

Package ‘Characterization’

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Type Package

Title Implement Descriptive Studies Using the Common Data Model

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Description An end-to-end framework that enables users to implement various descriptive studies for a given set of target and outcome cohorts for data mapped to the Observational Medical Outcomes Partnership Common Data Model.

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URL <https://ohdsi.github.io/Characterization/>,
<https://github.com/OHDSI/Characterization>

BugReports <https://github.com/OHDSI/Characterization/issues>

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cleanIncremental	<i>Removes csv files from folders that have not been marked as completed and removes the record of the execution file</i>
------------------	---

Description

Removes csv files from folders that have not been marked as completed and removes the record of the execution file

Usage

```
cleanIncremental(executionFolder, ignoreWhenEmpty = FALSE)
```

Arguments

- executionFolder The folder that has the execution files
- ignoreWhenEmpty When TRUE, if there are no incremental logs then nothing is run

Value

A list with the settings

See Also

Other Incremental: [cleanNonIncremental\(\)](#)

Examples

```
cleanIncremental(  
  file.path(tempdir(), 'incremental'),  
  ignoreWhenEmpty = TRUE  
)
```

cleanNonIncremental	<i>Removes csv files from the execution folder as there should be no csv files when running in non-incremental model</i>
---------------------	--

Description

Removes csv files from the execution folder as there should be no csv files when running in non-incremental model

Usage

```
cleanNonIncremental(executionFolder)
```

Arguments

executionFolder
The folder that has the execution files

Value

A list with the settings

See Also

Other Incremental: [cleanIncremental\(\)](#)

Examples

```
# example code  
  
cleanNonIncremental(file.path(tempdir(), 'incremental'))
```

```
computeDechallengeRechallengeAnalyses
    Compute dechallenge rechallenge study
```

Description

Compute dechallenge rechallenge study

Usage

```
computeDechallengeRechallengeAnalyses(
  connectionDetails = NULL,
  targetDatabaseSchema,
  targetTable,
  outcomeDatabaseSchema = targetDatabaseSchema,
  outcomeTable = targetTable,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),
  settings,
  databaseId = "database 1",
  outputFolder,
  minCellCount = 0,
  ...
)
```

Arguments

connectionDetails	An object of type 'connectionDetails' as created using the [DatabaseConnector::createConnectionDetails()] function.
targetDatabaseSchema	Schema name where your target cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
targetTable	Name of the target cohort table.
outcomeDatabaseSchema	Schema name where your outcome cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
outcomeTable	Name of the outcome cohort table.
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created
settings	The settings for the timeToEvent study
databaseId	An identifier for the database (string)
outputFolder	A directory to save the results as csv files

minCellCount The minimum cell value to display, values less than this will be replaced by -1
 ... extra inputs

Value

An `Andromeda::andromeda()` object containing the dechallenge rechallenge results

See Also

Other DechallengeRechallenge: [computeRechallengeFailCaseSeriesAnalyses\(\)](#), [createDechallengeRechallengeSe](#)

Examples

```
conDet <- exampleOmopConnectionDetails()

drSet <- createDechallengeRechallengeSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)

computeDechallengeRechallengeAnalyses(
  connectionDetails = conDet,
  targetDatabaseSchema = 'main',
  targetTable = 'cohort',
  settings = drSet,
  outputFolder = tempdir()
)
```

```
computeRechallengeFailCaseSeriesAnalyses
```

Compute fine the subjects that fail the dechallenge rechallenge study

Description

Compute fine the subjects that fail the dechallenge rechallenge study

Usage

```
computeRechallengeFailCaseSeriesAnalyses(
  connectionDetails = NULL,
  targetDatabaseSchema,
  targetTable,
  outcomeDatabaseSchema = targetDatabaseSchema,
  outcomeTable = targetTable,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),
  settings,
  databaseId = "database 1",
```

```

    showSubjectId = FALSE,
    outputFolder,
    minCellCount = 0,
    ...
)

