

Package ‘CohortDiagnostics’

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Type Package

Title Diagnostics for OHDSI Cohorts

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Description Diagnostics for cohorts that use the OMOP Common Data Model and the OHDSI tools.

Depends DatabaseConnector (>= 4.0.0),
FeatureExtraction (>= 3.1.1),
R (>= 4.0.0)

Imports Andromeda,
checkmate,
clock,
digest,
dplyr (>= 1.0.0),
methods,
ParallelLogger (>= 2.0.0),
readr (>= 1.4.0),
RJSONIO,
rlang,
ROhdsiWebApi (>= 1.2.0),
SqlRender (>= 1.7.0),
stringr,
tidyr (>= 1.1.3)

Suggests CirceR,
DT,
Eunomia,
ggiraph,
ggplot2,
htmltools,
knitr,
lubridate,
plotly,
pool,
purrr,
RColorBrewer,
rmarkdown,
RSQLite (>= 2.2.1),
scales,

shiny,
shinydashboard,
shinyWidgets,
testthat,
withr,
zip

Remotes ohdsi/Eunomia,
ohdsi/FeatureExtraction,
ohdsi/ROhdsiWebApi,
ohdsi/CirceR

License Apache License

VignetteBuilder knitr

URL <https://ohdsi.github.io/CohortDiagnostics>, <https://github.com/OHDSI/CohortDiagnostics>

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

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Encoding UTF-8

Language en-US

R topics documented:

checkIfCohortInstantiated	3
checkInputFileEncoding	4
computeCohortOverlap	4
createDatabaseDataSource	5
createFileDataSource	6
createResultsDataModel	6
getCohortCharacteristics	7
getCohortCounts	8
getConceptDetails	9
getResultsCovariateValue	9
getResultsDataModelSpecifications	10
getResultsFromCohortCount	11
getResultsFromIncidenceRate	11
getResultsFromIncludedConcept	12
getResultsFromInclusionRuleStatistics	13
getResultsFromIndexEventBreakdown	13
getResultsFromOrphanConcept	14
getResultsFromTimeDistribution	15
getResultsFromTimeSeries	15
getResultsFromVisitContext	16
getResultsResolveMappedConceptSet	17
instantiateCohortSet	17
launchCohortExplorer	20
launchDiagnosticsExplorer	21
preMergeDiagnosticsFiles	22
runCohortDiagnostics	22
uploadResults	26

`checkIfCohortInstantiated`*Checks if a set of cohortId(s) are instantiated in the cohort table*

Description

Given a set of one or more cohortIds and a single cohort table, checks if all cohortIds in the set are instantiated.

Usage

```
checkIfCohortInstantiated(  
    connectionDetails = NULL,  
    connection = NULL,  
    cohortDatabaseSchema,  
    cohortTable,  
    cohortIds  
)
```

Arguments

- | | |
|-----------------------------------|--|
| <code>connectionDetails</code> | An object of type <code>connectionDetails</code> as created using the createConnectionDetails function in the DatabaseConnector package. Can be left NULL if connection is provided. |
| <code>connection</code> | An object of type <code>connection</code> as created using the connect function in the DatabaseConnector package. Can be left NULL if <code>connectionDetails</code> is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes. |
| <code>cohortDatabaseSchema</code> | Schema name where your cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'. |
| <code>cohortTable</code> | Name of the cohort table. |
| <code>cohortIds</code> | Provide a set of cohort IDs to check if instantiated. |

Value

Returns TRUE if all cohortIds are instantiated.

 checkInputFileEncoding

Check character encoding of input file

Description

For its input files, CohortDiagnostics only accepts UTF-8 or ASCII character encoding. This function can be used to check whether a file meets these criteria.

Usage

```
checkInputFileEncoding(fileName)
```

Arguments

fileName The path to the file to check

Value

Throws an error if the input file does not have the correct encoding.

 computeCohortOverlap *Given two sets of cohorts get relationships between the cohorts.*

Description

Given two cohorts, get data to compare relationships between the cohorts - such as overlap, temporal relationships between cohort start date(s). Note: only the first occurrence of subject_id in the cohort is used.

