

# Guidelines on Cohort Definition Set R Object

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2022-08-15

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PhenotypeLibrary is part of HADES

*This document is a DRAFT guidance.*

## 1 How to create a cohort definition set object

### 1.1 Structure

#### 1.1.1 Downloading cohorts from ATLAS

We can create cohorts using ATLAS and extract them using ROhdsiWebApi package:

```
cohortIds <- c(1778211,1778212,1778213)
ROhdsiWebApi::authorizeWebApi(baseUrl = baseUrl, authMethod = "windows")
cohortDefinitionSet <- ROhdsiWebApi::exportCohortDefinitionSet(baseUrl = baseUrl,
                                                                cohortIds = cohortIds)
```

The code above connects to ATLAS' WebAPI, retrieves the `cohortDefinitions` as returns a `data.frame` object with required fields. The following columns are considered required for OHDSI submission.

- **cohortId**: The cohortId will be the same as the atlasId upon export from ATLAS. We provide this column in case you'd like to alter the numbering scheme for your cohort definition set.
- **cohortName**: The name of the cohort in ATLAS.
- **json**: The Circe compliant JSON representation of the cohort definition

When cohort json is submitted, the PhenotypeLibrary will create the SQL using Circe. The only instance when the submitted SQL will be used are when the cohort definitions does not conform to circe/atlas cohort definition standard.