

# Running cohort diagnostics

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## 1 Configuring the connection to the server

We need to tell R how to connect to the server where the data are. `CohortDiagnostics` uses the `DatabaseConnector` package, which provides the `createConnectionDetails` function. Type `?createConnectionDetails` for the specific settings required for the various database management systems (DBMS). For example, one might connect to a PostgreSQL database using this code:

```
connectionDetails <- createConnectionDetails(dbms = "postgresql",
                                             server = "localhost/ohdsi",
                                             user = "joe",
                                             password = "supersecret")

cdmDatabaseSchema <- "my_cdm_data"
tempEmulationSchema <- NULL
cohortDatabaseSchema <- "my_schema"
cohortTable <- "my_cohort_table"
```

The last four lines define the `cdmDatabaseSchema`, `tempEmulationSchema`, `cohortDatabaseSchema`, and `cohortTable` variables. We'll use the `cdmDatabaseSchema` later to tell R where the data in CDM format live. The `tempEmulationSchema` is needed only for Oracle users, since Oracle does not support temporary tables. The `cohortDatabaseSchema`, and `cohortTable` specify where we want to instantiate our cohorts. Note that for Microsoft SQL Server, databaseschemas need to specify both the database and the schema, so for example `cdmDatabaseSchema <- "my_cdm_data.dbo"`.

### 1.1 Creating a new cohort table

In order to run most of the cohort diagnostics, we need to instantiate the cohorts. The best way is to instantiate the cohorts in a new cohort table. We can use the `createCohortTable` to create an empty cohort table:

```
createCohortTable(connectionDetails = connectionDetails,  
                  cohortDatabaseSchema = cohortDatabaseSchema,  
                  cohortTable = cohortTable)
```

Note this this function will **delete the table if it already exists** before creating it.

## 1.2 Inclusion rules

We have the option to also generate inclusion rule statistics while the cohorts are instantiated (recommended). If we want to do this, we need to provide a folder where the inclusion rule statistics will be stored for later use.

## 2 Cohort Diagnostics Output

Once diagnostics is completed, a zip file will have been created in the specified export folder. This zip file can be shared between sites, as it does not contain patient-identifiable information. When unzipped, the zip file will contain several .csv files that maybe easily audited. Note that cell counts smaller than 5 have been removed, as specified using the `minCellCount` argument, to ensure non-identifiability.

### 2.1 Creating a pre merged file

Assuming you completed the steps described above for one or more databases, you should now have a set of zip files, one per database. Make sure to place all zip files in a single folder, for example `c:/temp/allZipFiles`.

Optionally, we can pre-merge the zip files, so we can view results in the Shiny app:

```
preMergeDiagnosticsFiles("C:/temp/allZipFiles")
```