Usage

```
computeCohortOverlap(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema,
  cohortTable = "cohort",
  targetCohortIds,
  comparatorCohortIds,
  batchSize = 200
)
```

Arguments

connectionDetails

An object of type connectionDetails as created using the [createConnectionDetails](#) function in the DatabaseConnector package. Can be left NULL if connection is provided.

connection	An object of type connection as created using the connect function in the DatabaseConnector package. Can be left NULL if connectionDetails is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes.
cohortDatabaseSchema	Schema name where your cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
cohortTable	Name of the cohort table.
targetCohortIds	A list of cohort ids to be used as target cohorts.
comparatorCohortIds	A list of cohort ids to be used as comparator cohorts.
batchSize	Optional, default set to 200. If running diagnostics on target set of cohorts, this function allows you to batch them into chunks that run as a batch.

```
createDatabaseDataSource
```

Return a database data source object

Description

Collects a list of objects needed to connect to a database datasource. This includes one of DatabaseConnector::createConnection object, or a DBI database connection created using either DatabaseConnector::connection or pool::dbPool, and a names of resultsDatabaseSchema and vocabularyDatabaseSchema

Usage

```
createDatabaseDataSource(
  connection = NULL,
  connectionDetails = NULL,
  resultsDatabaseSchema,
  vocabularyDatabaseSchema = resultsDatabaseSchema
)
```

Arguments

connection	An object of type connection as created using the connect function in the DatabaseConnector package. Can be left NULL if connectionDetails is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes.
connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package. Can be left NULL if connection is provided.
resultsDatabaseSchema	Schema name where the output of your Cohort Diagnostics result set is uploaded. This is commonly uploaded using CohortDiagnostics::uploadResults function. The schema may be initiated using CohortDiagnostics::resultsDatabaseSchema.
vocabularyDatabaseSchema	Schema name where your OMOP vocabulary data resides. This is commonly the same as cdmDatabaseSchema. Note that for SQL Server, this should include both the database and schema name, for example 'vocabulary.dbo'.

Value

Returns a list with information on database data source

`createFileDataSource` *Return a file data source object*

Description

Given a premerged file (an `.RData/rds` object the output of `CohortDiagnostics::preMergeDiagnosticsFiles` reads the object into memory and makes it available for query.

Usage

```
createFileDataSource(premergedDataFile, envir = .GlobalEnv)
```

Arguments

<code>premergedDataFile</code>	an <code>.RData/rds</code> object the output of <code>CohortDiagnostics::preMergeDiagnosticsFiles</code>
<code>envir</code>	(optional) R-environment to read premerged data. By default this is the global environment.

Value

R environment containing data conforming to Cohort Diagnostics results data model specifications.

`createResultsDataModel`
Create the results data model tables on a database server.

Description

Create the results data model tables on a database server.

Usage

```
createResultsDataModel(connection = NULL, connectionDetails = NULL, schema)
```

Arguments

<code>connection</code>	An object of type <code>connection</code> as created using the connect function in the <code>DatabaseConnector</code> package. Can be left <code>NULL</code> if <code>connectionDetails</code> is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes.
<code>connectionDetails</code>	An object of type <code>connectionDetails</code> as created using the createConnectionDetails function in the <code>DatabaseConnector</code> package. Can be left <code>NULL</code> if <code>connection</code> is provided.
<code>schema</code>	The schema on the postgres server where the tables will be created.

Details

Only PostgreSQL servers are supported.

```
getCohortCharacteristics
```

Get Characteristics for a cohort

Description

Given a set of instantiated cohorts get Characteristics for the cohort using `FeatureExtraction::getDbCovariateData`.

If `runTemporalCohortCharacterization` argument is `TRUE`, then the following default covariateSettings object will be created using `RFeatureExtraction::createTemporalCovariateSettings`.

Usage

```
getCohortCharacteristics(
  connectionDetails = NULL,
  connection = NULL,
  cdmDatabaseSchema,
  tempEmulationSchema = NULL,
  cohortDatabaseSchema = cdmDatabaseSchema,
  cohortTable = "cohort",
  cohortIds = NULL,
  cdmVersion = 5,
  covariateSettings = createDefaultCovariateSettings(),
  batchSize = 100
)
```

Arguments

`connectionDetails`

An object of type `connectionDetails` as created using the [createConnectionDetails](#) function in the `DatabaseConnector` package. Can be left `NULL` if connection is provided.

`connection`

An object of type `connection` as created using the [connect](#) function in the `DatabaseConnector` package. Can be left `NULL` if `connectionDetails` is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes.

`cdmDatabaseSchema`

Schema name where your patient-level data in OMOP CDM format resides. Note that for SQL Server, this should include both the database and schema name, for example `'cdm_data.dbo'`.

`tempEmulationSchema`

Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.

