

# Package ‘AlendronateVsRaloxifene’

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**Type** Package

**Title** A Package for Comparative Effectiveness Study of Alendronate versus Raloxifene

**Version** 2.0.0

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**Description** updated from previous version (0.3.2)

**Depends** DatabaseConnector

**Imports** SqlRender,  
EmpiricalCalibration,  
Cyclops,  
FeatureExtraction,  
CohortMethod,  
ggplot2,  
ff,  
ffbase,  
MethodEvaluation,  
EvidenceSynthesis,  
OhdsiSharing,  
zip,  
OhdsiRTools (>= 1.5.0)

**Suggests** knitr,  
rmarkdown,  
DT,  
shiny

**License** Apache License 2.0

**VignetteBuilder** knitr

**LazyData** TRUE

**RoxygenNote** 6.0.1.9000

## R topics documented:

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

---

## Description

Create the exposure and outcome cohorts

## Usage

```
createCohorts(connectionDetails, cdmDatabaseSchema, cohortDatabaseSchema,
               cohortTable = "cohort", oracleTempSchema, 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'.                                     |
| cohortDatabaseSchema | 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'. |
| cohortTable          | 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.   |
| 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.

---

`createFiguresAndTables`*Generate diagnostics*

---

**Description**

Generate diagnostics

**Usage**

```
createFiguresAndTables(outputFolder, connectionDetails, cohortDatabaseSchema,  
    cohortTable, oracleTempSchema = oracleTempSchema)
```

**Arguments**

- |                                   |  |
|-----------------------------------|--|
| <code>outputFolder</code>         | Name of local folder where the results were generated; make sure to use forward slashes (/). Do not use a folder on a network drive since this greatly impacts performance.  |
| <code>connectionDetails</code>    | An object of type <code>connectionDetails</code> as created using the <a href="#">createConnectionDetails</a> function in the <code>DatabaseConnector</code> package.  |
| <code>cohortDatabaseSchema</code> | 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'. |
| <code>cohortTable</code>          | 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.  |
| <code>oracleTempSchema</code>     | Should be used in Oracle to specify a schema where the user has write privileges for storing temporary tables.   |

**Details**

This function generates figures and tables.

---

`createMetaData`*Create metadata file*

---

**Description**

Create metadata file

**Usage**

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

## 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'. |
| 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.

---

|         |                          |
|---------|--------------------------|
| execute | <i>Execute the Study</i> |
|---------|--------------------------|

---

## Description

Execute the Study

## Usage

```
execute(connectionDetails, cdmDatabaseSchema,
  cohortDatabaseSchema = cdmDatabaseSchema, cohortTable = "cohort",
  oracleTempSchema = cohortDatabaseSchema, outputFolder,
  createCohorts = TRUE, synthesizePositiveControls = TRUE,
  runAnalyses = TRUE, runDiagnostics = TRUE, packageResults = TRUE,
  maxCores = 4, minCellCount = 5)
```

## 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 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'. |
| cohortTable          | 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.   |

|                            |   |
|----------------------------|---|
| 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 cohortTable table with the exposure and outcome cohorts?   |
| synthesizePositiveControls | Should positive controls be synthesized?  |
| runAnalyses                | Perform the cohort method analyses?   |
| runDiagnostics             | Compute study diagnostics?  |
| packageResults             | Should results be packaged for later sharing?   |
| maxCores                   | How many parallel cores should be used? If more cores are made available this can speed up the analyses.  |
| minCellCount               | The minimum number of subjects contributing to a count before it can be included in packaged results.   |

## Details

This function executes the SkeletonCompativeEffectStudy Study.

The createCohorts, synthesizePositiveControls, runAnalyses, and runDiagnostics arguments are intended to be used to run parts of the full study at a time, but none of the parts are considered to be optional.

## Examples

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

execute(connectionDetails,
        cdmDatabaseSchema = "cdm_data",
        cohortDatabaseSchema = "study_results",
        cohortTable = "cohort",
        oracleTempSchema = NULL,
        outputFolder = "c:/temp/study_results",
        maxCores = 4)

## End(Not run)
```

