

# 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 (>= 2.0.2),  
readr (>= 1.4.0),  
RJSONIO,  
rlang,  
ROhdsiWebApi (>= 1.2.0),  
SqlRender (>= 1.7.0),  
stringr,  
tidyr (>= 1.1.3),  
tsibble

**Suggests** CirceR,  
DT,  
Eunomia,  
ggiraph,  
ggplot2,  
htmltools,  
knitr,  
lubridate,  
plotly,  
pool,  
purrr,  
RColorBrewer,  
markdown,  
rmarkdown,

RSQLite ( $\geq 2.2.1$ ),  
 scales,  
 shiny,  
 shinydashboard,  
 shinyWidgets,  
 testthat,  
 withr,  
 zip,  
 R.utils

**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>

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**Language** en-US

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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

connectionDetails	An object of type connectionDetails as created using the <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the <a href="#">connect</a> 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	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.

---

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::createC 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**

- premergedDataFile** an .RData/rds object the output of CohortDiagnostics::preMergeDiagnosticsFiles
- envir** (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

connection	An object of type connection as created using the <a href="#">connect</a> 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 <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.
schema	The schema on the postgres server where the tables will be created.

### Details

Only PostgreSQL servers are supported.

---

```
exportFeatureExtractionOutput
```

*Export Feature Extraction output to csv*

---

### Description

Exports the output of `FeatureExtraction::getDbCovariateData` into CSV.

### Usage

```
exportFeatureExtractionOutput(
  featureExtractionDbCovariateData,
  databaseId,
  incremental = FALSE,
  covariateValueFileName = "covariate_value.csv",
  covariateValueContFileName = "covariate_value_dist.csv",
  covariateRefFileName = "covariate_ref.csv",
  analysisRefFileName = "analysis_ref.csv",
  timeDistributionFileName = NULL,
  timeRefFileName = NULL,
  cohortCounts,
  cutOff = 1e-04,
  minCellCount = 5
)
```

**Arguments**

featureExtractionDbCovariateData	An Andromeda object returned by CohortDiagnostics::runCohortCharacterizationDiagnostics
databaseId	A short string for identifying the database (e.g. 'Synpuf').
incremental	Create only cohort diagnostics that haven't been created before?
covariateValueFileName	The full path (including file name) for the csv file with covariate value data. e.g. "covariate_value.csv" or "temporal_covariate_value.csv"
covariateValueContFileName	The full path (including file name) for the csv file with covariate value distribution data. e.g. "covariate_value_dist.csv" or "temporal_covariate_value_dist.csv"
covariateRefFileName	The full path (including file name) for the csv file with covariate reference data. e.g. "covariate_ref.csv" or "temporal_covariate_ref.csv"
analysisRefFileName	The full path (including file name) for the csv file with analysis reference data. e.g. "analysis_ref.csv" or "temporal_analysis_ref.csv"
timeDistributionFileName	The full path (including file name) for the csv file with time distribution data. e.g. "time_distribution.csv"
timeRefFileName	The full path (including file name) for the csv file with time reference data. e.g. "temporal_time_ref.csv"
cohortCounts	Output CohortDiagnostics::getCohortCounts
cutOff	Minimum value of the covariate value, below which data is censored.
minCellCount	(Optional). Default value = 5. The minimum cell count for fields contains person counts or fractions.

---

getCdmDataSourceInformation

*Returns information from CDM source table.*


---

**Description**

Returns CDM source name, description, release date, CDM release date, version and vocabulary version, where available.

**Usage**

```
getCdmDataSourceInformation(
  connectionDetails = NULL,
  connection = NULL,
  cdmDatabaseSchema
)
```

**Arguments**

connectionDetails	An object of type connectionDetails as created using the <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the <a href="#">connect</a> 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'.

**Value**

Returns a data frame from CDM Data source.