`cohortDatabaseSchema`

Schema name where your cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example `'scratch.dbo'`.

cohortTable	Name of the cohort table.
cohortIds	Optionally, provide a subset of cohort IDs to restrict the diagnostics to.
cdmVersion	The version of the OMOP CDM. Default 5. (Note: only 5 is supported.)
covariateSettings	Either an object of type covariateSettings as created using one of the createCovariateSettings (createTemporalCovariateSettings if temporal characterization) function in the FeatureExtraction package, or a list of such objects. If unspecified, default covariate settings as specified by FeatureExtraction is computed, this is sufficient for presenting default table 1. See documentation of FeatureExtraction on how to specify CovariateSettings object.
batchSize	Optional, default set to 100 If running characterization on largset set of cohorts, this function allows you to batch them into chunks that run as a batch.

getCohortCounts	<i>Count the cohort(s)</i>
-----------------	----------------------------

Description

Computes the subject and entry count per cohort

Usage

```
getCohortCounts(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema,
  cohortTable = "cohort",
  cohortIds = c()
)
```

Arguments

connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the connect function in the DatabaseConnector package. Can be left NULL if connectionDetails is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes.
cohortDatabaseSchema	Schema name where your cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
cohortTable	Name of the cohort table.
cohortIds	The cohort Id(s) used to reference the cohort in the cohort table. If left empty, all cohorts in the table will be included.

Value

A tibble with cohort counts

getConceptDetails	<i>Returns data from concept table of Cohort Diagnostics results data model</i>
-------------------	---

Description

Returns data from concept table of Cohort Diagnostics results data model

Usage

```
getConceptDetails(
  dataSource = .GlobalEnv,
  vocabularyDatabaseSchema = NULL,
  conceptIds
)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
vocabularyDatabaseSchema	Schema name where your OMOP vocabulary data resides. This is commonly the same as cdmDatabaseSchema. Note that for SQL Server, this should include both the database and schema name, for example 'vocabulary.dbo'.
conceptIds	A vector of one or more Concept Ids.

Value

Returns a data frame (tibble) with results that conform to concept table in Cohort Diagnostics results data model.

getResultsCovariateValue	<i>Returns covariate_value and covariate_value_dist output of feature extraction</i>
--------------------------	--

Description

Returns covariate_value and covariate_value_dist output of feature extraction. The covariate_value and temporal_covariate_value are appended with timeId = 0 assigned to covariate_value. Similarly, covariate_value_dist and temporal_covariate_value_dist are also appended with timeId = 0 in covariate_value_dist.

Usage

```
getResultsCovariateValue(dataSource = .GlobalEnv, cohortIds, databaseIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
cohortIds	A vector of one or more Cohort Ids.
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.

Value

Returns a list object with two data frames (tibble) covariate_value and covariate_value_dist

```
getResultsDataModelSpecifications
```

Get specifications for Cohort Diagnostics results data model

Description

Get specifications for Cohort Diagnostics results data model

Usage

```
getResultsDataModelSpecifications()
```

Value

A tibble data frame object with specifications

`getResultsFromCohortCount`*Returns data from cohort_count table of Cohort Diagnostics results data model*

Description

Returns data from cohort_count table of Cohort Diagnostics results data model

Usage

```
getResultsFromCohortCount(dataSource, cohortIds, databaseIds)
```

Arguments

- | | |
|--------------------------|--|
| <code>dataSource</code> | A list object that is the output of <code>createDatabaseDataSource</code> or <code>createFileDataSource</code> function. This object helps direct the function to query data from the database (created by <code>createDatabaseDataSource</code>) or a local premerged file (created by <code>createFileDataSource</code>). Premerged files are output of <code>cohortDiagnostics</code> compiled into RData using <code>preMergeDiagnosticsFiles</code> . Database DataSources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function <code>createResultsDataModel</code> and uploaded using <code>uploadResults</code> |
| <code>cohortIds</code> | A vector of one or more Cohort Ids. |
| <code>databaseIds</code> | A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model. |

Value

Returns a data frame (tibble) with results that conform to cohort counts table in Cohort Diagnostics results data model.

`getResultsFromIncidenceRate`*Returns data from incidence_rate table of Cohort Diagnostics results data model*

Description

Returns data from incidence_rate table of Cohort Diagnostics results data model

Usage

```
getResultsFromIncidenceRate(dataSource, cohortIds, databaseIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
cohortIds	A vector of one or more Cohort Ids.
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.

Value

Returns a data frame (tibble) with results that conform to incidence_rate table in Cohort Diagnostics results data model.

getResultsFromIncludedConcept

Returns data from included_concept table of Cohort Diagnostics results data model

Description

Returns data from included_concept table of Cohort Diagnostics results data model

Usage

```
getResultsFromIncludedConcept(dataSource, cohortIds, databaseIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
cohortIds	A vector of one or more Cohort Ids.
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.

Value

Returns a data frame (tibble) with results that conform to included_concept table in Cohort Diagnostics results data model.

