Executing a study using the TreatmentPatterns package

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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

3. In extras -> CodeToRun.R: specify connection details (if OMOP-CDM) or cohort location (if Other format).

A) Manually filling the inst folder in the package

Full example:

```r
library(TreatmentPatterns)

connectionDetails <- DatabaseConnector::createConnectionDetails(dbms = Sys.getenv('dbms'),
                                                                server = Sys.getenv('server'),
                                                                user = Sys.getenv('user'),
                                                                password = Sys.getenv('password'),
                                                                port = Sys.getenv('port'))


cdmDatabaseSchema <- 'cdm'
cohortDatabaseSchema <- 'results'
databaseName <- 'IPCI'
cohortTable <- 'treatment_patterns'
```

```
instFolder <- paste0(system.file(package = "TreatmentPatterns"),"/examples/OMOP CDM/inst")
outputFolder <- paste0(getwd(), "/output")
tempFolder <- paste0(getwd(), "/temp")

TreatmentPatterns::executeTreatmentPatterns(OMOP_CDM = TRUE,
                                            connectionDetails = connectionDetails,
                                            cdmDatabaseSchema = cdmDatabaseSchema,
                                            cohortDatabaseSchema = cohortDatabaseSchema,
                                            databaseName = databaseName,
                                            cohortTable = paste0(cohortTable, "_", databaseName),
                                            instFolder = instFolder,
                                            outputFolder = outputFolder,
                                            tempFolder = tempFolder)
```

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

Full example:

```
library(TreatmentPatterns)

connectionDetails <- DatabaseConnector::createConnectionDetails(dbms = Sys.getenv('dbms'),
                                                               server = Sys.getenv('server'),
                                                               user = Sys.getenv('user'),
                                                               password = Sys.getenv('password'),
                                                               port = Sys.getenv('port'))

cdmDatabaseSchema <- 'cdm'
cohortDatabaseSchema <- 'results'
databaseName <- 'IPCI'
cohortTable <- 'treatment_patterns'

rootFolder <- getwd()

targetCohorts <- data.frame(cohortId = c(1),
                            atlasId = c(1777380),
                            cohortName = c('Hypertension'))

eventCohorts <- data.frame(cohortId = c(10, 11, 12, 13, 14),
                           atlasId = c(1777381,1777382, 1777383, 1777384, 1777385),
                           cohortName = c('Hydrochlorothiazide', 'Metorolol',
                                          'Amlodipine', 'Lisinopril', 'Losartan'))

characterizationSettings <- data.frame(covariate_name = c('Male', 'Age',
                                                          'Charlson comorbidity index score'),
                                       covariate_id = c(8507001, 1002, 1901),
                                       concept_set = c('', '', ''))

studySettings <- data.frame(studyName = c("default", "analysis1"),
                            targetCohortId = c(1,1),
                            eventCohortIds = c("10,11,12,13,14","10,11,12,13,14"),
                            includeTreatmentsPriorToIndex = c(0,0),
                            minEraDuration = c(0,5),
```

```
                             splitEventCohorts = c("",""),
                             eraCollapseSize = c(0,30),
                             combinationWindow = c(30,30),
                             minStepDuration = c(30,30),
                             filterTreatments = c("First","Changes"),
                             maxPathLength = c(5,5),
                             minCellCount = c(0,5),
                             minCellMethod = c("Remove","Adjust"),
                             groupCombinations = c(10,10),
                             addNoPaths = c(FALSE, TRUE))

baseUrl <- "http://atlas-demo.ohdsi.org/WebAPI"

TreatmentPatterns::executeTreatmentPatterns(connectionDetails = connectionDetails,
                             cdmDatabaseSchema = cdmDatabaseSchema,
                             cohortDatabaseSchema = cohortDatabaseSchema,
                             databaseName = databaseName,
                             cohortTable = paste0(cohortTable, "_", databaseName),
                             rootFolder = rootFolder,
                             targetCohorts = targetCohorts,
                             eventCohorts = eventCohorts,
                             characterizationSettings = characterizationSettings,
                             studySettings = studySettings,
                             loadCohorts = TRUE,
                             baseUrl = baseUrl)
```

2.2 Databases in other formats

A) Manually filling the inst folder in the package

Full example:

```
databaseName <- 'IPCI'

instFolder <- paste0(system.file(package = "TreatmentPatterns"),"/examples/other format/inst")
outputFolder <- paste0(getwd(), "/output")
tempFolder <- paste0(getwd(), "/temp")

cohortLocation <- paste0(instFolder, "/cohorts/input_cohorts.csv"),

TreatmentPatterns::executeTreatmentPatterns(OMOP_CDM = FALSE,
                             databaseName = databaseName,
                             instFolder = instFolder,
                             outputFolder = outputFolder,
                             tempFolder = tempFolder,
                             cohortLocation = cohortLocation,
                             runCohortCharacterization = FALSE)
```

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

```r
databaseName <- 'IPCI'

rootFolder <- getwd()

cohortLocation <- paste0(system.file(package = "TreatmentPatterns"),"/examples/other format/inst/cohorts

targetCohorts <- data.frame(cohortId = c(1),
                            atlasId = c(""),
                            cohortName = c('Hypertension'))

eventCohorts <- data.frame(cohortId = c(10, 11, 12, 13, 14),
                           atlasId = c("","", "", "", ""),
                           cohortName = c('Hydrochlorothiazide', 'Metorolol',
                                          'Amlodipine', 'Lisinopril', 'Losartan'))

studySettings <- data.frame(studyName = c("default", "analysis1"),
                            targetCohortId = c(1,1),
                            eventCohortIds = c("10,11,12,13,14","10,11,12,13,14"),
                            includeTreatmentsPriorToIndex = c(0,0),
                            minEraDuration = c(0,5),
                            splitEventCohorts = c("",""),
                            eraCollapseSize = c(0,30),
                            combinationWindow = c(30,30),
                            minStepDuration = c(30,30),
                            filterTreatments = c("First","Changes"),
                            maxPathLength = c(5,5),
                            minCellCount = c(0,5),
                            minCellMethod = c("Remove","Adjust"),
                            groupCombinations = c(10,10),
                            addNoPaths = c(FALSE, TRUE))

TreatmentPatterns::executeTreatmentPatterns(OMOP_CDM = FALSE,
                                            databaseName = databaseName,
                                            rootFolder = rootFolder,
                                            cohortLocation = cohortLocation,
                                            targetCohorts = targetCohorts,
                                            eventCohorts = eventCohorts,
                                            studySettings = studySettings,
                                            runCohortCharacterization = FALSE)
```

3. Results

- The results are located in the output folder (default: '~/output').

- Run the Shiny App for an interactive visualization of the results:

```r
TreatmentPatterns::launchShinyApplication(rootFolder)
```

- Share the results in the automatically generated zip folder.