---

```
getCohortAsFeatureTemporalCharacterizationResults
```

*Returns cohort temporal feature characterization*

---

**Description**

Returns a list object with temporalCovariateValue, temporalCovariateRef, temporalAnalysisRef, temporalRef output of cohort as features.

**Usage**

```
getCohortAsFeatureTemporalCharacterizationResults(
  dataSource = .GlobalEnv,
  cohortIds = NULL,
  databaseIds = NULL,
  temporalTimeRef = getResultsTemporalTimeRef(dataSource = dataSource)
)
```

**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.



temporalTimeRef

A dataframe object with three columns timeId (integer), startDay (integer), endDay (integer)

## Value

Returns a list object with temporalCovariateValue, temporalCovariateRef, temporalAnalysisRef, temporalRef output of cohort as features.

---

getCohortCounts	<i>Count of unique subjects and records in 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 <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the <a href="#">connect</a> 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

---

```
getCohortOverlapData
```

*Returns data for use in cohort\_overlap*

---

### Description

Returns data for use in cohort\_overlap

### Usage

```
getCohortOverlapData(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 DataSources 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 data for use in cohort\_overlap

---

```
getCohortRelationshipCharacterizationResults
```

*Returns cohort as feature characterization*

---

### Description

Returns a list object with covariateValue, covariateRef, analysisRef output of cohort as features.

### Usage

```
getCohortRelationshipCharacterizationResults(
  dataSource = .GlobalEnv,
  cohortIds = NULL,
  databaseIds = NULL
)
```

**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 DataSources 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 covariateValue, covariateRef, analysisRef output of cohort as features. To avoid clash with covaraiteId and conceptId returned from Feature Extraction the output is a negative integer.

---

getFeatureExtractionCharacterization

*Returns cohort characterization output of feature extraction*

---

**Description**

Returns a list object with covariateValue, covariateValueDist, covariateRef, analysisRef output of feature extraction.

**Usage**

```
getFeatureExtractionCharacterization(
  dataSource = .GlobalEnv,
  cohortIds = NULL,
  databaseIds = NULL
)
```

**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 DataSources 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 covariateValue, covariateValueDist, covariateRef, analysisRef output of feature extraction along with concept information.

---

```
getFeatureExtractionTemporalCharacterization
```

*Returns temporal cohort characterization output of feature extraction*

---

**Description**

Returns a list object with temporalCovariateValue, temporalCovariateValueDist, temporalCovariateRef, temporalAnalysisRef, temporalRef output of feature extraction along with concept information.

**Usage**

```
getFeatureExtractionTemporalCharacterization(
  dataSource = .GlobalEnv,
  cohortIds = NULL,
  databaseIds = NULL
)
```

**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 DataSources 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 temporalCovariateValue, temporalCovariateValueDist, temporalCovariateRef, temporalAnalysisRef, temporalTimeRef, Concept output of feature extraction.

---

getMultipleCharacterizationResults

*Returns multiple characterization output*


---

### Description

Returns multiple characterization output

### Usage

```
getMultipleCharacterizationResults(
  dataSource = .GlobalEnv,
  cohortIds = NULL,
  databaseIds = NULL
)
```

### 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 DataSources 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 multiple characterization output

---

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

---

getResultsFromCalendarIncidence

*Returns data from calendar\_incidence table of Cohort Diagnostics results data model*


---

### Description

Returns data from calendar\_incidence table of Cohort Diagnostics results data model

### Usage

```
getResultsFromCalendarIncidence(
  dataSource,
  cohortIds = NULL,
  databaseIds = NULL
)
```

### 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.

---

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 = NULL, databaseIds = NULL)
```

**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 cohort counts table in Cohort Diagnostics results data model.

---

getResultsFromCohortRelationships

*Returns data from cohort\_relationships table of Cohort Diagnostics results data model*

---

**Description**

Returns data from cohort\_relationships table of Cohort Diagnostics results data model

**Usage**

```
getResultsFromCohortRelationships(
  dataSource,
  cohortIds = NULL,
  databaseIds = NULL
)
```

**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 cohort\_relationships table in Cohort Diagnostics results data model.