`getResultsFromInclusionRuleStatistics`*Returns data from inclusion_rule_stats table of Cohort Diagnostics results data model*

Description

Returns data from inclusion_rule_stats table of Cohort Diagnostics results data model

Usage

```
getResultsFromInclusionRuleStatistics(dataSource, cohortIds, databaseIds)
```

Arguments

- | | |
|--------------------------|--|
| <code>dataSource</code> | A list object that is the output of <code>createDatabaseDataSource</code> or <code>createFileDataSource</code> function. This object helps direct the function to query data from the database (created by <code>createDatabaseDataSource</code>) or a local premerged file (created by <code>createFileDataSource</code>). Premerged files are output of <code>cohortDiagnostics</code> compiled into RData using <code>preMergeDiagnosticsFiles</code> . Database DataSources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function <code>createResultsDataModel</code> and uploaded using <code>uploadResults</code> |
| <code>cohortIds</code> | A vector of one or more Cohort Ids. |
| <code>databaseIds</code> | A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model. |

Value

Returns a data frame (tibble) with results that conform to inclusion_rule_stats table in Cohort Diagnostics results data model.

`getResultsFromIndexEventBreakdown`*Returns data from index_event_breakdown table of Cohort Diagnostics results data model*

Description

Returns data from index_event_breakdown table of Cohort Diagnostics results data model

Usage

```
getResultsFromIndexEventBreakdown(dataSource, cohortIds, databaseIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
cohortIds	A vector of one or more Cohort Ids.
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.

Value

Returns a data frame (tibble) with results that conform to index_event_breakdown table in Cohort Diagnostics results data model.

getResultsFromOrphanConcept

Returns data from orphan_concept table of Cohort Diagnostics results data model

Description

Returns data from orphan_concept table of Cohort Diagnostics results data model

Usage

```
getResultsFromOrphanConcept(dataSource, cohortIds, databaseIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
cohortIds	A vector of one or more Cohort Ids.
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.

Value

Returns a data frame (tibble) with results that conform to orphan_concept table in Cohort Diagnostics results data model.

`getResultsFromTimeDistribution`*Returns data from time_distribution table of Cohort Diagnostics results data model*

Description

Returns data from time_distribution table of Cohort Diagnostics results data model

Usage

```
getResultsFromTimeDistribution(dataSource, cohortIds, databaseIds)
```

Arguments

- | | |
|--------------------------|--|
| <code>dataSource</code> | A list object that is the output of <code>createDatabaseDataSource</code> or <code>createFileDataSource</code> function. This object helps direct the function to query data from the database (created by <code>createDatabaseDataSource</code>) or a local premerged file (created by <code>createFileDataSource</code>). Premerged files are output of <code>cohortDiagnostics</code> compiled into RData using <code>preMergeDiagnosticsFiles</code> . Database DataSources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function <code>createResultsDataModel</code> and uploaded using <code>uploadResults</code> |
| <code>cohortIds</code> | A vector of one or more Cohort Ids. |
| <code>databaseIds</code> | A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model. |

Value

Returns a data frame (tibble) with results that conform to time_distribution table in Cohort Diagnostics results data model.

`getResultsFromTimeSeries`*Returns data from time_series table of Cohort Diagnostics results data model*

Description

Returns data from time_series table of Cohort Diagnostics results data model

Usage

```
getResultsFromTimeSeries(dataSource, cohortIds, databaseIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
cohortIds	A vector of one or more Cohort Ids.
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.

Value

Returns a data frame (tibble) with results that conform to time series table in Cohort Diagnostics results data model.

```
getResultsFromVisitContext
```

Returns data from visit_context table of Cohort Diagnostics results data model

Description

Returns data from visit_context table of Cohort Diagnostics results data model

Usage

```
getResultsFromVisitContext(dataSource, cohortIds, databaseIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
cohortIds	A vector of one or more Cohort Ids.
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.

Value

Returns a data frame (tibble) with results that conform to visit_context table in Cohort Diagnostics results data model.

getResultsResolveMappedConceptSet

Returns resolved and mapped concepts for concept set expression in a cohort

Description

Returns a list object with resolved and mapped concepts for all concept sets in one cohort from one or more data sources. This is being returned from the results data model of Cohort Diagnostics and is precomputed.

Usage

```
getResultsResolveMappedConceptSet(dataSource, databaseIds, cohortIds)
```

Arguments

dataSource	A list object that is the output of createDatabaseDataSource or createFileDataSource function. This object helps direct the function to query data from the database (created by createDatabaseDataSource) or a local premerged file (created by createFileDataSource). Premerged files are output of cohortDiagnostics compiled into RData using preMergeDiagnosticsFiles. Database Data-Sources are data inserted into a remote database (only a postgres database is supported) with tables created with DDL function createResultsDataModel and uploaded using uploadResults
databaseIds	A vector one or more databaseIds to retrieve the results for. This is a character field values from the 'databaseId' field of the 'database' table of the results data model.
cohortIds	A vector of one or more Cohort Ids.

