

Package ‘ROhdsiWebApi’

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Type Package

Title R package to allow interactivity with a WebApi instance

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Description Includes R wrappers for calling WebAPI web services.

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

Suggests testthat,
knitr,
rmarkdown

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

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

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R topics documented:

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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 | <i>Get a cohort definition</i> |
|---------------------|--------------------------------|

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 | <i>Get a cohort definition expression</i> |
|-------------------------------|---|

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

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).

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

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.

`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](#).

| | |
|-------------------|---|
| resolveConceptSet | <i>Resolve a concept set to the included standard concept IDs</i> |
|-------------------|---|

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 getConceptSetDefinition 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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