

# Package ‘ROhdsiWebApi’

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**Type** Package

**Title** R package to allow interactivity with a WebApi instance

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**Maintainer** Gowtham Rao <gowthamrao@gmail.com>

**Description** Includes R wrappers for calling WebAPI web services.

**License** Apache License 2.0

**Depends** R (>= 3.1.0),

**Imports** checkmate,  
dplyr,  
httr (>= 1.3.1),  
jsonlite,  
lubridate,  
magrittr,  
openxlsx (>= 4.0.17),  
purrr,  
readr,  
RJSONIO,  
SqlRender,  
stringr,  
tibble,  
tidyr

**Suggests** testthat

**URL** <https://github.com/OHDSI/ROhdsiWebApi>

**BugReports** <https://github.com/OHDSI/ROhdsiWebApi/issues>

**NeedsCompilation** no

**RoxygenNote** 7.1.0

**Encoding** UTF-8

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---

convertConceptSetDefinitionToTable

*Convert a concept set definition to a table*

---

### Description

Convert a concept set definition to a table

### Usage

```
convertConceptSetDefinitionToTable(
    conceptSetDefinition,
    snakeCaseToCamelCase = TRUE
)
```

### Arguments

conceptSetDefinition

A concept set definition, for example as obtained through the [getConceptSetDefinition](#) function, or taken from a cohort definition.

snakeCaseToCamelCase

Should the column names of the result be converted to camelCase?

**Value**

A tibble representing the concept set expression.

**Examples**

```
## Not run:
conceptSetDefinition <- getConceptSetDefinition(conceptSetId = 282, baseUrl = "http://server.org:80/WebAPI")
convertConceptSetDefinitionToTable(conceptSetDefinition = conceptSetDefinition)

## End(Not run)
```

---

```
createConceptSetWorkbook
```

*Save a set of concept sets expressions, included concepts, and mapped concepts into a workbook*

---

**Description**

Save a set of concept sets expressions, included concepts, and mapped concepts into a workbook

**Usage**

```
createConceptSetWorkbook(
  conceptSetIds,
  fileName,
  baseUrl,
  included = FALSE,
  mapped = FALSE
)
```

**Arguments**

conceptSetIds	A vector of concept set IDs.
fileName	The name of the XLSX workbook file.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
included	Should included concepts be included in the workbook?
mapped	Should mapped concepts be included in the workbook?

**Value**

A xlsx workbook that includes a list of all concept set IDs and names and a worksheet for the concepts in each set. Options to include an included concepts and mapped concepts worksheet for each concept set are available.

deleteCohortCharacterizationDefinition

*Delete a cohort characterization definition and results*

---

### Description

Delete a cohort characterization definition and results

### Usage

```
deleteCohortCharacterizationDefinition(  
    characterizationId,  
    baseUrl,  
    silent = FALSE,  
    stopOnError = FALSE  
)
```

### Arguments

characterizationId	The number indicating which characterization definition to fetch.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
silent	[OPTIONAL, Default = FALSE] If TRUE, function will work silently without showing any warning or error message.
stopOnError	[OPTIONAL, Default = FALSE] If silent = TRUE, then this will be ignored.

### Details

Deletes cohort characterization definition and results from WebAPI for a given characterization id

### Value

NA. A status message will be shown.

### Examples

```
## Not run:  
deleteCohortCharacterizationDefinition(characterizationId = 282, baseUrl = "http://server.org:80/WebAPI")  
  
## End(Not run)
```

---

`deleteCohortDefinition`*Delete a cohort definition*

---

**Description**

Delete a cohort definition

**Usage**

```
deleteCohortDefinition(cohortId, baseUrl, silent = FALSE, stopOnError = FALSE)
```

**Arguments**

<code>cohortId</code>	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
<code>silent</code>	[OPTIONAL, Default = FALSE] If TRUE, function will work silently without showing any warning or error message.
<code>stopOnError</code>	[OPTIONAL, Default = FALSE] If silent = TRUE, then this will be ignored.

**Details**

Deletes cohort definition from WebAPI for a given cohort id

**Value**

NA. A status message will be shown.