```

Arguments

connectionDetails	An object of type 'connectionDetails' as created using the [DatabaseConnector::createConnectionDetails()] function.
targetDatabaseSchema	Schema name where your target cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
targetTable	Name of the target cohort table.
outcomeDatabaseSchema	Schema name where your outcome cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
outcomeTable	Name of the outcome cohort table.
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created
settings	The settings for the timeToEvent study
databaseId	An identifier for the database (string)
showSubjectId	if F then subject_ids are hidden (recommended if sharing results)
outputFolder	A directory to save the results as csv files
minCellCount	The minimum cell value to display, values less than this will be replaced by -1
...	extra inputs

Value

An `Andromeda::andromeda()` object with the case series details of the failed rechallenge

See Also

Other DechallengeRechallenge: [computeDechallengeRechallengeAnalyses\(\)](#), [createDechallengeRechallengeSettings\(\)](#)

Examples

```

conDet <- exampleOmopConnectionDetails()

drSet <- createDechallengeRechallengeSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)

```

```
computeRechallengeFailCaseSeriesAnalyses(
  connectionDetails = conDet,
  targetDatabaseSchema = 'main',
  targetTable = 'cohort',
  settings = drSet,
  outputFolder = tempdir()
)
```

```
computeTimeToEventAnalyses
```

Compute time to event study

Description

Compute time to event study

Usage

```
computeTimeToEventAnalyses(
  connectionDetails = NULL,
  targetDatabaseSchema,
  targetTable,
  outcomeDatabaseSchema = targetDatabaseSchema,
  outcomeTable = targetTable,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),
  cdmDatabaseSchema,
  settings,
  databaseId = "database 1",
  outputFolder,
  minCellCount = 0,
  ...
)
```

Arguments

connectionDetails	An object of type 'connectionDetails' as created using the [DatabaseConnector::createConnectionDetails()] function.
targetDatabaseSchema	Schema name where your target cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
targetTable	Name of the target cohort table.
outcomeDatabaseSchema	Schema name where your outcome cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.

outcomeTable	Name of the outcome cohort table.
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created
cdmDatabaseSchema	The database schema containing the OMOP CDM data
settings	The settings for the timeToEvent study
databaseId	An identifier for the database (string)
outputFolder	A directory to save the results as csv files
minCellCount	The minimum cell value to display, values less than this will be replaced by -1
...	extra inputs

Value

An `Andromeda::andromeda()` object containing the time to event results.

See Also

Other TimeToEvent: [createTimeToEventSettings\(\)](#)

Examples

```
# example code

conDet <- exampleOmopConnectionDetails()

tteSet <- createTimeToEventSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)

result <- computeTimeToEventAnalyses(
  connectionDetails = conDet,
  targetDatabaseSchema = 'main',
  targetTable = 'cohort',
  cdmDatabaseSchema = 'main',
  settings = tteSet,
  outputFolder = file.path(tempdir(), 'tte')
)
```

createAggregateCovariateSettings

Create aggregate covariate study settings

Description

Create aggregate covariate study settings

Usage

```
createAggregateCovariateSettings(
  targetIds,
  outcomeIds,
  minPriorObservation = 0,
  outcomeWashoutDays = 0,
  riskWindowStart = 1,
  startAnchor = "cohort start",
  riskWindowEnd = 365,
  endAnchor = "cohort start",
  covariateSettings = FeatureExtraction::createCovariateSettings(useDemographicsGender =
    TRUE, useDemographicsAge = TRUE, useDemographicsAgeGroup = TRUE, useDemographicsRace
    = TRUE, useDemographicsEthnicity = TRUE, useDemographicsIndexYear = TRUE,
    useDemographicsIndexMonth = TRUE, useDemographicsTimeInCohort = TRUE,
    useDemographicsPriorObservationTime = TRUE, useDemographicsPostObservationTime =
    TRUE, useConditionGroupEraLongTerm = TRUE, useDrugGroupEraOverlapping = TRUE,
    useDrugGroupEraLongTerm = TRUE, useProcedureOccurrenceLongTerm = TRUE,

    useMeasurementLongTerm = TRUE, useObservationLongTerm = TRUE,
    useDeviceExposureLongTerm = TRUE, useVisitConceptCountLongTerm = TRUE,
    useConditionGroupEraShortTerm = TRUE, useDrugGroupEraShortTerm = TRUE,
    useProcedureOccurrenceShortTerm = TRUE, useMeasurementShortTerm = TRUE,
    useObservationShortTerm = TRUE, useDeviceExposureShortTerm = TRUE,
    useVisitConceptCountShortTerm = TRUE, endDays = 0, longTermStartDays = -365,
    shortTermStartDays = -30),
  caseCovariateSettings = createDuringCovariateSettings(useConditionGroupEraDuring =
    TRUE, useDrugGroupEraDuring = TRUE, useProcedureOccurrenceDuring = TRUE,
    useDeviceExposureDuring = TRUE, useMeasurementDuring = TRUE, useObservationDuring =
    TRUE, useVisitConceptCountDuring = TRUE),
  casePreTargetDuration = 365,
  casePostOutcomeDuration = 365,
  extractNonCaseCovariates = TRUE
)
```

