

# Package ‘KeppraAngioedema’

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**Title** Keppra and the Risk of Angioedema

**Version** 0.0.1

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**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),  
RJDBC,  
Cyclops

**License** Apache License 2.0

**LazyData** true

**RoxygenNote** 5.0.1

## R topics documented:

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|                 |   |
|-----------------|---|
| addOutcomeNames | <i>Add names to a data frame with outcome IDs</i> |
|-----------------|---|

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**Description**

Add names to a data frame with outcome IDs

**Usage**

```
addOutcomeNames(data, outcomeIdColumnName = "outcomeId")
```

**Arguments**

|                     |  |
|---------------------|--|
| data                | The data frame to add the outcome names to                           |
| outcomeIdColumnName | The name of the column in the data frame that holds the outcome IDs. |

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

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**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.

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|               |  |
|---------------|--|
| createCohorts | <i>Create the exposure and outcome cohorts</i> |
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## 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 <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'.                                     |
| 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.

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|                |                      |
|----------------|----------------------|
| createMetaData | Create metadata file |
|----------------|----------------------|

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**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.

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|                       |                           |
|-----------------------|---------------------------|
| createTableAndFigures | Create tables and figures |
|-----------------------|---------------------------|

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**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

*Execute OHDSI Keppra and the Risk of Angioedema study***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)
```

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|                  |                     |
|------------------|---------------------|
| KeppraAngioedema | <i>CohortMethod</i> |
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Description

CohortMethod

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

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

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**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.

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