

# Executing a study using the TreatmentPatterns package

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2021-08-11

This vignette describes how to run a custom treatment patterns study.

## 1. Setting up

Make sure you have TreatmentPatterns installed and all dependencies (see instructions in README).

## 2. Executing the study

If you like to execute the customized study package against a database follow these instructions:

- Download and open the R package using RStudio.
- Build the package (packages required are listed in DESCRIPTION file).
- Design a study (see vignette "Designing a study using the TreatmentPatterns package).

### 2.1 Databases in OMOP CDM format

#### A) Manually filling the inst folder in the package

Full example:

```
library(TreatmentPatterns)
dataSettings <- createDataSettings(OMOP_CDM = TRUE,
                                   connectionDetails = DatabaseConnector::createConnectionDetails(dbms = "mysql",
                                                       server = "localhost",
                                                       user = "root",
                                                       password = "password",
                                                       port = 3306),
                                   cdmDatabaseSchema = 'cdm',
                                   cohortDatabaseSchema = 'amarkus',
                                   cohortTable = "treatmentpatterns_cohorts")

cohortSettings <- createCohortSettings(cohortsToCreate_location = file.path(system.file(package = "TreatmentPatterns",
                                              "examples", "OMOP CDM", "inst"),
characterizationSettings <- createCharacterizationSettings(baselineCovariates_location = file.path(system.file(package = "TreatmentPatterns",
                                                                 "examples", "OMOP CDM", "inst"),
```

```

pathwaySettings <- createPathwaySettings(pathwaySettings_location = file.path(system.file(package = "TreatmentPatterns", "examples", "OMOP_CDM", "pathwaySettings_location"),
saveSettings <- createSaveSettings(databaseName = "IPCI")

TreatmentPatterns::executeTreatmentPatterns(dataSettings = dataSettings,
                                             cohortSettings = cohortSettings,
                                             characterizationSettings = characterizationSettings,
                                             pathwaySettings = pathwaySettings,
                                             saveSettings = saveSettings)

```

## B) Using function arguments when calling the main function of the package

Full example:

```

library(TreatmentPatterns)
dataSettings <- createDataSettings(OMOP_CDM = TRUE,
                                   connectionDetails = DatabaseConnector::createConnectionDetails(dbms = "mysql",
                                                                                               server = "localhost",
                                                                                               user = "root",
                                                                                               password = "root",
                                                                                               port = 3306),
                                   cdmDatabaseSchema = 'cdm',
                                   cohortDatabaseSchema = 'amarkus',
                                   cohortTable = "treatmentpatterns_cohorts")

cohortSettings <- createCohortSettings(targetCohorts = data.frame(cohortId = c(1),
                                                                  atlasId = c(590),
                                                                  cohortName = c('Hypertension'),
                                                                  conceptSet = ""),
                                       eventCohorts = data.frame(cohortId = c(10, 11, 12, 13, 14),
                                                                  atlasId = c(1777381, 1777382, 1777383, 1777384, 1777385),
                                                                  cohortName = c('Hydrochlorothiazide', 'Amlodipine', 'Lisinopril', 'Metoprolol', 'Valsartan'),
                                                                  conceptSet = c("", "", "", "", "")),
                                       baseUrl = "http://Res-Srv-Lin-01:8080/WebAPI",
                                       loadCohorts = TRUE)

characterizationSettings <- createCharacterizationSettings(baselineCovariates = data.frame(covariateName = "Age",
                                                                                          covariateId = 1),
                                                         eventCovariates = data.frame(covariateName = "Blood Pressure",
                                                                                       covariateId = 2),
                                                         treatmentCovariates = data.frame(covariateName = "Treatment",
                                                                                             covariateId = 3))

pathwaySettings <- createPathwaySettings(targetCohortId = 590, eventCohortIds = c(10, 11, 12, 13, 14))

saveSettings <- createSaveSettings(databaseName = "IPCI")

TreatmentPatterns::executeTreatmentPatterns(dataSettings = dataSettings,
                                             cohortSettings = cohortSettings,
                                             characterizationSettings = characterizationSettings,
                                             pathwaySettings = pathwaySettings,
                                             saveSettings = saveSettings)

```

## 2.2 Databases in other formats

### A) Manually filling the inst folder in the package

Full example:

```
dataSettings <- createDataSettings(OMOP_CDM = FALSE,
                                   cohortLocation = file.path(system.file(package = "TreatmentPatterns",
                                   "cohorts", "input_cohorts.csv"))

cohortSettings <- createCohortSettings(cohortsToCreate_location = paste0(system.file(package = "TreatmentPatterns",
cohortSettings, "cohorts", "input_cohorts.csv"))

pathwaySettings <- createPathwaySettings(pathwaySettings_location = file.path(system.file(package = "TreatmentPatterns",
pathwaySettings, "examples", "other_format.csv"))

saveSettings <- createSaveSettings(databaseName = "IPCI")

TreatmentPatterns::executeTreatmentPatterns(dataSettings = dataSettings,
                                             cohortSettings = cohortSettings,
                                             pathwaySettings = pathwaySettings,
                                             saveSettings = saveSettings)
```

### B) Using function arguments when calling the main function of the package

```
library(TreatmentPatterns)
dataSettings <- createDataSettings(OMOP_CDM = FALSE,
                                   cohortLocation = file.path(system.file(package = "TreatmentPatterns",
                                   "cohorts", "input_cohorts.csv"))

cohortSettings <- createCohortSettings(targetCohorts = data.frame(cohortId = c(1),
                                                                  atlasId = c(1777380),
                                                                  cohortName = c('Hypertension'),
                                                                  conceptSet = ""),
                                     eventCohorts = data.frame(cohortId = c(10, 11, 12, 13, 14),
                                                                  atlasId = c(1777381, 1777382, 1777383, 1777384, 1777385),
                                                                  cohortName = c('Hydrochlorothiazide', 'Amlodipine', 'Lisinopril', 'Metoprolol', 'Nifedipine'),
                                                                  conceptSet = c("", "", "", "", "")))

characterizationSettings <- createCharacterizationSettings(baselineCovariates = data.frame(covariateName = c("Age", "Sex", "Race", "Ethnicity", "Marital Status", "Education", "Income", "Health Insurance", "Comorbidities", "Medications", "Lifestyle Factors", "Social Determinants of Health"),
                                                                                          covariateId = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20)))

pathwaySettings <- createPathwaySettings(targetCohortId = 590, eventCohortIds = c(10, 11, 12, 13, 14))

saveSettings <- createSaveSettings(databaseName = "IPCI")

TreatmentPatterns::executeTreatmentPatterns(dataSettings = dataSettings,
                                             cohortSettings = cohortSettings,
                                             pathwaySettings = pathwaySettings,
                                             saveSettings = saveSettings)
```

### 3. Results

- The results are combined in the automatically generated zip file
- Select the folder containing the zip files and run the Shiny App for an interactive visualization of the results:

```
TreatmentPatterns::launchResultsExplorer(zipFolder)
```

- Share the results in the automatically generated zip folder.