

# How to Use PhenotypeLibrary R Package

Gowtham A. Rao

2023-08-24

## Contents

1	Installation	1
2	Retrieval	1
3	Use	2

PhenotypeLibrary is part of HADES

## 1 Installation

- This is an installable R-package that may be installed as follows:

```
remotes::install_github("OHDSI/PhenotypeLibrary")
```

## 2 Retrieval

- The list of cohort definitions available may be retrieved as follows:

```
PhenotypeLibrary::listPhenotypes()
```

```
#> # A tibble: 569 x 27
#>   cohortId cohortName      cohortNameFormatted cohortNameLong cohortNameAtlas librarian status added
#>   <dbl> <chr>          <chr>          <chr>          <chr>          <chr>    <chr> <chr>
#> 1     2 [W] COVID-19 ~ COVID-19 diagnosis~ COVID-19 diag~ [W] COVID-19 d~ rao@ohds~ Withd~ <NA>
#> 2     3 [P] Cough or ~ Cough or Sputum   Cough or Sput~ [P] Cough or S~ rao@ohds~ Pendi~ <NA>
#> 3     4 [P] Diarrhea   Diarrhea          Diarrhea       [P] Diarrhea    rao@ohds~ Pendi~ <NA>
#> 4     5 [P] Dyspnea   Dyspnea           Dyspnea        [P] Dyspnea     rao@ohds~ Pendi~ <NA>
#> 5     6 [P] Fever     Fever             Fever          [P] Fever       rao@ohds~ Pendi~ <NA>
#> 6     7 [P] Headache ~ Headache or Headac~ Headache or H~ [P] Headache o~ rao@ohds~ Pendi~ <NA>
#> 7     8 [P] Altered s~ Altered smell or t~ Altered smell~ [P] Altered sm~ rao@ohds~ Pendi~ <NA>
#> 8     9 [P] Sore thro~ Sore throat       Sore throat    [P] Sore throat rao@ohds~ Pendi~ <NA>
#> 9    10 [P] Nausea or~ Nausea or Vomiting Nausea or Vom~ [P] Nausea or ~ rao@ohds~ Pendi~ <NA>
#> 10   11 [P] Malaise a~ Malaise and or fat~ Malaise and o~ [P] Malaise an~ rao@ohds~ Pendi~ <NA>
#> # i 559 more rows
```

```
#> # i 15 more variables: contributorOrcIds <chr>, contributorOrganizations <chr>, peerReviewers <chr>,
#> #   recommendedEraPersistenceDurations <chr>, recommendedEraCollapseDurations <chr>, recommendSubset
#> #   ohdsiForumPost <chr>, metaDataAll <chr>, createdAt <date>, modifiedDate <date>, lastModifiedBy
```

- You can extract one or more cohort definitions into a cohortDefinitionSet object as

```
cohortDefinitionSet <- PhenotypeLibrary::getPlCohortDefinitionSet(cohortIds = c(1, 2, 3))

cohortDefinitionSet
```

```
#> # A tibble: 2 x 4
#>   cohortId cohortName                                json
#>   <dbl> <chr>                                <chr>
#> 1       2 [W] COVID-19 diagnosis or SARS-CoV-2 test (1pos) "{\n\t\"cdmVersionRange\" : \">=5.0.0\",
#> 2       3 [P] Cough or Sputum                        "{\n\t\"cdmVersionRange\" : \">=5.0.0\",
```

- cohortDefinitionSet is now a data.frame with specifications for the cohort ids 1, 2 and 3. For cohorts that conform to OHDSI Circe specifications, the field json is the cohort json specification that may be posted into your Atlas instance. The SQL is the SQL rendered from the JSON. For cohorts that do not conform to OHDSI Circe specification, only the SQL is provided and the json is left empty.

### 3 Use

- You can instantiate the cohorts in your environment as follows using (OHDSI/CohortGenerator)[<https://github.com/OHDSI/CohortGenerator>].

```
connectionDetails <-
  DatabaseConnector::createConnectionDetails(
    dbms = "postgresql",
    server = "some.server.com/ohdsi",
    user = "joe",
    password = "secret"
  )
cdmDatabaseSchema <- "cdm_synpuf"
cohortDatabaseSchema <- "scratch.dbo"
cohortTables <- CohortGenerator::getCohortTableNames()
CohortGenerator::generateCohortSet(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = cdmDatabaseSchema,
  cohortDatabaseSchema = cohortDatabaseSchema,
  cohortTableNames = cohortTables,
  cohortDefinitionSet = cohortDefinitionSet
)
```

- You can also run cohort diagnostics on this cohortDefinitionSet object as follows:

```
databaseId <- "synpuf"

databaseName <-
  "Medicare Claims Synthetic Public Use Files (SynPUFs)"
```

```
databaseDescription <-  
  "Medicare Claims Synthetic Public Use Files (SynPUFs) were created to allow interested parties to gain  
  
CohortDiagnostics::executeDiagnostics(  
  cohortDefinitionSet = cohortDefinitionSet,  
  exportFolder = outputFolder,  
  databaseId = databaseId,  
  databaseName = databaseName,  
  databaseDescription = databaseDescription,  
  cohortDatabaseSchema = cohortDatabaseSchema,  
  cdmDatabaseSchema = cdmDatabaseSchema,  
  connectionDetails = connectionDetails,  
  cohortTableNames = cohortTableNames  
)
```