Arguments

targetIds	A list of cohortIds for the target cohorts
outcomeIds	A list of cohortIds for the outcome cohorts

<code>minPriorObservation</code>	The minimum time (in days) in the database a patient in the target cohorts must be observed prior to index
<code>outcomeWashoutDays</code>	Patients with the outcome within outcomeWashout days prior to index are excluded from the risk factor analysis
<code>riskWindowStart</code>	The start of the risk window (in days) relative to the 'startAnchor'.
<code>startAnchor</code>	The anchor point for the start of the risk window. Can be "cohort start" or "cohort end".
<code>riskWindowEnd</code>	The end of the risk window (in days) relative to the 'endAnchor'.
<code>endAnchor</code>	The anchor point for the end of the risk window. Can be "cohort start" or "cohort end".
<code>covariateSettings</code>	An object created using <code>FeatureExtraction::createCovariateSettings</code>
<code>caseCovariateSettings</code>	An object created using <code>createDuringCovariateSettings</code>
<code>casePreTargetDuration</code>	The number of days prior to case index we use for FeatureExtraction
<code>casePostOutcomeDuration</code>	The number of days prior to case index we use for FeatureExtraction
<code>extractNonCaseCovariates</code>	Whether to extract aggregate covariates and counts for patients in the targets and outcomes in addition to the cases

Value

A list with the settings

Examples

```
aggregateSetting <- createAggregateCovariateSettings(
  targetIds = c(1,2),
  outcomeIds = c(3),
  minPriorObservation = 365,
  outcomeWashoutDays = 90,
  riskWindowStart = 1,
  startAnchor = "cohort start",
  riskWindowEnd = 365,
  endAnchor = "cohort start",
  casePreTargetDuration = 365,
  casePostOutcomeDuration = 365
)
```

`createCharacterizationSettings`*Create the settings for a large scale characterization study*

Description

This function creates a list of settings for different characterization studies

Usage

```
createCharacterizationSettings(  
  timeToEventSettings = NULL,  
  dechallengeRechallengeSettings = NULL,  
  aggregateCovariateSettings = NULL  
)
```

Arguments

`timeToEventSettings`
A list of timeToEvent settings

`dechallengeRechallengeSettings`
A list of dechallengeRechallenge settings

`aggregateCovariateSettings`
A list of aggregateCovariate settings

Details

Specify one or more timeToEvent, dechallengeRechallenge and aggregateCovariate settings

Value

Returns the connection to the sqlite database

See Also

Other LargeScale: [loadCharacterizationSettings\(\)](#), [runCharacterizationAnalyses\(\)](#), [saveCharacterizationSet](#)

Examples

```
# example code  
  
drSet <- createDechallengeRechallengeSettings(  
  targetIds = c(1,2),  
  outcomeIds = 3  
)  
  
cSet <- createCharacterizationSettings(  
  dechallengeRechallengeSettings = drSet
```

)

createCharacterizationTables

Create the results tables to store characterization results into a database

Description

This function executes a large set of SQL statements to create tables that can store results

Usage

```
createCharacterizationTables(
    connectionDetails,
    resultSchema,
    targetDialect = "postgresql",
    deleteExistingTables = TRUE,
    createTables = TRUE,
    tablePrefix = "c_",
    tempEmulationSchema = getOption("sqlRenderTempEmulationSchema")
)
```

Arguments

connectionDetails	The connectionDetails to a database created by using the function createConnectDetails in the DatabaseConnector package.
resultSchema	The name of the database schema that the result tables will be created.
targetDialect	The database management system being used
deleteExistingTables	If true any existing tables matching the Characterization result tables names will be deleted
createTables	If true the Characterization result tables will be created
tablePrefix	A string appended to the Characterization result tables
tempEmulationSchema	The temp schema used when the database management system is oracle

Details

This function can be used to create (or delete) Characterization result tables

Value

Returns NULL but creates the required tables into the specified database schema.