**Examples**

```
## Not run:  
deleteCohortDefinition(cohortId = 282, baseUrl = "http://server.org:80/WebAPI")  
  
## End(Not run)
```

---

`getCdmSources`*Get the data sources in the WebAPI instance*

---

**Description**

Get the data sources in the WebAPI instance

**Usage**

```
getCdmSources(baseUrl)
```

**Arguments**

`baseUrl` The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.

**Details**

Obtains the data sources configured in the WebAPI instance.

**Value**

A data frame.

---

`getCohortCharacterizationDefinition`

*Get a characterization definition expression*

---

**Description**

Get a characterization definition expression

**Usage**

```
getCohortCharacterizationDefinition(
  characterizationId,
  baseUrl,
  generationId = NULL
)
```

**Arguments**

`characterizationId`

The number indicating which characterization definition to fetch.

`baseUrl`

The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.

`generationId`

(OPTIONAL) Used to specify the id of a particular generation of a cohort characterization. If `generationId` is provided, then `characterizationId` is ignored.

**Details**

Obtain the characterization definition expression from WebAPI as R-object for a given characterization id/generation id

**Value**

A R-object representing the `characterizationId/generationId` definition returned by WebApi. A warning will be shown if the `characterizationId/generationId` does not exist.

## Examples

```
## Not run:
getCohortCharacterizationDefinition(characterizationId = 282, baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

getCohortCharacterizationResults

*Get Cohort Characterization Results*

---

## Description

Get Cohort Characterization Results

## Usage

```
getCohortCharacterizationResults(
  characterizationId,
  baseUrl,
  generationId = NULL,
  sourceKey,
  cohortIds = c(),
  domains = c(),
  analysisNames = c()
)
```

## Arguments

characterizationId	The id of the cohort characterization in WebApi
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI".
generationId	Used to specify the id of a particular generation of a cohort characterization. By default, the latest execution is retrieved
sourceKey	The source key for a CDM instance in WebAPI, as defined in the Configuration page
cohortIds	(OPTIONAL) Which cohort definition ids would you like to retrieve? By default, all cohorts are retrieved.
domains	(OPTIONAL) Which feature domains would you like to retrieve? By default, all domains are retrieved.
analysisNames	(OPTIONAL) Which feature analysis names would you like to retrieve? By default, all analyses are retrieved.

---

getCohortDefinition      *Get a cohort definition*

---

**Description**

Get a cohort definition

**Usage**

```
getCohortDefinition(cohortId, baseUrl)
```

**Arguments**

cohortId	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.

**Details**

Obtain the cohort definition from WebAPI for a given cohort id

**Value**

An R object representing the cohort definition

**Examples**

```
## Not run:
getCohortDefinition(cohortId = 282, baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

getCohortDefinitionExpression  
                            *Get a cohort definition expression*

---

**Description**

Get a cohort definition expression

**Usage**

```
getCohortDefinitionExpression(cohortId, baseUrl)
```

**Arguments**

cohortId	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.



## Details

Obtain the JSON expression from WebAPI for a given cohort id

## Value

A JSON list object representing the cohort definition This function has been deprecated. As an alternative please use the following steps as in the example below: 1) cohortDefinition <- getCohortDefinition(baseUrl = baseUrl, cohortId = 15873) 2) validJsonExpression <- RJSONIO::toJSON(cohortDefinition\$expression) 3) save validJsonExpression object as .txt"

## Examples

```
## Not run:
# This will obtain a cohort definition's JSON expression:

getCohortDefinitionExpression(cohortId = 282, baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

getCohortDefinitionName

*(Deprecated) Get a cohort definition's name from WebAPI*

---

## Description

(Deprecated) Get a cohort definition's name from WebAPI

## Usage

```
getCohortDefinitionName(baseUrl, cohortId, formatName = FALSE)
```

## Arguments

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
cohortId	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
formatName	Should the name be formatted to remove prefixes and underscores?

## Details

(Deprecated) Obtains the name of a cohort. This function has been deprecated. As an alternative please use getCohortDefinition

## Value

The name of the cohort.

---

`getCohortDefinitionSql`*Get a cohort definition's SQL from WebAPI*

---

**Description**

Get a cohort definition's SQL from WebAPI

**Usage**

```
getCohortDefinitionSql(baseUrl, cohortId, generateStats = TRUE)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
<code>cohortId</code>	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
<code>generateStats</code>	Should the SQL include the code for generating inclusion rule statistics? Note that if TRUE, several additional tables are expected to exist as described in the details. By default this is TRUE.