---

getResultsFromConcept	<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**

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

**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.



---

getResultsFromFixedTimeSeries

*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. The returned object is a tsibble, but to use in time series analysis, gaps need to be filled. Only absolute values are returned i.e. negative values are converted to positives.

### Usage

```
getResultsFromFixedTimeSeries(dataSource, cohortIds = NULL, databaseIds = NULL)
```

### 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 of tsibble (time series) objects with results that conform to time series table in Cohort Diagnostics results data model. There are three list objects, labelled m for monthly, q for quarterly and y for yearly. The periodBegin variable is in the format of tsibble::yearmonth for monthly, tsibble::yearquarter for quarter and integer for year.

---

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 = NULL, databaseIds = NULL)
```

**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 = NULL, databaseIds = NULL)
```

**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 = NULL,  
  databaseIds = NULL  
)
```

## 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 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 = NULL,
  databaseIds = NULL
)
```

**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 DataSources 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 = NULL, databaseIds = NULL)
```

**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 DataSources 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 = NULL,
  databaseIds = NULL
)
```

**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\_distribution 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 = NULL, databaseIds = NULL)
```

### 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 = NULL,
  cohortIds = NULL
)
```

**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 DataSources 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,
  cohortToCreateFile = "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 <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the <a href="#">connect</a> 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.
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 (i.e. webapi mode takes precedence).
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.
generateInclusionStats	Compute and store inclusion rule statistics?
inclusionStatisticsFolder	The folder where the inclusion rule statistics are stored. Can be left NULL if generateInclusionStats = FALSE.
createCohortTable	Create the cohort table? If incremental = TRUE and the table already exists this will be skipped.
incremental	Create only cohorts that haven't been created before?



`incrementalFolder`

If `incremental = TRUE`, 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, e.g. by hydrating a the `SkeletonCohortDiagnosticsStudy` package using `Hydra::hydrate` or inserting cohort specifications using `ROhdsiWebApi::insertCohortDefinitionSetInPackage`, or (2) [WebApi Mode] By using a WebApi interface to retrieve the cohort definitions. Note: WebApi mode takes precedence over package mode.

Structure of `cohortSetReference` or `cohortToCreateFile`

**cohortId** (required) The cohort Id in Atlas for the cohort you want to diagnose.

**cohortName** (optional) The full name of the cohort. This will be shown in the Shiny app. If not provided, the name used in Atlas will be displayed.

In addition - `cohortToCreateFile` is able to accept additional optional columns

**metaData** (optional) A JSON with metadata of the cohort that you would like to provided. Logic description may be a metadata object. Other types of metadata objects may include project code, author, version, key words etc.

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.

The `cohortSetReference` argument maybe a vector of atlas ids or it maybe a data frame object. If `cohortSetReference` is a data frame object:

**cohortId** (required) The cohort Id in Atlas for the cohort you want to diagnose.

**cohortName** (optional) The full name of the cohort. This will be shown in the Shiny app. If not provided, the cohort id will be displayed.

## 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 <a href="#">createConnectionDetails</a> 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 <a href="#">preMergeDiagnosticsFiles</a> 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 <a href="#">createConnectionDetails</a> function in the DatabaseConnector package, specifying how to connect to the server where the CohortDiagnostics results have been uploaded using the <a href="#">uploadResults</a> 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 <a href="#">runCohortDiagnostics</a> 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.

---

```
runCohortCharacterizationDiagnostics
```

*Get Feature Extraction output for set of cohorts*

---

**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`. Because of the large file size, the returned object is an `Andromeda::andromeda` class object. Use `CohortDiagnostics::exportFeatureExtractionOutput` to export the characterization results to csv.

