

# Package ‘CohortDiagnostics’

June 28, 2021

**Type** Package

**Title** Diagnostics for OHDSI Cohorts

**Version** 2.2.0

**Date** 2021-06-15

**Maintainer** Gowtham Rao <rao@ohdsi.org>

**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),  
tsibble

**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>

**RoxygenNote** 7.1.1

**Encoding** UTF-8

**Language** en-US

## R topics documented:

checkIfCohortInstantiated . . . . .	3
checkInputFileEncoding . . . . .	4
computeCohortOverlap . . . . .	4
computeCohortTemporalRelationship . . . . .	5
createDatabaseDataSource . . . . .	6
createFileDataSource . . . . .	7
createResultsDataModel . . . . .	7
getCdmDataSourceInformation . . . . .	8
getCohortAsFeatureCharacterizationResults . . . . .	8
getCohortAsFeatureTemporalCharacterizationResults . . . . .	9
getCohortCharacteristics . . . . .	10
getCohortCharacterizationResults . . . . .	11
getCohortCounts . . . . .	12
getMultipleCharacterizationResults . . . . .	12
getResultsDataModelSpecifications . . . . .	13
getResultsFromCalendarIncidence . . . . .	14
getResultsFromCohortCount . . . . .	14
getResultsFromCohortRelationships . . . . .	15
getResultsFromConcept . . . . .	16
getResultsFromIncidenceRate . . . . .	17
getResultsFromIncludedConcept . . . . .	17
getResultsFromInclusionRuleStatistics . . . . .	18
getResultsFromIndexEventBreakdown . . . . .	19
getResultsFromOrphanConcept . . . . .	20
getResultsFromTimeDistribution . . . . .	20
getResultsFromTimeSeries . . . . .	21
getResultsFromVisitContext . . . . .	22

<i>checkIfCohortInstantiated</i>	3
getResultsResolveMappedConceptSet . . . . .	22
getTemporalCohortCharacterizationResults . . . . .	23
instantiateCohortSet . . . . .	24
launchCohortExplorer . . . . .	26
launchDiagnosticsExplorer . . . . .	27
preMergeDiagnosticsFiles . . . . .	28
runCohortDiagnostics . . . . .	29
runConceptSetDiagnostics . . . . .	33
uploadResults . . . . .	35
<b>Index</b>	<b>36</b>

---

checkIfCohortInstantiated	<i>Checks if a set of cohortId(s) are instantiated in the cohort table</i>
---------------------------	--

---

## 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.

---

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


---

### Description

Given two sets of cohorts, get data on overlap between the cohorts. Note: only the first occurrence of subject\_id in the cohort is used.

### Usage

```
computeCohortOverlap(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema,
  cohortTable = "cohort",
  cohortIds,
  batchSize = 50
)
```

### 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	A vector of one or more Cohort Ids.
batchSize	Optional, default set to 50. If running diagnostics on large set of cohorts, this function allows you to batch them into chunks that by default run over 50 target cohorts (and all comparator cohorts).

---

computeCohortTemporalRelationship

*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

```
computeCohortTemporalRelationship(
  connectionDetails = NULL,
  connection = NULL,
  cohortDatabaseSchema,
  cohortTable = "cohort",
  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	A vector of one or more Cohort Ids.

---

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 <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.  |
| 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 [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.

`schema`    The schema on the postgres server where the tables will be created.

### Details

Only PostgreSQL servers are supported.

---

```
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 [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'.

### Value

Returns a data frame from CDM Data source.

---

```
getCohortAsFeatureCharacterizationResults
```

*Returns cohort as feature characterization*

---

### Description

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

### Usage

```
getCohortAsFeatureCharacterizationResults(  
  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 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 covariateValue, covariateRef, analysisRef output of cohort as features.

---

```
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
)
```

**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 temporalCovariateValue, temporalCovariateRef, temporalAnalysisRef, temporalRef output of cohort as features.

---

```
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 <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'.   |

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.

---

getCohortCharacterizationResults

*Returns cohort characterization output of feature extraction*


---

## Description

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

## Usage

```
getCohortCharacterizationResults(
  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.

---

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 <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

---

getMultipleCharacterizationResults	<i>Returns multiple characterization output</i>
------------------------------------	---

---

### 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 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 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 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 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.



---

`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**

- |                          |  |
|--------------------------|--|
| <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 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.

---

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. 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**

```
getResultsFromTimeSeries(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.

---

```
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 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 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 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.

---

```
getTemporalCohortCharacterizationResults
```

*Returns temporal cohort characterization output of feature extraction*

---

**Description**

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

**Usage**

```
getTemporalCohortCharacterizationResults(
  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, temporalRef output of feature extraction.

---

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. 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.
generateInclusionStats	Compute and store inclusion rule statistics?
inclusionStatisticsFolder	The folder where the inclusion rule statistics are stored. Can be left NULL if generateInclusionStats = FALSE.

<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 <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.

---

runCohortDiagnostics	<i>Run cohort diagnostics</i>
----------------------	-------------------------------

---

**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,
runCohortTemporalRelationship = 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 <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?
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.
runCohortTemporalRelationship	Do you want to compute temporal relationship between the cohorts being diagnosed. This diagnostics is needed for cohort as feature characterization.
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::insertCohortD` 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



---

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.
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.

## 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::insertCohortD` 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	<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 connectionDetails as created using the <a href="#">createConnectionDetails</a> 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](#)  
computeCohortTemporalRelationship, [5](#)  
connect, [3–8](#), [10](#), [12](#), [25](#), [30](#), [33](#)  
createConnectionDetails, [3–8](#), [10](#), [12](#), [25](#),  
[27](#), [28](#), [30](#), [33](#), [35](#)  
createDatabaseDataSource, [6](#)  
createFileDataSource, [7](#)  
createResultsDataModel, [7](#), [35](#)  
  
getCdmDataSourceInformation, [8](#)  
getCohortAsFeatureCharacterizationResults,  
[8](#)  
getCohortAsFeatureTemporalCharacterizationResults,  
[9](#)  
getCohortCharacteristics, [10](#)  
getCohortCharacterizationResults, [11](#)  
getCohortCounts, [12](#)  
getMultipleCharacterizationResults, [12](#)  
getResultsDataModelSpecifications, [13](#)  
getResultsFromCalendarIncidence, [14](#)  
getResultsFromCohortCount, [14](#)  
getResultsFromCohortRelationships, [15](#)  
getResultsFromConcept, [16](#)  
getResultsFromIncidenceRate, [17](#)  
getResultsFromIncludedConcept, [17](#)  
getResultsFromInclusionRuleStatistics,  
[18](#)  
getResultsFromIndexEventBreakdown, [19](#)  
getResultsFromOrphanConcept, [20](#)  
getResultsFromTimeDistribution, [20](#)  
getResultsFromTimeSeries, [21](#)  
getResultsFromVisitContext, [22](#)  
getResultsResolveMappedConceptSet, [22](#)  
getTemporalCohortCharacterizationResults,  
[23](#)  
  
instantiateCohortSet, [24](#)  
  
launchCohortExplorer, [26](#)  
launchDiagnosticsExplorer, [27](#)  
  
preMergeDiagnosticsFiles, [28](#), [28](#)  
  
runCohortDiagnostics, [29](#), [29](#)  
runConceptSetDiagnostics, [33](#)  
  
uploadResults, [28](#), [35](#)