---

|                     |                             |
|---------------------|-----------------------------|
| generateDiagnostics | <i>Generate diagnostics</i> |
|---------------------|-----------------------------|

---

## Description

Generate diagnostics

## Usage

```
generateDiagnostics(outputFolder)
```

**Arguments**

`outputFolder` Name of local folder where the results were generated; make sure to use forward slashes (/). Do not use a folder on a network drive since this greatly impacts performance.

**Details**

This function generates analyses diagnostics. Requires the study to be executed first.

---

`launchEvidenceExplorer`

*Launch the SqlRender Developer Shiny app*

---

**Description**

Launch the SqlRender Developer Shiny app

**Usage**

```
launchEvidenceExplorer(studyFolder, blind = TRUE, launch.browser = TRUE)
```

**Arguments**

`studyFolder` The root folder containing the study results. The app expects each database to have a subfolder in this folder, containing the packaged results.

`blind` Should the user be blinded to the main results?

`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 evidence

---

`packageResults`

*Package the results for sharing with OHDSI researchers*

---

**Description**

Package the results for sharing with OHDSI researchers

**Usage**

```
packageResults(connectionDetails, cdmDatabaseSchema, outputFolder,
  minCellCount = 5)
```

**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'. |
| outputFolder      | Name of local folder to place results; make sure to use forward slashes (/)  |
| minCellCount      | The minimum number of subjects contributing to a count before it can be included in the results.   |

**Details**

This function packages the results.

---

```
prepareForEvidenceExplorer
```

*Prepare results for the Evidence Explorer Shiny app.*

---

**Description**

Prepare results for the Evidence Explorer Shiny app.

**Usage**

```
prepareForEvidenceExplorer(studyFolder)
```

**Arguments**

|             |  |
|-------------|--|
| studyFolder | The root folder containing the study results. The app expects each database to have a subfolder in this folder, containing the packaged results. |
|-------------|--|

---

```
SkeletonCompativeEffectStudy
```

*SkeletonCompativeEffectStudy*

---

**Description**

```
SkeletonCompativeEffectStudy
```

---

|               |  |
|---------------|--|
| 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(outputFolder, key, secret)
```

### Arguments

|              |   |
|--------------|---|
| outputFolder | Name of local folder where the results were generated; make sure to use forward slashes (/). Do not use a folder on a network drive since this greatly impacts performance. |
| 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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|                            |                                     |
|----------------------------|-------------------------------------|
| synthesizePositiveControls | <i>Synthesize positive controls</i> |
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---

### Description

Synthesize positive controls

### Usage

```
synthesizePositiveControls(connectionDetails, cdmDatabaseSchema,
  cohortDatabaseSchema, cohortTable = "cohort", oracleTempSchema,
  outputFolder, maxCores = 1)
```



## Arguments

|                                   |  |
|-----------------------------------|--|
| <code>connectionDetails</code>    | An object of type <code>connectionDetails</code> as created using the <a href="#">createConnectionDetails</a> function in the <code>DatabaseConnector</code> package.  |
| <code>cdmDatabaseSchema</code>    | 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 <code>'cdm_data.dbo'</code> .                                     |
| <code>cohortDatabaseSchema</code> | 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 <code>'cdm_data.dbo'</code> . |
| <code>cohortTable</code>          | 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.  |
| <code>oracleTempSchema</code>     | Should be used in Oracle to specify a schema where the user has write privileges for storing temporary tables.   |
| <code>outputFolder</code>         | Name of local folder to place results; make sure to use forward slashes (/)  |
| <code>maxCores</code>             | How many parallel cores should be used? If more cores are made available this can speed up the analyses.   |

## Details

This function will synthesize positive controls based on the negative controls. The simulated outcomes will be added to the cohort table.

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