

# Package ‘DataQualityDashboard’

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**Type** Package

**Title** Execute and View Data Quality Checks on OMOP CDM Database

**Version** 2.5.0

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**Description** An R package for assessing data quality in standardized OMOP Common Data Model data sources.

**License** Apache License (>= 2)

**Config/build/clean-inst-doc** FALSE

**VignetteBuilder** knitr

**Config/testthat/edition** 3

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

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

**Depends** R (>= 3.2.2),  
DatabaseConnector (>= 2.0.2)

**Imports** magrittr,  
ParallelLogger,  
dplyr,  
jsonlite,  
rJava,  
SqlRender (>= 1.10.1),  
plyr,  
stringr,  
rlang,  
tidyselect,  
readr

**Suggests** testthat,  
knitr,  
rmarkdown,  
markdown,  
shiny,  
ggplot2,  
Eunomia,  
R.utils

**Remotes** ohdsi/Eunomia

**RoxygenNote** 7.2.2  
**Encoding** UTF-8

**R topics documented:**

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convertJsonResultsFileCase
<i>Convert JSON results file case</i>

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**Description**

Convert a DQD JSON results file between camelcase and (all-caps) snakecase. Enables viewing of pre-v.2.1.0 results files in later DQD versions, and vice versa

**Usage**

```
convertJsonResultsFileCase(  
  jsonFilePath,  
  writeToFile,  
  outputFolder = NA,  
  outputFile = "",  
  targetCase  
)
```

**Arguments**

jsonFilePath	Path to the JSON results file to be converted
writeToFile	Whether or not to write the converted results back to a file (must be either TRUE or FALSE)
outputFolder	The folder to output the converted JSON results file to
outputFile	(OPTIONAL) File to write converted results JSON object to. Default is name of input file with a "_camel" or "_snake" postfix
targetCase	Case into which the results file parameters should be converted (must be either "camel" or "snake")

**Value**

DQD results object (a named list)

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executeDqChecks	<i>Execute DQ checks</i>
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## Description

This function will connect to the database, generate the sql scripts, and run the data quality checks against the database. By default, results will be written to a json file as well as a database table.

## Usage

```
executeDqChecks(
  connectionDetails,
  cdmDatabaseSchema,
  resultsDatabaseSchema,
  vocabDatabaseSchema = cdmDatabaseSchema,
  cdmSourceName,
  numThreads = 1,
  sqlOnly = FALSE,
  sqlOnlyUnionCount = 1,
  sqlOnlyIncrementalInsert = FALSE,
  outputFolder,
  outputFile = "",
  verboseMode = FALSE,
  writeToTable = TRUE,
  writeTableName = "dqdashboard_results",
  writeToCsv = FALSE,
  csvFile = "",
  checkLevels = c("TABLE", "FIELD", "CONCEPT"),
  checkNames = c(),
  cohortDefinitionId = c(),
  cohortDatabaseSchema = resultsDatabaseSchema,
  cohortTableName = "cohort",
  tablesToExclude = c("CONCEPT", "VOCABULARY", "CONCEPT_ANCESTOR",
    "CONCEPT_RELATIONSHIP", "CONCEPT_CLASS", "CONCEPT_SYNONYM", "RELATIONSHIP", "DOMAIN"),
  cdmVersion = "5.3",
  tableCheckThresholdLoc = "default",
  fieldCheckThresholdLoc = "default",
  conceptCheckThresholdLoc = "default"
)
```

## Arguments

connectionDetails	A connectionDetails object for connecting to the CDM database
cdmDatabaseSchema	The fully qualified database name of the CDM schema
resultsDatabaseSchema	The fully qualified database name of the results schema
vocabDatabaseSchema	The fully qualified database name of the vocabulary schema (default is to set it as the cdmDatabaseSchema)

cdmSourceName	The name of the CDM data source
numThreads	The number of concurrent threads to use to execute the queries
sqlOnly	Should the SQLs be executed (FALSE) or just returned (TRUE)?
sqlOnlyUnionCount	(OPTIONAL) In sqlOnlyIncrementalInsert mode, how many SQL commands to union in each query to insert check results into results table (can speed processing when queries done in parallel). Default is 1.
sqlOnlyIncrementalInsert	(OPTIONAL) In sqlOnly mode, boolean to determine whether to generate SQL queries that insert check results and associated metadata into results table. Default is FALSE (for backwards compatibility to <= v2.2.0)
outputFolder	The folder to output logs, SQL files, and JSON results file to
outputFile	(OPTIONAL) File to write results JSON object
verboseMode	Boolean to determine if the console will show all execution steps. Default is FALSE
writeToTable	Boolean to indicate if the check results will be written to the dqdashboard_results table in the resultsDatabaseSchema. Default is TRUE
writeTableName	The name of the results table. Defaults to 'dqdashboard_results'. Used when sqlOnly or writeToTable is True.
writeToCsv	Boolean to indicate if the check results will be written to a csv file. Default is FALSE
csvFile	(OPTIONAL) CSV file to write results
checkLevels	Choose which DQ check levels to execute. Default is all 3 (TABLE, FIELD, CONCEPT)
checkNames	(OPTIONAL) Choose which check names to execute. Names can be found in inst/csv/OMOP_CDM_v[cdmVersion]_Check_Descriptions.csv. Note that "cdmTable", "cdmField" and "measureValueCompleteness" are always executed.
cohortDefinitionId	The cohort definition id for the cohort you wish to run the DQD on. The package assumes a standard OHDSI cohort table with the fields cohort_definition_id and subject_id.
cohortDatabaseSchema	The schema where the cohort table is located.
cohortTableName	The name of the cohort table. Defaults to 'cohort'.
tablesToExclude	(OPTIONAL) Choose which CDM tables to exclude from the execution.
cdmVersion	The CDM version to target for the data source. Options are "5.2", "5.3", or "5.4". By default, "5.3" is used.
tableCheckThresholdLoc	The location of the threshold file for evaluating the table checks. If not specified the default thresholds will be applied.
fieldCheckThresholdLoc	The location of the threshold file for evaluating the field checks. If not specified the default thresholds will be applied.
conceptCheckThresholdLoc	The location of the threshold file for evaluating the concept checks. If not specified the default thresholds will be applied.