**Details**

Obtains the template SQL of a cohort. When using `generateStats = TRUE`, the following tables are required to exist when executing the SQL: `cohort_inclusion`, `cohort_inclusion_result`, `cohort_inclusion_stats`, and `cohort_summary_stats`. Also note that the `cohort_inclusion` table should be populated with the names of the rules prior to executing the cohort definition SQL.

**Value**

The templated SQL to generate the cohort

---

`getCohortGenerationInformation`*Get cohort generation information*

---

**Description**

Get cohort generation information

**Usage**

```
getCohortGenerationInformation(cohortIds, baseUrl, sourceKeys = NULL)
```

**Arguments**

cohortIds	A list of cohortIds
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
sourceKeys	(OPTIONAL) A list of CDM source keys. These can be found in Atlas -> Configure. Otherwise, all CDM source keys will be used.

**Details**

Obtains cohort generation statuses for a collection of cohort definition Ids and CDM sources. Useful if running multiple cohort generation jobs that are long-running.

**Value**

A data frame of cohort generation statuses, start times, and execution durations per definition id and source key.

---

`getCohortInclusionRulesAndCounts`*Get cohort inclusion rules and person counts*

---

**Description**

Get cohort inclusion rules and person counts

**Usage**

```
getCohortInclusionRulesAndCounts(baseUrl, cohortId, sourceKey)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
cohortId	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
sourceKey	The source key for a CDM instance in WebAPI, as defined in the Configuration page

**Details**

Obtains the inclusion rules from a cohort definition and summarizes the person counts per rule

---

getCohortResults	<i>Get cohort generation results</i>
------------------	--------------------------------------

---

**Description**

Get cohort generation results

**Usage**

```
getCohortResults(cohortId, baseUrl, sourceKey, mode = 0)
```

**Arguments**

cohortId	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
sourceKey	The source key for a CDM instance in WebAPI, as defined in the Configuration page
mode	Mode is used to differentiate between inclusion rules and count by events (mode = 0, default) or persons (mode = 1). Default value = 0.

**Details**

Obtains a list with data frame containing details of output for cohort generation

**Value**

A list of data frames containing cohort generation report

**Examples**

```
## Not run:
getCohortGeneratioInformation(cohortId = 282, baseUrl = "http://server.org:80/WebAPI", sourceKey = "HCUP", mode = 0)

## End(Not run)
```

---

getConcepts	<i>Get concepts</i>
-------------	---------------------

---

**Description**

Get concepts

**Usage**

```
getConcepts(
  conceptIds,
  baseUrl,
  vocabularySourceKey = NULL,
  snakeCaseToCamelCase = TRUE
)
```

**Arguments**

conceptIds	A vector of concept IDs.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
vocabularySourceKey	The source key of the Vocabulary. By default, the priority Vocabulary is used.
snakeCaseToCamelCase	Should the column names of the result be converted to camelCase?

**Value**

A tibble containing information on the concepts.

**Examples**

```
## Not run:
conceptSet <- getConceptSet(conceptSetId = 282, baseUrl = "http://server.org:80/WebAPI")
conceptIds <- resolveConceptSet(conceptSet = conceptSet,
                               baseUrl = "http://server.org:80/WebAPI")
concepts <- getConcepts(conceptIds = conceptIds,
                        baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

```
getConceptSetDefinition
```

*Get a concept set definition*

---

**Description**

Get a concept set definition

**Usage**

```
getConceptSetDefinition(conceptSetId, baseUrl)
```

**Arguments**

conceptSetId	An integer id representing the id that uniquely identifies a concept set definition in a WebApi instance.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.

**Details**

Obtain a concept set from WebAPI.

**Value**

An R object representing the concept set.

