

Package ‘KeppraAngioedema’

May 13, 2016

Title Keppra and the Risk of Angioedema

Version 0.1.1

Author Martijn Schuemie [aut, cre],
Patrick Ryan [aut],
Jon Duke [aut],
Marc Suchard [aut]

Maintainer Martijn J. Schuemie <schuemie@ohdsi.org>

Description This study aims to evaluate angioedema risk in seizure disorder patients exposed to Keppra (levetiracetam) compared with those exposed to phenytoin sodium. A potential link between levetiracetam and angioedema has been recently raised by the Food and Drug Administration in their review of spontaneous reporting data. In this study, we will analyze data from a distributed network using the OHDSI CohortMethod package.

Depends R (>= 3.2.2),
DatabaseConnector (>= 1.4.0)

Imports SqlRender (>= 1.1.3),
FeatureExtraction (>= 1.0.0),
CohortMethod (>= 2.0.2),
EmpiricalCalibration,
OhdsiSharing (>= 0.1.0),
OhdsiRTools,
RJDBC,
Cyclops

License Apache License 2.0

LazyData true

RoxygenNote 5.0.1

R topics documented:

createAnalysesDetails	2
createCohorts	2
createMetaData	3
createTableAndFigures	4
execute	4
KeppraAngioedema	5
packageResults	6
submitResults	6

Index[7](#)

createAnalysesDetails	<i>Create the analyses details</i>
-----------------------	------------------------------------

Description

Create the analyses details

Usage

```
createAnalysesDetails(outputFolder)
```

Arguments

outputFolder	Name of local folder to place results; make sure to use forward slashes (/)
--------------	---

Details

This function creates files specifying the analyses that will be performed.

createCohorts	<i>Create the exposure and outcome cohorts</i>
---------------	--

Description

Create the exposure and outcome cohorts

Usage

```
createCohorts(connectionDetails, cdmDatabaseSchema, workDatabaseSchema,
  studyCohortTable = "ohdsi_keppra_angioedema", oracleTempSchema,
  cdmVersion = 5, outputFolder)
```

Arguments

connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package.
cdmDatabaseSchema	Schema name where your patient-level data in OMOP CDM format resides. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
workDatabaseSchema	Schema name where intermediate data can be stored. You will need to have write privileges in this schema. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
studyCohortTable	The name of the table that will be created in the work database schema. This table will hold the exposure and outcome cohorts used in this study.

oracleTempSchema	Should be used in Oracle to specify a schema where the user has write privileges for storing temporary tables.
cdmVersion	Version of the CDM. Can be "4" or "5"
outputFolder	Name of local folder to place results; make sure to use forward slashes (/).

Details

This function will create the exposure and outcome cohorts following the definitions included in this package.

createMetaData	<i>Create metadata file</i>
----------------	-----------------------------

Description

Create metadata file

Usage

```
createMetaData(connectionDetails, cdmDatabaseSchema, exportFolder)
```

Arguments

connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package.
cdmDatabaseSchema	Schema name where your patient-level data in OMOP CDM format resides. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
exportFolder	The name of the folder where the metadata file should be created.

Details

Creates a file containing metadata about the source data (taken from the cdm_source table) and R package versions.

createTableAndFigures	<i>Create tables and figures</i>
-----------------------	----------------------------------

Description

Create tables and figures

Usage

```
createTableAndFigures(exportFolder)
```

Arguments

exportFolder The path to the export folder containing the results.

Details

Creates tables and figures for viewing and interpreting the results. Requires that the [execute](#) function has completed first.

execute	<i>Execute OHDSI Keppra and the Risk of Angioedema study</i>
---------	--

Description

Execute OHDSI Keppra and the Risk of Angioedema study

Usage

```
execute(connectionDetails, cdmDatabaseSchema,
        workDatabaseSchema = cdmDatabaseSchema,
        studyCohortTable = "ohdsi_keppra_angioedema",
        oracleTempSchema = workDatabaseSchema, cdmVersion = 5, outputFolder,
        createCohorts = TRUE, runAnalyses = TRUE, packageResults = TRUE,
        maxCores = 4)
```

Arguments

connectionDetails An object of type connectionDetails as created using the [createConnectionDetails](#) function in the DatabaseConnector package.

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

workDatabaseSchema Schema name where intermediate data can be stored. You will need to have write privileges in this schema. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.

studyCohortTable	The name of the table that will be created in the work database schema. This table will hold the exposure and outcome cohorts used in this study.
oracleTempSchema	Should be used in Oracle to specify a schema where the user has write privileges for storing temporary tables.
cdmVersion	Version of the CDM. Can be "4" or "5"
outputFolder	Name of local folder to place results; make sure to use forward slashes (/). Do not use a folder on a network drive since this greatly impacts performance.
createCohorts	Create the studyCohortTable table with the exposure and outcome cohorts?
runAnalyses	Perform the cohort method analyses?
packageResults	Package the results for sharing?
maxCores	How many parallel cores should be used? If more cores are made available this can speed up the analyses.

Details

This function executes the OHDSI Keppra and the Risk of Angioedema study.

Examples

```
## Not run:
connectionDetails <- createConnectionDetails(dbms = "postgresql",
                                             user = "joe",
                                             password = "secret",
                                             server = "myserver")

execute(connectionDetails,
        cdmDatabaseSchema = "cdm_data",
        workDatabaseSchema = "results",
        studyCohortTable = "ohdsi_keppra_angioedema",
        oracleTempSchema = NULL,
        outputFolder = "c:/temp/study_results",
        maxCores = 4)

## End(Not run)
```

KeppraAngioedema

CohortMethod

Description

CohortMethod

packageResults	<i>Package the results for sharing with OHDSI researchers</i>
----------------	---

Description

Package the results for sharing with OHDSI researchers

Usage

```
packageResults(connectionDetails, cdmDatabaseSchema, outputFolder)
```

Arguments

connectionDetails	An object of type connectionDetails as created using the createConnectionDetails function in the DatabaseConnector package.
cdmDatabaseSchema	Schema name where your patient-level data in OMOP CDM format resides. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.
outputFolder	Name of local folder to place results; make sure to use forward slashes (/)

Details

This function packages the results.

submitResults	<i>Submit the study results to the study coordinating center</i>
---------------	--

Description

Submit the study results to the study coordinating center

Usage

```
submitResults(exportFolder, key, secret)
```

Arguments

exportFolder	The path to the folder containing the StudyResults.zip file.
key	The key string as provided by the study coordinator
secret	The secret string as provided by the study coordinator

Details

This will upload the file StudyResults.zip to the study coordinating center using Amazon S3. This requires an active internet connection.

Value

TRUE if the upload was successful.

Index

`createAnalysesDetails`, [2](#)
`createCohorts`, [2](#)
`createConnectionDetails`, [2–4](#), [6](#)
`createMetaData`, [3](#)
`createTableAndFigures`, [4](#)

`execute`, [4](#), [4](#)

`KepraAngioedema`, [5](#)
`KepraAngioedema-package`
 (`KepraAngioedema`), [5](#)

`packageResults`, [6](#)

`submitResults`, [6](#)