Value

Returns a list object with resolved and mapped concepts for all concept sets in one cohort from one or more data sources. There will be two objects in the returned list object resolved, mapped - each will be tibble.

instantiateCohortSet *Instantiate a set of cohort(s)*

Description

This function instantiates a set of cohort(s) in specified cohort table, using definitions that are fetched from a WebApi interface. Optionally, the inclusion rule statistics are computed and stored in the inclusionStatisticsFolder.

Usage

```

instantiateCohortSet(
  connectionDetails = NULL,
  connection = NULL,
  cdmDatabaseSchema,
  vocabularyDatabaseSchema = cdmDatabaseSchema,
  tempEmulationSchema = NULL,
  oracleTempSchema = NULL,
  cohortDatabaseSchema = cdmDatabaseSchema,
  cohortTable = "cohort",
  cohortIds = NULL,
  packageName = NULL,
  cohortToFile = "settings/CohortsToCreate.csv",
  baseUrl = NULL,
  cohortSetReference = NULL,
  generateInclusionStats = FALSE,
  inclusionStatisticsFolder = NULL,
  createCohortTable = TRUE,
  incremental = FALSE,
  incrementalFolder = NULL
)

```

Arguments

- | | |
|--------------------------|--|
| connectionDetails | An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package. Can be left NULL if connection is provided. |
| connection | An object of type connection as created using the connect function in the DatabaseConnector package. Can be left NULL if connectionDetails is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes. |
| cdmDatabaseSchema | Schema name where your patient-level data in OMOP CDM format resides. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'. |
| vocabularyDatabaseSchema | Schema name where your OMOP vocabulary data resides. This is commonly the same as cdmDatabaseSchema. Note that for SQL Server, this should include both the database and schema name, for example 'vocabulary.dbo'. |
| tempEmulationSchema | Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created. |
| oracleTempSchema | DEPRECATED by DatabaseConnector: use tempEmulationSchema instead. |
| cohortDatabaseSchema | Schema name where your cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'. |
| cohortTable | Name of the cohort table. |
| cohortIds | Optionally, provide a subset of cohort IDs to restrict the construction to. |

<code>packageName</code>	The name of the package containing the cohort definitions. Can be left NULL if <code>baseUrl</code> and <code>cohortSetReference</code> have been specified.
<code>cohortToCreateFile</code>	The location of the cohortToCreate file within the package. Is ignored if <code>baseUrl</code> and <code>cohortSetReference</code> have been specified. The cohortToCreateFile must be .csv file that is expected to be read into a dataframe object identical to requirements for <code>cohortSetReference</code> argument. This csv file is expected to be encoded in either ASCII or UTF-8, if not, an error message will be displayed and process stopped.
<code>baseUrl</code>	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Can be left NULL if <code>packageName</code> and <code>cohortToCreateFile</code> have been specified.
<code>cohortSetReference</code>	A data frame with four columns, as described in the details. Can be left NULL if <code>packageName</code> and <code>cohortToCreateFile</code> have been specified.
<code>generateInclusionStats</code>	Compute and store inclusion rule statistics?
<code>inclusionStatisticsFolder</code>	The folder where the inclusion rule statistics are stored. Can be left NULL if <code>generateInclusionStats = FALSE</code> .
<code>createCohortTable</code>	Create the cohort table? If <code>incremental = TRUE</code> and the table already exists this will be skipped.
<code>incremental</code>	Create only cohorts that haven't been created before?
<code>incrementalFolder</code>	If <code>incremental = TRUE</code> , specify a folder where records are kept of which definition has been executed.

Details

Currently two ways of executing this function are supported, either (1) [Package Mode] embedded in a study package, assuming the cohort definitions are stored in that package using the `ROhdsiWebApi::insertCohortDefinition` or (2) [WebApi Mode] By using a WebApi interface to retrieve the cohort definitions.

When using this function in Package Mode: Use the `packageName` and `cohortToCreateFile` to specify the name of the study package, and the name of the cohortToCreate file within that package, respectively

When using this function in WebApi Mode: use the `baseUrl` and `cohortSetReference` to specify how to connect to the WebApi, and which cohorts to fetch, respectively.

Note: if the parameters for both Package Mode and WebApi Mode are provided, then Package mode is preferred.

