

# Running cohort diagnostics using WebAPI

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## Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
<b>2</b>	<b>Running the cohort diagnostics</b>	<b>1</b>
2.1	Defining the set of cohorts to diagnose . . . . .	1
2.2	Instantiating the cohorts . . . . .	3
2.3	Generating the diagnostics in WebApi mode . . . . .	3
2.4	Incremental mode . . . . .	4

## 1 Introduction

There are currently two approaches to run Cohort Diagnostics. - Embed in an OHDSI study package, where all the cohort definitions are stored as part of that study package, or - WebAPI mode - where cohort diagnostics dynamically pulls the cohort definition from a webapi instance. WebAPI is the backend of the OHDSI ATLAS application, allowing programmatic access to the cohort definitions created in ATLAS.

This vignette describes the latter approach (webapi): how to run CohortDiagnostics using the WebAPI.

## 2 Running the cohort diagnostics

### 2.1 Defining the set of cohorts to diagnose

The first step is to define the set of cohorts we wish to create diagnostics for. We do this by creating a data frame with four columns:

- **atlasId**: The cohort ID in ATLAS.
- **atlasName**: The full name of the cohort. This will be shown in the Shiny app.
- **cohortId**: The cohort ID to use in the package. Usually the same as the cohort ID in ATLAS.
- **name**: A short name for the cohort, to use to create file names. do not use special characters.

One way to create such a data frame is to create a CSV file, and load it into R. Here is an example table we assume is stored in `cohortsToDiagnose.csv`:

atlasId	atlasName	cohortId	name
1770710	New users of ACE inhibitors as first-line monotherapy for hypertension	1770710	ace_inhibitors
1770711	New users of Thiazide-like diuretics as first-line monotherapy for hypertension	1770711	thz
1770712	Angioedema outcome	1770712	angioedema
1770713	Acute myocardial infarction outcome	1770713	ami

We can read the table using

```
library(CohortDiagnostics)
cohortSetReference <- read.csv("cohortsToDiagnose.csv")
```

An easy way to create this csv file is to use ROhdsiWebApi

```
library(magrittr)
# Set up
baseUrl <- Sys.getenv("BaseUrl")
# list of cohort ids
cohortIds <- c(18345,18346)

# get specifications for the cohortIds above
webApiCohorts <-
  ROhdsiWebApi::getCohortDefinitionsMetaData(baseUrl = baseUrl) %>%
  dplyr::filter(.data$id %in% cohortIds)

cohortsToCreate <- list()
for (i in (1:nrow(webApiCohorts))) {
  cohortId <- webApiCohorts$id[[i]]
  cohortDefinition <-
    ROhdsiWebApi::getCohortDefinition(cohortId = cohortId,
                                       baseUrl = baseUrl)
  cohortsToCreate[[i]] <- tidyr::tibble(
    atlasId = webApiCohorts$id[[i]],
    atlasName = stringr::str_trim(stringr::str_squish(cohortDefinition$name)),
    cohortId = webApiCohorts$id[[i]],
    name = stringr::str_trim(stringr::str_squish(cohortDefinition$name))
  )
}
cohortsToCreate <- dplyr::bind_rows(cohortsToCreate)

readr::write_excel_csv(x = cohortsToCreate, na = "",
                      file = "D:/temp/CohortsToCreate.csv",
                      append = FALSE)
```

See Vignette on ‘Running Cohort Diagnostics’ on how to connect cohort diagnostics to CDM and creating cohort table.

## 2.2 Instantiating the cohorts

To instantiate the cohorts we specified in the `cohortSetReference` we need to communicate with the WebAPI instance, as well as the database server.

To connect to the WebAPI, we need to provide the base URL. This is a URL that looks something like “http://server.org:80/WebAPI”. If you do not know the WebAPI’s base URL, contact the ATLAS administrator. Note: there is no trailing ‘/’.

To instantiate the cohorts:

```
baseUrl <- "http://server.org:80/WebAPI"
inclusionStatisticsFolder <- "c:/temp/incStats"

instantiateCohortSet(connectionDetails = connectionDetails,
                     cdmDatabaseSchema = cdmDatabaseSchema,
                     tempEmulationSchema = tempEmulationSchema,
                     cohortDatabaseSchema = cohortDatabaseSchema,
                     cohortTable = cohortTable,
                     baseUrl = baseUrl,
                     cohortSetReference = cohortSetReference,
                     generateInclusionStats = TRUE,
                     inclusionStatisticsFolder = inclusionStatisticsFolder)
```

This command will contact the WebApi to obtain the cohort definitions, instantiate them in the cohort table, and write the inclusion rule statistics to the specified folder.

## 2.3 Generating the diagnostics in WebApi mode

Next we generate the cohort diagnostics:

```
databaseId <- "MyData"
exportFolder <- "c:/temp/export"

runCohortDiagnostics(baseUrl = baseUrl,
                     cohortSetReference = cohortSetReference,
                     connectionDetails = connectionDetails,
                     cdmDatabaseSchema = cdmDatabaseSchema,
                     tempEmulationSchema = tempEmulationSchema,
                     cohortDatabaseSchema = cohortDatabaseSchema,
                     cohortTable = cohortTable,
                     inclusionStatisticsFolder = inclusionStatisticsFolder,
                     exportFolder = exportFolder,
                     databaseId = databaseId,
                     runInclusionStatistics = TRUE,
                     runIncludedSourceConcepts = TRUE,
                     runOrphanConcepts = TRUE,
                     runTimeDistributions = TRUE,
                     runBreakdownIndexEvents = TRUE,
                     runIncidenceRate = TRUE,
                     runCohortOverlap = TRUE,
                     runCohortCharacterization = TRUE,
                     minCellCount = 5)
```

The `databaseId` is a short string that will be used to identify the data from this database in the Shiny app. Make sure to give it a name you can easily recognize.

## **2.4 Incremental mode**

Although possible, we don't recommend using incremental mode in WebApi mode, as the cohort definitions may change in the target webapi instance.