## Examples

```
## Not run:  
conceptSetDefinition <- getConceptSetDefinition(conceptSetId = 282, baseUrl = "http://server.org:80/WebAPI")  
  
## End(Not run)
```

---

getEstimationDefinition

*Get the estimation definition*

---

## Description

Get the estimation definition

## Usage

```
getEstimationDefinition(baseUrl, estimationId)
```

## Arguments

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
estimationId	The WebApi id for the estimation specification

## Details

Get an R object representing the estimation definition.

## Value

An R object.

## Examples

```
## Not run:  
getEstimationDefinition(baseUrl = "http://server.org:80/WebAPI", estimationId = 3434)  
  
## End(Not run)
```

---

`getIncidenceRateDefinition`*Get definitions for incident rate analysis*

---

**Description**

Get definitions for incident rate analysis

**Usage**

```
getIncidenceRateDefinition(baseUrl, incidenceRateId)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
<code>incidenceRateId</code>	The WebApi ID for incidence rate analysis.

**Details**

Returns an R-objects with definitions for incident rate analysis

**Value**

Get definitions for incident rate analysis

**Examples**

```
## Not run:
getIncidenceRateDefinition <- function(baseUrl "http://server.org:80/WebAPI",
                                           incidenceRateId = 296)
)

## End(Not run)
```

---

`getIncidenceRateGenerationInformation`*Get incident rate generation information*

---

**Description**

Get incident rate generation information

**Usage**

```
getIncidenceRateGenerationInformation(incidenceRateId, baseUrl)
```

**Arguments**

incidenceRateId	The WebApi ID for incidence rate analysis.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.

**Details**

Get incident rate generation information

**Value**

A tibble data-frame R-object with incidence rate generation information.

**Examples**

```
## Not run:
getIncidenceRateGenerationInformation(incidenceRateId = 296, baseUrl = baseUrl)
)

## End(Not run)
```

---

getIncidenceRateResults

*Get results from incidence rate analysis.*

---

**Description**

Get results from incidence rate analysis.

**Usage**

```
getIncidenceRateResults(
  incidenceRateId,
  baseUrl,
  sourceKey,
  targetCohortId,
  outcomeCohortId
)
```

**Arguments**

incidenceRateId	The WebApi ID for incidence rate analysis.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
sourceKey	The sourceKey for the incident rate analysis.
targetCohortId	The cohort id of the target cohort in the incident rate analysis.
outcomeCohortId	The cohort id of the outcome cohort in the incidence rate analysis.



**Details**

Given a sourceKey, targetCohortId, outcomeCohortId combinations, this function will return the results of incidence rate analysis.

**Value**

A list with incident rate results summary, stratified results and treemap data.

**Examples**

```
## Not run:
getIncidenceRateResults(incidenceRateId = 296,
                        baseUrl = "http://server.org:80/WebAPI",
                          targetCohortId = 432423,
                          outcomeCohortId = 324,
                          sourceKey = "HCUP"
                        )

## End(Not run)
```

---

getMetadataForAllSpecifications

*Retrieve the meta data of all WebApi definitions*

---

**Description**

Retrieve the meta data of all WebApi definitions

**Usage**

```
getMetadataForAllSpecifications(baseUrl)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
---------	--

**Details**

Obtains the meta data of WebApi specifications such as id, name, created/modified details, hash object, etc. The following function categories are supported. Concept-set, Cohort-definition, Cohort-characterization, Pathway-analysis, Incidence rate (ir), estimation and prediction. This function is useful to retrieve the current specifications.

**Value**

A tibble of specification metadata. Note: modifiedDate and createdDate are returned as text/character.