**Usage**

```
runCohortCharacterizationDiagnostics(
  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 <code>connectionDetails</code> as created using the <a href="#">createConnectionDetails</a> function in the <code>DatabaseConnector</code> package. Can be left <code>NULL</code> if connection is provided.
connection	An object of type <code>connection</code> as created using the <a href="#">connect</a> 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.

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 large set of cohorts, this function allows you to batch them into chunks that run as a batch.

---

runCohortDiagnostics    *Run cohort diagnostics*

---

## Description

Runs cohort diagnostics on cohorts specified in cohortToCreateFile (file) or cohortSetReference. The function checks if the specified cohorts are instantiated, and only runs diagnostics on the instantiated cohorts (i.e. > 0 rows in cohort table).

Characterization: If runTemporalCohortCharacterization argument is TRUE, then RFeatureExtraction::createTemporalCohortCharacterization is used as default.

## 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,
runVisitContext = TRUE,
runBreakdownIndexEvents = TRUE,
runIncidenceRate = TRUE,
runCohortTimeSeries = TRUE,
runDataSourceTimeSeries = TRUE,
runCohortRelationship = TRUE,
runCohortCharacterization = TRUE,
covariateSettings = list(FeatureExtraction::createDefaultCovariateSettings(),
  FeatureExtraction::createCovariateSettings(useVisitCountLongTerm = TRUE,
    useVisitCountShortTerm = TRUE, useVisitConceptCountLongTerm = TRUE,
    useVisitConceptCountShortTerm = TRUE, useDemographicsPriorObservationTime = TRUE,
    useDemographicsPostObservationTime = TRUE, useDemographicsTimeInCohort = TRUE,
    useDemographicsIndexYearMonth = TRUE, )),
runTemporalCohortCharacterization = TRUE,

temporalCovariateSettings = FeatureExtraction::createTemporalCovariateSettings(useConditionOccurrence
= TRUE, useDrugEraStart = 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 (i.e. webapi mode takes precedence).
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 <a href="#">createConnectionDetails</a>

	function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the <a href="#">connect</a> 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?
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?

<code>runCohortTimeSeries</code>	Generate and export the cohort level time series?
<code>runDataSourceTimeSeries</code>	Generate and export the Data source level time series? i.e. using all persons found in observation period table.
<code>runCohortRelationship</code>	Do you want to compute temporal relationship between the cohorts being diagnosed. This diagnostics is needed for cohort as feature characterization.
<code>runCohortCharacterization</code>	Generate and export the cohort characterization? Only records with values greater than 0.0001 are returned.
<code>covariateSettings</code>	Either an object of type <code>covariateSettings</code> as created using one of the <code>createCovariateSettings</code> function in the <code>FeatureExtraction</code> package, or a list of such objects.
<code>runTemporalCohortCharacterization</code>	Generate and export the temporal cohort characterization? Only records with values greater than 0.001 are returned.
<code>temporalCovariateSettings</code>	Either an object of type <code>covariateSettings</code> as created using one of the <code>createTemporalCovariateSettings</code> function in the <code>FeatureExtraction</code> package, or a list of such objects.
<code>minCellCount</code>	The minimum cell count for fields contains person counts or fractions.
<code>incremental</code>	Create only cohort diagnostics that haven't been created before?
<code>incrementalFolder</code>	If <code>incremental = TRUE</code> , 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, e.g. by hydrating a the `SkeletonCohortDiagnosticsStudy` package using `Hydra::hydrate` or inserting cohort specifications using `ROhdsiWebApi::insertCohortDefinitionSetInPackage`, or (2) [WebApi Mode] By using a WebApi interface to retrieve the cohort definitions. Note: WebApi mode takes precedence over package mode.

Structure of `cohortSetReference` or `cohortToCreateFile`

**cohortId** (required) The cohort Id in Atlas for the cohort you want to diagnose.

**cohortName** (optional) The full name of the cohort. This will be shown in the Shiny app. If not provided, the name used in Atlas will be displayed.

In addition - `cohortToCreateFile` is able to accept additional optional columns

**metaData** (optional) A JSON with metadata of the cohort that you would like to provided. Logic description may be a metadata object. Other types of metadata objects may include project code, author, version, key words etc.

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.



The cohortSetReference argument maybe a vector of atlas ids or it maybe a data frame object. If cohortSetReference is a data frame object:

**cohortId** (required) The cohort Id in Atlas for the cohort you want to diagnose.

**cohortName** (optional) The full name of the cohort. This will be shown in the Shiny app. If not provided, the cohort id will be displayed.

---

runCohortRelationshipDiagnostics

*Given a set of cohorts get relationships between the cohorts.*

---

## Description

Given a set of cohorts, get temporal relationships between the cohort\_start\_date of the cohorts.

## Usage