The `cohortSetReference` argument must be a data frame with the following columns:

referentConceptId A standard omop concept id that serves as the referent phenotype definition for the cohort Id.

cohortId The cohort Id is the id used to identify a cohort definition. This is required to be unique. It will be used to create file names. It is recommended to be $(\text{referentConceptId} * 1000) + \text{a number between 3 to 999}$

webApiCohortId Cohort Id in the webApi/atlas instance. It is a required field to run Cohort Diagnostics in WebApi mode. It is discarded in package mode.

cohortName The full name of the cohort. This will be shown in the Shiny app.

logicDescription A human understandable brief description of the cohort definition. This logic does not have to a fully specified description of the cohort definition, but should provide enough context to help user understand the meaning of the cohort definition

Value

A data frame with cohort counts

launchCohortExplorer *Launch the CohortExplorer Shiny app*

Description

Launch the CohortExplorer Shiny app

Usage

```
launchCohortExplorer(
  connectionDetails,
  cdmDatabaseSchema,
  cohortDatabaseSchema,
  cohortTable,
  cohortId,
  sampleSize = 100,
  subjectIds = NULL
)
```

Arguments

connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package.
cdmDatabaseSchema	Schema name where your patient-level data in OMOP CDM format resides. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
cohortDatabaseSchema	Schema name where your cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
cohortTable	Name of the cohort table.
cohortId	The ID of the cohort.
sampleSize	Number of subjects to sample from the cohort. Ignored if subjectIds is specified.
subjectIds	A vector of subject IDs to view.

Details

Launches a Shiny app that allows the user to explore a cohort of interest.

 launchDiagnosticsExplorer

Launch the Diagnostics Explorer Shiny app

Description

Launch the Diagnostics Explorer Shiny app

Usage

```
launchDiagnosticsExplorer(
  dataFolder = "data",
  dataFile = "PreMerged.RData",
  connectionDetails = NULL,
  resultsDatabaseSchema = NULL,
  vocabularyDatabaseSchema = NULL,
  vocabularyDatabaseSchemas = resultsDatabaseSchema,
  aboutText = NULL,
  runOverNetwork = FALSE,
  port = 80,
  launch.browser = FALSE
)
```

Arguments

- | | |
|---------------------------|--|
| dataFolder | A folder where the premerged file is stored. Use the preMergeDiagnosticsFiles function to generate this file. |
| dataFile | (Optional) The name of the .RData file with results. It is commonly known as the Premerged file. |
| connectionDetails | An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package, specifying how to connect to the server where the CohortDiagnostics results have been uploaded using the uploadResults function. |
| resultsDatabaseSchema | The schema on the database server where the CohortDiagnostics results have been uploaded. |
| vocabularyDatabaseSchema | (Deprecated) Please use vocabularyDatabaseSchemas. |
| vocabularyDatabaseSchemas | (optional) A list of one or more schemas on the database server where the vocabulary tables are located. The default value is the value of the resultsDatabaseSchema. We can provide a list of vocabulary schema that might represent different versions of the OMOP vocabulary tables. It allows us to compare the impact of vocabulary changes on Diagnostics. |
| aboutText | Text (using HTML markup) that will be displayed in an About tab in the Shiny app. If not provided, no About tab will be shown. |
| runOverNetwork | (optional) Do you want the app to run over your network? |
| port | (optional) Only used if runOverNetwork = TRUE. |
| launch.browser | Should the app be launched in your default browser, or in a Shiny window. Note: copying to clipboard will not work in a Shiny window. |

Details

Launches a Shiny app that allows the user to explore the diagnostics

```
preMergeDiagnosticsFiles
```

Premerge Shiny diagnostics files

Description

This function combines diagnostics results from one or more databases into a single file. The result is a single file that can be used as input for the Diagnostics Explorer Shiny app.

It also checks whether the results conform to the results data model specifications.

Usage

```
preMergeDiagnosticsFiles(dataFolder, tempFolder = tempdir())
```

Arguments

dataFolder	folder where the exported zip files for the diagnostics are stored. Use the runCohortDiagnostics function to generate these zip files. Zip files containing results from multiple databases may be placed in the same folder.
tempFolder	A folder on the local file system where the zip files are extracted to. Will be cleaned up when the function is finished. Can be used to specify a temp folder on a drive that has sufficient space if the default system temp space is too limited.

```
runCohortDiagnostics
```

Run cohort diagnostics

Description

Runs the cohort diagnostics on all (or a subset of) the cohorts instantiated using the `ROhdsiWebApi::insertCohortDefinition` function. Assumes the cohorts have already been instantiated.

Characterization: If `runTemporalCohortCharacterization` argument is `TRUE`, then the following default covariateSettings object will be created using `RFeatureExtraction::createTemporalCovariateSettings`. Alternatively, a covariate setting object may be created using the above as an example.