**Examples**

```
## Not run:
getMetadataForAllSpecifications(baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

getPersonProfile	<i>Get person profile data</i>
------------------	--------------------------------

---

**Description**

Get person profile data

**Usage**

```
getPersonProfile(baseUrl, sourceKey, personId, indexCohortId = NULL)
```

**Arguments**

baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
sourceKey	The source key for a CDM instance in WebAPI, as defined in the Configuration page
personId	The personId of the person whose profile is being reviewed
indexCohortId	<OPTIONAL> Do you want to use a particular cohortId as the index cohort? If left NULL, the WebApi will identify the earliest cohort for the person by cohort start date and use it as the index cohort. WebApi uses the cohort start date of the index cohort to calculate the person's index age (ageAtIndex). WebApi will also return the relative position, in days, for each event compared to the index cohorts start date. These relative positions are useful to study the relationship of various events with respect to the index cohort start date.

**Details**

Get a R object with person profile data. This function may be used for visualizing a patients profile in tables or visualization.

**Value**

A list of tibble data frame objects corresponding to cohorts, observationPeriod, records and person.

**Examples**

```
## Not run: #'
getPersonProfile(baseUrl = "http://server.org:80/WebAPI",
  sourceKey = 'sourceKey',
  personId = 342342)

## End(Not run)
```

---

`getPriorityVocabularyKey`*Get Priority Vocabulary Source Key*

---

**Description**

Get Priority Vocabulary Source Key

**Usage**

```
getPriorityVocabularyKey(baseUrl)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
----------------------	--

**Details**

Obtains the source key of the default OMOP Vocabulary in WebApi.

**Value**

A string.

---

`getSourceConcepts`*Get source concepts that map to standard concepts*

---

**Description**

Get source concepts that map to standard concepts

**Usage**

```
getSourceConcepts(  
    conceptIds,  
    baseUrl,  
    vocabularySourceKey = NULL,  
    snakeCaseToCamelCase = TRUE  
)
```

**Arguments**

<code>conceptIds</code>	A list of concept IDs referring to standard concepts.
<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
<code>vocabularySourceKey</code>	The source key of the Vocabulary. By default, the priority Vocabulary is used.
<code>snakeCaseToCamelCase</code>	Should the column names of the result be converted to camelCase?

**Value**

A tibble containing information on the source concepts.

**Examples**

```
## Not run:
conceptSet <- getConceptSetDefinition(conceptSetId = 282, baseUrl = "http://server.org:80/WebAPI")
conceptIds <- resolveConceptSet(conceptSet = conceptSet,
                               baseUrl = "http://server.org:80/WebAPI")
sourceConcepts <- getSourceConcepts(conceptIds = conceptIds,
                                     baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

getWebApiVersion	<i>Get the WebAPI version number</i>
------------------	--------------------------------------

---

**Description**

Get the WebAPI version number

**Usage**

```
getWebApiVersion(baseUrl)
```

**Arguments**

**baseUrl**            The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.

**Details**

Obtains the WebAPI version number.

**Value**

A string.

---

insertCohortDefinitionInPackage	<i>Load a cohort definition and insert it into this package</i>
---------------------------------	---

---

**Description**

Load a cohort definition and insert it into this package

**Usage**

```
insertCohortDefinitionInPackage(
    cohortId,
    name = NULL,
    jsonFolder = "inst/cohorts",
    sqlFolder = "inst/sql/sql_server",
    baseUrl,
    generateStats = FALSE
)
```

**Arguments**

cohortId	An integer id representing the id that uniquely identifies a cohort definition in a WebApi instance.
name	The name that will be used for the json and SQL files. If not provided, the name in cohort will be used, but this may not lead to valid file names.
jsonFolder	Path to the folder where the JSON representation will be saved.
sqlFolder	Path to the folder where the SQL representation will be saved.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
generateStats	Should the SQL include the code for generating inclusion rule statistics? Note that if TRUE, several additional tables are expected to exist as described in the details.

**Details**

Load a cohort definition from a WebApi instance and insert it into this package. This will fetch the json object and store it in a folder (defaults to 'the inst/cohorts' folder), and fetch the template SQL and store it in another folder (defaults to the 'inst/sql/sql\_server' folder). Both folders will be created if they don't exist. When using generateStats = TRUE, the following tables are required to exist when executing the SQL: cohort\_inclusion, cohort\_inclusion\_result, cohort\_inclusion\_stats, and cohort\_summary\_stats. Also note that the cohort\_inclusion table should be populated with the names of the rules prior to executing the cohort definition SQL.

**Examples**