```
runCohortRelationshipDiagnostics(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema,
  tempEmulationSchema = NULL,
  cohortTable = "cohort",
  targetCohortIds,
  comparatorCohortIds
)
```

## Arguments

- |                      |  |
|----------------------|--|
| connectionDetails    | An object of type connectionDetails as created using the <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.  |
| connection           | An object of type connection as created using the <a href="#">connect</a> 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'.   |
| 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.  |
| cohortTable          | Name of the cohort table.  |
| targetCohortIds      | A vector of one or more Cohort Ids for use as target cohorts.  |
| comparatorCohortIds  | A vector of one or more Cohort Ids for use as feature/comparator cohorts.  |

---

```
runCohortTimeSeriesDiagnostics
```

*Given a set of instantiated cohorts get time series for the cohorts.*

---

## Description

This function first generates a calendar period table, that has calendar intervals between the `timeSeriesMinDate` and `timeSeriesMaxDate`. Calendar Month, Quarter and year are supported. For each of the calendar interval, time series data are computed. The returned object is a R dataframe that will need to be converted to a time series object to perform time series analysis.

Data Source time series: computes time series at the data source level i.e. observation period table. This output is NOT limited to individuals in the cohort table but is for ALL people in the datasource (i.e. present in observation period table)

## Usage

```
runCohortTimeSeriesDiagnostics(
  connectionDetails = NULL,
  connection = NULL,
  tempEmulationSchema = NULL,
  cdmDatabaseSchema,
  cohortDatabaseSchema = cdmDatabaseSchema,
  cohortTable = "cohort",
  runCohortTimeSeries = TRUE,
  runDataSourceTimeSeries = TRUE,
  timeSeriesMinDate = as.Date("1980-01-01"),
  timeSeriesMaxDate = as.Date(Sys.Date()),
  cohortIds = NULL
)
```

## Arguments

- |                                   |  |
|-----------------------------------|--|
| <code>connectionDetails</code>    | An object of type <code>connectionDetails</code> as created using the <a href="#">createConnectionDetails</a> 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 <a href="#">connect</a> 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>tempEmulationSchema</code>  | 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.  |
| <code>cdmDatabaseSchema</code>    | 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 <code>'cdm_data.dbo'</code> .   |
| <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 <code>'scratch.dbo'</code> .   |

cohortTable	Name of the cohort table.
runCohortTimeSeries	Generate and export the cohort level time series?
runDataSourceTimeSeries	Generate and export the Data source level time series? i.e. using all persons found in observation period table.
timeSeriesMinDate	(optional) Minimum date for time series. Default value January 1st 1980.
timeSeriesMaxDate	(optional) Maximum date for time series. Default value System date.
cohortIds	A vector of one or more Cohort Ids to compute time distribution for.

---

runConceptSetDiagnostics

*Run concept set diagnostics*


---

## Description

Runs concept set diagnostics on a set of cohorts. For index event breakdown, the cohorts need to be instantiated.

## Usage