Usage

```
runCohortDiagnostics(
  packageName = NULL,
  cohortToCreateFile = "settings/CohortsToCreate.csv",
  baseUrl = NULL,
  cohortSetReference = NULL,
  connectionDetails = NULL,
  connection = NULL,
  cdmDatabaseSchema,
  oracleTempSchema = NULL,
```

```

tempEmulationSchema = NULL,
cohortDatabaseSchema,
vocabularyDatabaseSchema = cdmDatabaseSchema,
cohortTable = "cohort",
cohortIds = NULL,
inclusionStatisticsFolder = file.path(exportFolder, "inclusionStatistics"),
exportFolder,
databaseId,
databaseName = databaseId,
databaseDescription = databaseId,
cdmVersion = 5,
runInclusionStatistics = TRUE,
runIncludedSourceConcepts = TRUE,
runOrphanConcepts = TRUE,
runTimeDistributions = TRUE,
runVisitContext = TRUE,
runBreakdownIndexEvents = TRUE,
runIncidenceRate = TRUE,
runTimeSeries = TRUE,
runCohortOverlap = TRUE,
runCohortCharacterization = TRUE,
covariateSettings = createDefaultCovariateSettings(),
runTemporalCohortCharacterization = TRUE,
temporalCovariateSettings = createTemporalCovariateSettings(useConditionOccurrence =
  TRUE, useDrugEraStart = TRUE, useDrugEraOverlap = TRUE, useVisitCount = TRUE,
  useVisitConceptCount = TRUE, useProcedureOccurrence = TRUE, useMeasurement = TRUE,
  temporalStartDays = c(-365, -30, 0, 1, 31, seq(from = -421, to = -31, by = 30),
    seq(from = 0, to = 390, by = 30)), temporalEndDays = c(-31, -1, 0, 30, 365, seq(from
    = -391, to = -1, by = 30), seq(from = 30, to = 420, by = 30))),
minCellCount = 5,
incremental = FALSE,
incrementalFolder = file.path(exportFolder, "incremental")
)

```

Arguments

packageName	The name of the package containing the cohort definitions. Can be left NULL if baseUrl and cohortSetReference have been specified.
cohortToCreateFile	The location of the cohortToCreate file within the package. Is ignored if baseUrl and cohortSetReference have been specified. The cohortToCreateFile must be .csv file that is expected to be read into a dataframe object identical to requirements for cohortSetReference argument. This csv file is expected to be encoded in either ASCII or UTF-8, if not, an error message will be displayed and process stopped.
baseUrl	The base URL for the WebApi instance, for example: "http://server.org:80/WebAPI". Can be left NULL if packageName and cohortToCreateFile have been specified.
cohortSetReference	A data frame with four columns, as described in the details. Can be left NULL if packageName and cohortToCreateFile have been specified.

connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the connect function in the DatabaseConnector package. Can be left NULL if connectionDetails is provided, in which case a new connection will be opened at the start of the function, and closed when the function finishes.
cdmDatabaseSchema	Schema name where your patient-level data in OMOP CDM format resides. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
oracleTempSchema	DEPRECATED by DatabaseConnector: use tempEmulationSchema instead.
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.
cohortDatabaseSchema	Schema name where your cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
vocabularyDatabaseSchema	Schema name where your OMOP vocabulary data resides. This is commonly the same as cdmDatabaseSchema. Note that for SQL Server, this should include both the database and schema name, for example 'vocabulary.dbo'.
cohortTable	Name of the cohort table.
cohortIds	Optionally, provide a subset of cohort IDs to restrict the diagnostics to.
inclusionStatisticsFolder	The folder where the inclusion rule statistics are stored. Can be left NULL if runInclusionStatistics = FALSE.
exportFolder	The folder where the output will be exported to. If this folder does not exist it will be created.
databaseId	A short string for identifying the database (e.g. 'Synpuf').
databaseName	The full name of the database. If NULL, defaults to databaseId.
databaseDescription	A short description (several sentences) of the database. If NULL, defaults to databaseId.
cdmVersion	The version of the OMOP CDM. Default 5. (Note: only 5 is supported.)
runInclusionStatistics	Generate and export statistic on the cohort inclusion rules?
runIncludedSourceConcepts	Generate and export the source concepts included in the cohorts?
runOrphanConcepts	Generate and export potential orphan concepts?
runTimeDistributions	Generate and export cohort time distributions?
runVisitContext	Generate and export index-date visit context?

runBreakdownIndexEvents	Generate and export the breakdown of index events?
runIncidenceRate	Generate and export the cohort incidence rates?
runTimeSeries	Generate and export the cohort prevalence rates?
runCohortOverlap	Generate and export the cohort overlap? Overlaps are checked within cohortIds that have the same phenotype ID sourced from the CohortSetReference or cohortToCreateFile.
runCohortCharacterization	Generate and export the cohort characterization? Only records with values greater than 0.0001 are returned.
covariateSettings	Either an object of type covariateSettings as created using one of the createCovariateSettings function in the FeatureExtraction package, or a list of such objects.
runTemporalCohortCharacterization	Generate and export the temporal cohort characterization? Only records with values greater than 0.001 are returned.
temporalCovariateSettings	Either an object of type covariateSettings as created using one of the createTemporalCovariateSettings function in the FeatureExtraction package, or a list of such objects.
minCellCount	The minimum cell count for fields contains person counts or fractions.
incremental	Create only cohort diagnostics that haven't been created before?
incrementalFolder	If incremental = TRUE, specify a folder where records are kept of which cohort diagnostics has been executed.