See Also

Other Database: [createSqliteDatabase\(\)](#), [insertResultsToDatabase\(\)](#)

Examples

```
# create sqlite database
charResultDbCD <- createSqliteDatabase()

# create database results tables
createCharacterizationTables(
  connectionDetails = charResultDbCD,
  resultSchema = 'main'
)
```

```
createDechallengeRechallengeSettings
      Create dechallenge rechallenge study settings
```

Description

Create dechallenge rechallenge study settings

Usage

```
createDechallengeRechallengeSettings(
  targetIds,
  outcomeIds,
  dechallengeStopInterval = 30,
  dechallengeEvaluationWindow = 30
)
```

Arguments

targetIds	A list of cohortIds for the target cohorts
outcomeIds	A list of cohortIds for the outcome cohorts
dechallengeStopInterval	An integer specifying the how much time to add to the cohort_end when determining whether the event starts during cohort and ends after
dechallengeEvaluationWindow	An integer specifying the period of time after the cohort_end when you cannot see an outcome for a dechallenge success

Value

A list with the settings

See Also

Other DechallengeRechallenge: [computeDechallengeRechallengeAnalyses\(\)](#), [computeRechallengeFailCaseSeriesA](#)

Examples

```
drSet <- createDechallengeRechallengeSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)
```

```
createDuringCovariateSettings
```

Create during covariate settings

Description

Create during covariate settings

Usage

```
createDuringCovariateSettings(
  useConditionOccurrenceDuring = FALSE,
  useConditionOccurrencePrimaryInpatientDuring = FALSE,
  useConditionEraDuring = FALSE,
  useConditionGroupEraDuring = FALSE,
  useDrugExposureDuring = FALSE,
  useDrugEraDuring = FALSE,
  useDrugGroupEraDuring = FALSE,
  useProcedureOccurrenceDuring = FALSE,
  useDeviceExposureDuring = FALSE,
  useMeasurementDuring = FALSE,
  useObservationDuring = FALSE,
  useVisitCountDuring = FALSE,
  useVisitConceptCountDuring = FALSE,
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c()
)
```

Arguments

useConditionOccurrenceDuring

One covariate per condition in the condition_occurrence table starting between cohort start and cohort end. (analysis ID 109)

useConditionOccurrencePrimaryInpatientDuring	One covariate per condition observed as a primary diagnosis in an inpatient setting in the condition_occurrence table starting between cohort start and cohort end. (analysis ID 110)
useConditionEraDuring	One covariate per condition in the condition_era table starting between cohort start and cohort end. (analysis ID 217)
useConditionGroupEraDuring	One covariate per condition era rolled up to groups in the condition_era table starting between cohort start and cohort end. (analysis ID 218)
useDrugExposureDuring	One covariate per drug in the drug_exposure table between cohort start and end. (analysis ID 305)
useDrugEraDuring	One covariate per drug in the drug_era table between cohort start and end. (analysis ID 417)
useDrugGroupEraDuring	One covariate per drug rolled up to ATC groups in the drug_era table between cohort start and end. (analysis ID 418)
useProcedureOccurrenceDuring	One covariate per procedure in the procedure_occurrence table between cohort start and end. (analysis ID 505)
useDeviceExposureDuring	One covariate per device in the device exposure table starting between cohort start and end. (analysis ID 605)
useMeasurementDuring	One covariate per measurement in the measurement table between cohort start and end. (analysis ID 713)
useObservationDuring	One covariate per observation in the observation table between cohort start and end. (analysis ID 805)
useVisitCountDuring	The number of visits observed between cohort start and end. (analysis ID 926)
useVisitConceptCountDuring	The number of visits observed between cohort start and end, stratified by visit concept ID. (analysis ID 927)
includedCovariateConceptIds	A list of concept IDs that should be used to construct covariates.
addDescendantsToInclude	Should descendant concept IDs be added to the list of concepts to include?
excludedCovariateConceptIds	A list of concept IDs that should NOT be used to construct covariates.
addDescendantsToExclude	Should descendant concept IDs be added to the list of concepts to exclude?
includedCovariateIds	A list of covariate IDs that should be restricted to.

