Package 'Covid19Il6JakInhibitorsSccs'

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Type Package

Title Self-Controlled Case Series Analysis of the Safety of IL-6 and JAK Inhibitors

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Description

IL-6 and JAK inhibitors are being considered for use in treatment and prophylaxis of COVID-19 in rapid clinical trials across the world. However, the full safety profiles of these drugs is unknown, and the current trials are unlikely to be powered or have sufficient follow-up time to evaluate most safety outcomes. The aim of this OHDSI study is to use existing retrospective data to evaluate the safety of IL-6 and JAK inhibitors, using the self-controlled case series (SCCS) design.

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Depends DatabaseConnector

Imports SqlRender,
SelfControlledCaseSeries (>= 1.4.2),
ParallelLogger,
Cyclops,
FeatureExtraction,
EmpiricalCalibration (>= 2.0.2),
OhdsiSharing (>= 0.2.1),
ff,
ffbase,
plyr,
dplyr,
tibble,
readr

Suggests VennDiagram,
shiny,
DT

Remotes ohdsi/SelfControlledCaseSeries,
ohdsi/FeatureExtraction,
ohdsi/OhdsiSharing

NeedsCompilation no

RoxygenNote 7.1.0

Encoding UTF-8

R topics documented:

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createCohorts   *Create the exposure and outcome cohorts*

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 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'.

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.

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deleteHoiFiles	*Delete health outcomes of interest result files*

Description

Delete health outcomes of interest result files

Usage

```
deleteHoiFiles(outputFolder)
```

Arguments

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.

---

execute	*Execute the Study*

Description

Execute the Study

Usage

```
execute(
  connectionDetails,
  cdmDatabaseSchema,
  cohortDatabaseSchema = cdmDatabaseSchema,
  cohortTable = "cohort",
  oracleTempSchema = cohortDatabaseSchema,
  outputFolder,
  databaseId,
  databaseName = databaseId,
  databaseDescription = databaseId,
  minCellCount = 5,
  createCohorts = TRUE,
  runSccs = TRUE,
  createCharacterization = TRUE,
  runSccsDiagnostics = TRUE,
  exportResults = 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'.

cohortDatabaseSchema
> Schema name where intermediate data can be stored. You will need to have
> write priviliges 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.

databaseId
> A short unique identifier for the database. Will be used to generate file names.

databaseName
> The full name of the database (e.g. 'Medicare Claims Synthetic Public Use Files
> (SynPUFs)').

databaseDescription
> A short description (several sentences) of the database.

minCellCount
> The minimum cell count for fields contains person counts or fractions when
> exporting to CSV.

createCohorts
> Create the cohortTable table with the exposure and outcome cohorts?

runSccs
> Perform the SCCS analyses? Requires the cohorts have been created.

createCharacterization
> Generate the cohort characterizations?

runSccsDiagnostics
> Generate local SCCS diagnostics?

exportResults
> Export the results to CSV?

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 Covid19Il6JakInhibitorsSccs 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.

exportResults *Export all results to tables*

Description

Outputs all results to a folder called 'export', and zips them.

Usage

```
exportResults(
  outputFolder,
  databaseId,
  databaseName,
  databaseDescription,
  minCellCount = 5,
  exposureOfInterestLabel = "Exposure of interest",
  maxCores
)
```

Arguments

`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.
`databaseId`	A short string for identifying the database (e.g. 'Synpuf').
`databaseName`	The full name of the database.
`databaseDescription`	
	A short description (several sentences) of the database.
`minCellCount`	The minimum cell count for fields contains person counts or fractions.
`exposureOfInterestLabel`	
	The label used for the covariates that identify the exposure of interest, the
`maxCores`	How many parallel cores should be used? If more cores are made available this can speed up the analyses.

launchEvidenceExplorer
Launch the Evidence Explorer Shiny app

Description

Launch the Evidence Explorer Shiny app

Usage

```
launchEvidenceExplorer(dataFolder, blind = TRUE, launch.browser = FALSE)
```

Arguments

`dataFolder`	The folder where the Shiny data are stored. Use the [prepareForEvidenceExplorer](#) function to generate these files.
`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 study results.

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prepareForEvidenceExplorer

Prepare results for the Evidence Explorer Shiny app.

Description

Prepare results for the Evidence Explorer Shiny app.

Usage

```
prepareForEvidenceExplorer(resultsFolder, shinyDataFolder)
```

Arguments

`resultsFolder`	Folder where the exported zip files from one or more databases are stored.
`shinyDataFolder`	
	Folder where the data files for the Shiny app will be written.

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runSelfControlledCaseSeries

Execute the Self-Controlled Case Series analyses

Description

Execute the Self-Controlled Case Series analyses

Usage

```
runSelfControlledCaseSeries(
  connectionDetails,
  cdmDatabaseSchema,
  oracleTempSchema = NULL,
  outcomeDatabaseSchema = cdmDatabaseSchema,
  outcomeTable = "cohort",
  exposureDatabaseSchema = cdmDatabaseSchema,
  exposureTable = "drug_era",
  outputFolder,
  maxCores
)
```

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'.

oracleTempSchema
Should be used in Oracle to specify a schema where the user has write priviliges for storing temporary tables.

outcomeDatabaseSchema
Schema name where the outcome cohorts are stored. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.

outcomeTable
The name of the table in the outcome database schema that holds the outcome cohorts,

exposureDatabaseSchema
Schema name where the exposure cohorts are stored. Note that for SQL Server, this should include both the database and schema name, for example 'cdm_data.dbo'.

exposureTable
The name of the table in the exposure database schema that holds the exposure cohorts,

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.

maxCores
How many parallel cores should be used? If more cores are made available this can speed up the analyses.

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uploadResults   *Upload results to OHDSI server*

Description

Upload results to OHDSI server

Usage

```
uploadResults(outputFolder, privateKeyFileName, userName)
```

Arguments

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.

privateKeyFileName
A character string denoting the path to the RSA private key provided by the study coordinator.

userName
A character string containing the user name provided by the study coordinator.

Details

This function uploads the 'Results<databaseId>.zip' to the OHDSI SFTP server. Before sending, you can inspect the zip file, wich contains (zipped) CSV files. You can send the zip file from a different computer than the one on which is was created.

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