Details

Currently two ways of executing this function are supported, either (1) [Package Mode] embedded in a study package, assuming the cohort definitions are stored in that package using the `ROhdsiWebApi::insertCohortDefinitions` or (2) [WebApi Mode] By using a WebApi interface to retrieve the cohort definitions.

When using this function in Package Mode: Use the `packageName` and `cohortToCreateFile` to specify the name of the study package, and the name of the cohortToCreate file within that package, respectively

When using this function in WebApi Mode: use the `baseUrl` and `cohortSetReference` to specify how to connect to the WebApi, and which cohorts to fetch, respectively.

Note: if the parameters for both Package Mode and WebApi Mode are provided, then Package mode is preferred.

The `cohortSetReference` argument must be a data frame with the following columns:

referentConceptId A standard omop concept id that serves as the referent phenotype definition for the cohort Id.

cohortId The cohort Id is the id used to identify a cohort definition. This is required to be unique. It will be used to create file names. It is recommended to be (`referentConceptId * 1000`) + a number between 3 to 999

webApiCohortId Cohort Id in the webApi/atlas instance. It is a required field to run Cohort Diagnostics in WebApi mode. It is discarded in package mode.

cohortName The full name of the cohort. This will be shown in the Shiny app.

logicDescription A human understandable brief description of the cohort definition. This logic does not have to a fully specified description of the cohort definition, but should provide enough context to help user understand the meaning of the cohort definition

uploadResults

Upload results to the database server.

Description

Requires the results data model tables have been created using the [createResultsDataModel](#) function.

Set the POSTGRES_PATH environmental variable to the path to the folder containing the psql executable to enable bulk upload (recommended).

Usage

```
uploadResults(
  connectionDetails = NULL,
  schema,
  zipFileName,
  forceOverWriteOfSpecifications = FALSE,
  purgeSiteDataBeforeUploading = TRUE,
  tempFolder = tempdir()
)
```

Arguments

connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package.
schema	The schema on the postgres server where the tables have been created.
zipFileName	The name of the zip file.
forceOverWriteOfSpecifications	If TRUE, specifications of the phenotypes, cohort definitions, and analysis will be overwritten if they already exist on the database. Only use this if these specifications have changed since the last upload.
purgeSiteDataBeforeUploading	If TRUE, before inserting data for a specific databaseId all the data for that site will be dropped. This assumes the input zip file contains the full data for that data site.
tempFolder	A folder on the local file system where the zip files are extracted to. Will be cleaned up when the function is finished. Can be used to specify a temp folder on a drive that has sufficient space if the default system temp space is too limited.

Index

checkIfCohortInstantiated, [3](#)
checkInputFileEncoding, [4](#)
computeCohortOverlap, [4](#)
connect, [3](#), [5–8](#), [18](#), [24](#)
createConnectionDetails, [3–8](#), [18](#), [20](#), [21](#),
[24](#), [26](#)
createDatabaseDataSource, [5](#)
createFileDataSource, [6](#)
createResultsDataModel, [6](#), [26](#)

getCohortCharacteristics, [7](#)
getCohortCounts, [8](#)
getConceptDetails, [9](#)
getResultsCovariateValue, [9](#)
getResultsDataModelSpecifications, [10](#)
getResultsFromCohortCount, [11](#)
getResultsFromIncidenceRate, [11](#)
getResultsFromIncludedConcept, [12](#)
getResultsFromInclusionRuleStatistics,
[13](#)
getResultsFromIndexEventBreakdown, [13](#)
getResultsFromOrphanConcept, [14](#)
getResultsFromTimeDistribution, [15](#)
getResultsFromTimeSeries, [15](#)
getResultsFromVisitContext, [16](#)
getResultsResolveMappedConceptSet, [17](#)

instantiateCohortSet, [17](#)

launchCohortExplorer, [20](#)
launchDiagnosticsExplorer, [21](#)

preMergeDiagnosticsFiles, [21](#), [22](#)

runCohortDiagnostics, [22](#), [22](#)

uploadResults, [21](#), [26](#)