * condition_era group (ConditionGroupEraLongTerm) during day -365 through 0 days relative to index: Type 2 diabetes mellitus 0.911088  0.719973  1.151182 -0.093116  0.1197
## treatment * gender = FEMALE 1.073812  0.864245  1.334152  0.071215  0.1108
```

Note that you can use the `grepCovariateNames` to find covariate IDs.

It is prudent to verify that covariate balance has also been achieved in the subgroups of interest. For example, we can check the covariate balance in the subpopulation of females:

```
balanceFemale <- computeCovariateBalance(population = matchedPop,
                                         cohortMethodData = cohortMethodData,
                                         subgroupCovariateId = 8532001)
plotCovariateBalanceScatterPlot(balanceFemale)
```



### 7.3 Adding covariates to the outcome model

One final refinement would be to use the same covariates we used to fit the propensity model to also fit the outcome model. This way we are more robust against misspecification of the model, and more likely to remove bias. For this we use the regularized Cox regression in the `Cyclops` package. (Note that the treatment variable is automatically excluded from regularization.)

```
outcomeModel <- fitOutcomeModel(population = matchedPop,
                                 cohortMethodData = cohortMethodData,
                                 modelType = "cox",
                                 stratified = TRUE,
                                 useCovariates = TRUE)

outcomeModel
```

```
## Model type: cox
## Stratified: TRUE
## Use covariates: TRUE
## Use inverse probability of treatment weighting: FALSE
## Target estimand: att
## Status: OK
## Prior variance: 0.00999818614211261
##
##           Estimate lower .95 upper .95      logRr seLogRr
## treatment  0.943361  0.776675  1.141759 -0.058307  0.0983
```

## 7.4 Inspecting the outcome model

We can inspect more details of the outcome model:

```
exp(coef(outcomeModel))
```

```
## 4393168283078717  
## 0.9433607
```

```
exp(confint(outcomeModel))
```

```
## [1] 0.7766746 1.1417589
```

We can also see the covariates that ended up in the outcome model:

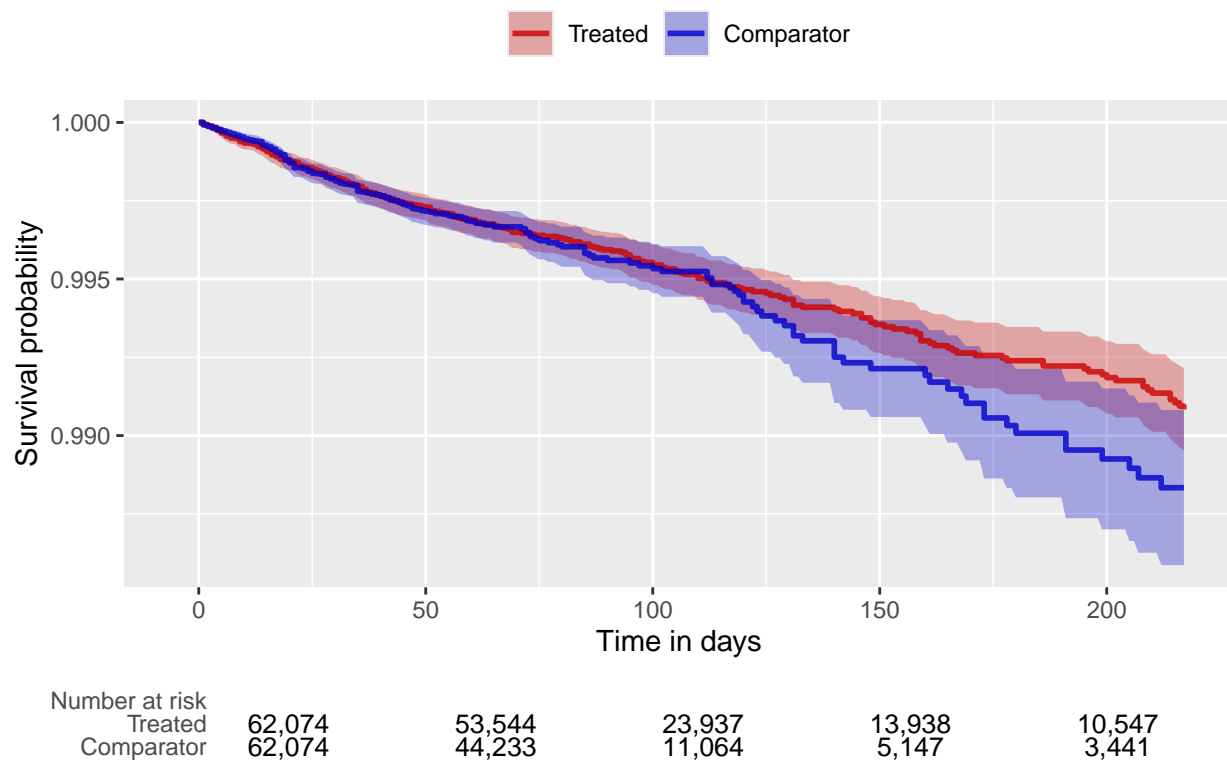
```
getOutcomeModel(outcomeModel, cohortMethodData)
```

```
## coefficient      id      name  
## 1 -0.05830653 4.393168e+15 Treatment
```

## 7.5 Kaplan-Meier plot

We can create the Kaplan-Meier plot:

```
plotKaplanMeier(matchedPop, includeZero = FALSE)
```

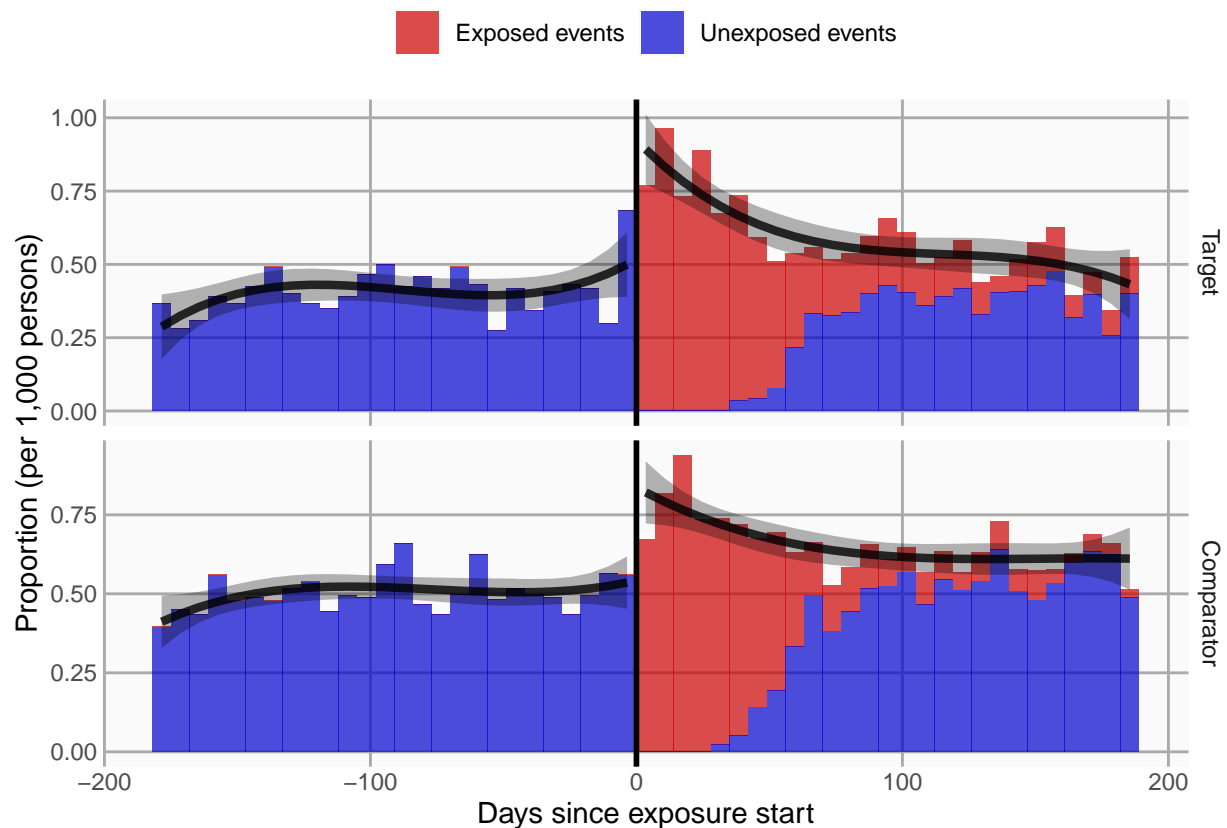


Note that the Kaplan-Meier plot will automatically adjust for any stratification, matching, or trimming that may have been applied.

## 7.6 Time-to-event plot

We can also plot time-to-event, showing both events before and after the index date, and events during and outside the defined time-at-risk window. This plot can provide insight into the temporal pattern of the outcome relative to the exposures:

```
plotTimeToEvent(cohortMethodData = cohortMethodData,
  outcomeId = 77,
  firstExposureOnly = FALSE,
  washoutPeriod = 0,
  removeDuplicateSubjects = "keep all",
  minDaysAtRisk = 1,
  riskWindowStart = 0,
  startAnchor = "cohort start",
  riskWindowEnd = 30,
  endAnchor = "cohort end")
```



Note that this plot does not show any adjustment for the propensity score.

## 8 Acknowledgments

Considerable work has been dedicated to provide the CohortMethod package.

```
citation("CohortMethod")
```

```
## To cite package 'CohortMethod' in publications use:
```

```
##
```

```
## Schuemie M, Suchard M, Ryan P (2025). _CohortMethod: New-User Cohort Method with Large Scale Proper
```

```
## https://github.com/OHDSI/CohortMethod, <https://ohdsi.github.io/CohortMethod>.
##
## A BibTeX entry for LaTeX users is
##
## @Manual{,
##   title = {CohortMethod: New-User Cohort Method with Large Scale Propensity and Outcome
## Models},
##   author = {Martijn Schuemie and Marc Suchard and Patrick Ryan},
##   year = {2025},
##   note = {R package version 5.5.2,
## https://github.com/OHDSI/CohortMethod},
##   url = {https://ohdsi.github.io/CohortMethod},
## }

```

Further, CohortMethod makes extensive use of the Cyclops package.

```
citation("Cyclops")

```

```
## To cite Cyclops in publications use:
##
## Suchard MA, Simpson SE, Zorych I, Ryan P, Madigan D (2013). "Massive parallelization of serial inference
## Modeling and Computer Simulation", 23, 10. doi:10.1145/2414416.2414791 <https://doi.org/10.1145/2414416.2414791>
##
## A BibTeX entry for LaTeX users is
##
## @Article{,
##   author = {M. A. Suchard and S. E. Simpson and I. Zorych and P. Ryan and D. Madigan},
##   title = {Massive parallelization of serial inference algorithms for complex generalized linear models},
##   journal = {ACM Transactions on Modeling and Computer Simulation},
##   volume = {23},
##   pages = {10},
##   year = {2013},
##   doi = {10.1145/2414416.2414791},
## }

```

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