**Value**

If sqlOnly = FALSE, a list object of results

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listDqChecks	<i>List DQ checks</i>
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**Description**

Details on all checks defined by the DataQualityDashboard Package.

**Usage**

```
listDqChecks(
  cdmVersion = "5.3",
  tableCheckThresholdLoc = "default",
  fieldCheckThresholdLoc = "default",
  conceptCheckThresholdLoc = "default"
)
```

**Arguments**

cdmVersion	The CDM version to target for the data source. By default, 5.3 is used.
tableCheckThresholdLoc	The location of the threshold file for evaluating the table checks. If not specified the default thresholds will be applied.
fieldCheckThresholdLoc	The location of the threshold file for evaluating the field checks. If not specified the default thresholds will be applied.
conceptCheckThresholdLoc	The location of the threshold file for evaluating the concept checks. If not specified the default thresholds will be applied.

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reEvaluateThresholds	<i>Re-evaluate Thresholds</i>
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**Description**

Re-evaluate an existing DQD result against an updated thresholds file.

**Usage**

```
reEvaluateThresholds(
  jsonFilePath,
  outputFolder,
  outputFile,
  tableCheckThresholdLoc = "default",
  fieldCheckThresholdLoc = "default",
  conceptCheckThresholdLoc = "default",
  cdmVersion = "5.3"
)
```

**Arguments**

jsonFilePath	Path to the JSON results file generated using the execute function
outputFolder	The folder to output new JSON result file to
outputFile	File to write results JSON object to
tableCheckThresholdLoc	The location of the threshold file for evaluating the table checks. If not specified the default thresholds will be applied.
fieldCheckThresholdLoc	The location of the threshold file for evaluating the field checks. If not specified the default thresholds will be applied.
conceptCheckThresholdLoc	The location of the threshold file for evaluating the concept checks. If not specified the default thresholds will be applied.
cdmVersion	The CDM version to target for the data source. By default, 5.3 is used.

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viewDqDashboard	<i>View DQ Dashboard</i>
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**Description**

View DQ Dashboard

**Usage**

```
viewDqDashboard(jsonPath, launch.browser = NULL, display.mode = NULL, ...)
```

**Arguments**

jsonPath	The path to the JSON file produced by <a href="#">executeDqChecks</a>
launch.browser	Passed on to shiny::runApp
display.mode	Passed on to shiny::runApp
...	Extra parameters for shiny::runApp() like "port" or "host"

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writeDBResultsToJson	<i>Write DQD results database table to json</i>
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**Description**

Write DQD results database table to json

**Usage**

```
writeDBResultsToJson(
  connection,
  resultsDatabaseSchema,
  cdmDatabaseSchema,
  writeTableName,
  outputFolder,
  outputFile
)
```

**Arguments**

connection	A connection object
resultsDatabaseSchema	The fully qualified database name of the results schema
cdmDatabaseSchema	The fully qualified database name of the CDM schema
writeTableName	Name of DQD results table in the database to read from
outputFolder	The folder to output the json results file to
outputFile	The output filename of the json results file

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writeJsonResultsToCsv    *Write JSON Results to CSV file*

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**Description**

Write JSON Results to CSV file

**Usage**

```
writeJsonResultsToCsv(
  jsonPath,
  csvPath,
  columns = c("checkId", "failed", "passed", "isError", "notApplicable", "checkName",
    "checkDescription", "thresholdValue", "notesValue", "checkLevel", "category",
    "subcategory", "context", "checkLevel", "cdmTableName", "cdmFieldName", "conceptId",
    "unitConceptId", "numViolatedRows", "pctViolatedRows", "numDenominatorRows",
    "executionTime", "notApplicableReason", "error", "queryText"),
  delimiter = ",",
)
```

**Arguments**

jsonPath	Path to the JSON results file generated using the execute function
csvPath	Path to the CSV output file
columns	(OPTIONAL) List of desired columns
delimiter	(OPTIONAL) CSV delimiter

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`writeJsonResultsToTable`*Write JSON Results to SQL Table*

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**Description**

Write JSON Results to SQL Table

**Usage**

```
writeJsonResultsToTable(  
  connectionDetails,  
  resultsDatabaseSchema,  
  jsonFilePath,  
  writeTableName = "dqdashboard_results",  
  cohortDefinitionId = c()  
)
```

**Arguments**

`connectionDetails`

A connectionDetails object for connecting to the CDM database

`resultsDatabaseSchema`

The fully qualified database name of the results schema

`jsonFilePath`

Path to the JSON results file generated using the execute function

`writeTableName`

Name of table in the database to write results to

`cohortDefinitionId`

If writing results for a single cohort this is the ID that will be appended to the table name