```
## Not run:
# This will create 'inst/cohorts/Angioedema.json' and 'inst/sql/sql_server/Angioedema.sql':

insertCohortDefinitionInPackage(cohortId = 282,
                                name = "Angioedema",
                                baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```

---

insertCohortDefinitionSetInPackage

*Insert a set of cohort definitions into package*


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## Description

Insert a set of cohort definitions into package

## Usage

```
insertCohortDefinitionSetInPackage(
  fileName = "inst/settings/CohortsToCreate.csv",
  baseUrl,
  jsonFolder = "inst/cohorts",
  sqlFolder = "inst/sql/sql_server",
  rFileName = "R/CreateCohorts.R",
  insertTableSql = TRUE,
  insertCohortCreationR = TRUE,
  generateStats = FALSE,
  packageName
)
```

## Arguments

fileName	Name of a CSV file specifying the cohorts to insert. See details for the expected file format.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
jsonFolder	Path to the folder where the JSON representations will be saved.
sqlFolder	Path to the folder where the SQL representations will be saved.
rFileName	Name of R file to generate when insertCohortCreationR = TRUE.
insertTableSql	Should the SQL for creating the cohort table be inserted into the package as well? This file will be called CreateCohortTable.sql.
insertCohortCreationR	Insert R code that will create the cohort table and instantiate the cohorts? This will create a file called R/CreateCohorts.R containing a function called .createCohorts.
generateStats	Should cohort inclusion rule statistics be created?
packageName	The name of the package (only needed when inserting the R code as well).

## Details

The CSV file should have at least the following fields:

**atlasId** The cohort ID in ATLAS.

**cohortId** The cohort ID that will be used when instantiating the cohort (can be different from atlasId).

**name** The name to be used for the cohort. This name will be used to generate file names, so please use letters and numbers only (no spaces).

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`invokeCohortSetGeneration`*Invoke the generation of a set of cohort definitions*

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**Description**

Invoke the generation of a set of cohort definitions

**Usage**

```
invokeCohortSetGeneration(baseUrl, sourceKeys, cohortIds)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
<code>sourceKeys</code>	A list of sourceKeys
<code>cohortIds</code>	A list of cohortIds

**Details**

Invokes the generation of a set of cohort definitions across a set of CDMs set up in WebAPI. Use `getCohortGenerationStatuses` to check the progress of the set.

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`postDefinition`*Post a definition into WebApi*

---

**Description**

Post a definition into WebApi

**Usage**

```
postDefinition(baseUrl, name, type = "cohort", object)
```

**Arguments**

<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
<code>name</code>	A valid name for the definition. WebApi will use this name (if valid) as the name of the definition. WebApi checks for validity, such as uniqueness, unaccepted character etc. An error might be thrown.
<code>type</code>	The type of expression in WebApi. Currently only 'cohort' is supported to refer cohort definition specification expression.
<code>object</code>	An R list object containing the expression for the specification. This will be converted to JSON by function and posted into the WebApi. Note: only limited checks are performed in R to check the validity of this expression.

**Details**

Post a definition into WebAPI

**Value**

This function will return a dataframe object with one row describing the posted WebApi expression and its details. If unsuccessful a STOP message will be shown. See [getMetadataForAllSpecifications](#).

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resolveConceptSet	<i>Resolve a concept set to the included standard concept IDs</i>
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**Description**

Resolve a concept set to the included standard concept IDs

**Usage**

```
resolveConceptSet(conceptSetDefinition, baseUrl, vocabularySourceKey = NULL)
```

**Arguments**

conceptSetDefinition	A concept set definition, for example as obtained through the <a href="#">getConceptSetDefinition</a> function, or taken from a cohort definition.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Note, there is no trailing '/'. If trailing '/' is used, you may receive an error.
vocabularySourceKey	The source key of the Vocabulary. By default, the priority Vocabulary is used.

**Value**

A vector of standard concept ids.

**Examples**

```
## Not run:
conceptSetDefinition <- getConceptSetDefinition(conceptSetId = 282, baseUrl = "http://server.org:80/WebAPI")
conceptIds <- resolveConceptSet(conceptSetDefinition = conceptSetDefinition,
                               baseUrl = "http://server.org:80/WebAPI")

## End(Not run)
```



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