```
runConceptSetDiagnostics(
  connection = NULL,
  connectionDetails = NULL,
  tempEmulationSchema = NULL,
  cdmDatabaseSchema,
  vocabularyDatabaseSchema = cdmDatabaseSchema,
  cohorts,
  cohortIds = NULL,
  cohortDatabaseSchema = NULL,
  cohortTable = NULL,
  runIncludedSourceConcepts,
  runOrphanConcepts,
  runBreakdownIndexEvents
)
```

## Arguments

connection	An object of type connection as created using the <a href="#">connect</a> 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 <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.

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.
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'.
cohorts	A dataframe object with required fields cohortId, sql, json, cohortName
cohortIds	Optionally, provide a subset of cohort IDs to restrict the diagnostics to.
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.
runIncludedSourceConcepts	Generate and export the source concepts included in the cohorts?
runOrphanConcepts	Generate and export potential orphan concepts?
runBreakdownIndexEvents	Generate and export the breakdown of index events? This is executed on instantiated cohorts only.

---

runIncidenceRateDiagnostics

*Given a set of instantiated cohorts get Incidence Rate for the cohorts.*

---

## Description

This function computes incidence rate, one cohort at a time.

## Usage

```
runIncidenceRateDiagnostics(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema,
  cohortTable,
  cdmDatabaseSchema,
  vocabularyDatabaseSchema = cdmDatabaseSchema,
  cdmVersion = 5,
  tempEmulationSchema = tempEmulationSchema,
  firstOccurrenceOnly = TRUE,
  washoutPeriod = 365,
  cohortId
)
```

**Arguments**

connectionDetails	An object of type connectionDetails as created using the <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the <a href="#">connect</a> 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.
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'.
cdmVersion	Only CDM version 5 is supported.
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.
firstOccurrenceOnly	Compute for first occurrence of subject in the cohort.
washoutPeriod	(Optional) Washout period to use. The default value is either 365 days or minimum prior observation period requirement specified in cohort definition.
cohortId	A Cohort Id to compute time distribution for.

---

runVisitContextDiagnostics

*Given a set of instantiated cohorts get the visit context in relation to cohort start date.*

---

**Description**

This function returns the types of visits experienced by persons in the cohort in relation to cohort start date.

**Usage**

```
runVisitContextDiagnostics(
  connectionDetails = NULL,
  connection = NULL,
  cdmDatabaseSchema,
```

```

tempEmulationSchema = NULL,
cohortDatabaseSchema,
vocabularyDatabaseSchema,
cohortTable = "cohort",
cohortIds,
cdmVersion = 5
)

```

## Arguments

connectionDetails	An object of type connectionDetails as created using the <a href="#">createConnectionDetails</a> function in the DatabaseConnector package. Can be left NULL if connection is provided.
connection	An object of type connection as created using the <a href="#">connect</a> 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'.
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	A vector of one or more Cohort Ids to compute visit context for.
cdmVersion	The version of the OMOP CDM. Default 5. (Note: only 5 is supported.)

---

takepackageDependencySnapshot

*Take a snapshot of the R environment*

---

## Description

Take a snapshot of the R environment

## Usage

```
takepackageDependencySnapshot()
```

## Details

This function records all versions used in the R environment as used by `runCohortDiagnostics`. This function was borrowed from `OhdsiRTools`

## Value

A data frame listing all the dependencies of the root package and their version numbers, in the order in which they should be installed.

---

uploadResults	<i>Upload results to the database server.</i>
---------------	---

---

## 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 <code>connectionDetails</code> as created using the <code>createConnectionDetails</code> function in the <code>DatabaseConnector</code> package.
schema	The schema on the postgres server where the tables have been created.
zipFileName	The name of the zip file.
forceOverWriteOfSpecifications	If <code>TRUE</code> , 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 <code>TRUE</code> , before inserting data for a specific <code>databaseId</code> 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.

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