Details

creates an object specifying how during covariates should be constructed from data in the CDM model.

Value

An object of type covariateSettings, to be used in other functions.

See Also

Other CovariateSetting: [getDbDuringCovariateData\(\)](#)

Examples

```
settings <- createDuringCovariateSettings(  
  useConditionOccurrenceDuring = TRUE,  
  useConditionOccurrencePrimaryInpatientDuring = FALSE,  
  useConditionEraDuring = FALSE,  
  useConditionGroupEraDuring = FALSE  
)
```

createSqliteDatabase *Create an sqlite database connection*

Description

This function creates a connection to an sqlite database

Usage

```
createSqliteDatabase(sqliteLocation = tempdir())
```

Arguments

sqliteLocation The location of the sqlite database

Details

This function creates a sqlite database and connection

Value

Returns the connection detail object to the sqlite database

See Also

Other Database: [createCharacterizationTables\(\)](#), [insertResultsToDatabase\(\)](#)

Examples

```
charResultDbCD <- createSqliteDatabase()
```

```
createTimeToEventSettings
```

Create time to event study settings

Description

Create time to event study settings

Usage

```
createTimeToEventSettings(targetIds, outcomeIds)
```

Arguments

targetIds A list of cohortIds for the target cohorts

outcomeIds A list of cohortIds for the outcome cohorts

Value

An list with the time to event settings

See Also

Other TimeToEvent: [computeTimeToEventAnalyses\(\)](#)

Examples

```
# example code

tteSet <- createTimeToEventSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)
```

```
exampleOmopConnectionDetails
```

create a connection detail for an example GI Bleed dataset from Euphonia

Description

This returns an object of class ‘ConnectionDetails’ that lets you connect via ‘DatabaseConnector::connect()’ to the example database.

Usage

```
exampleOmopConnectionDetails(exdir = tempdir())
```

Arguments

`exdir` a directory to unzip the example OMOP database into. Default is tempdir().

Details

Finds the location of the example database in the package and calls ‘DatabaseConnector::createConnectionDetails’ to create a ‘ConnectionDetails’ object for connecting to the database.

Value

An object of class ‘ConnectionDetails’ with the details to connect to the example OHDSI OMOP CDM database

Examples

```
conDet <- exampleOmopConnectionDetails()

connectionHandler <- ResultModelManager::ConnectionHandler$new(conDet)
```

```
getDbDuringCovariateData
```

Extracts covariates that occur during a cohort

Description

Extracts covariates that occur during a cohort

Usage

```
getDbDuringCovariateData(
  connection,
  oracleTempSchema = NULL,
  cdmDatabaseSchema,
  cdmVersion = "5",
  cohortTable = "#cohort_person",
  rowIdField = "subject_id",
  aggregated = TRUE,
  cohortIds = c(-1),
  covariateSettings,
  minCharacterizationMean = 0,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),
  ...
)
```

Arguments

connection	The database connection
oracleTempSchema	The temp schema if using oracle
cdmDatabaseSchema	The schema of the OMOP CDM data
cdmVersion	version of the OMOP CDM data
cohortTable	the table name that contains the target population cohort
rowIdField	string representing the unique identifier in the target population cohort
aggregated	whether the covariate should be aggregated
cohortIds	cohort id for the target cohort
covariateSettings	settings for the covariate cohorts and time periods
minCharacterizationMean	the minimum value for a covariate to be extracted
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created
...	additional arguments from FeatureExtraction

Details

The user specifies a what during covariates they want and this executes them using FE

Value

A 'FeatureExtraction' covariateData object containing the during covariates based on user settings

See Also

Other CovariateSetting: [createDuringCovariateSettings\(\)](#)

Examples

```
conDet <- exampleOmopConnectionDetails()
connection <- DatabaseConnector::connect(conDet)

settings <- createDuringCovariateSettings(
  useConditionOccurrenceDuring = TRUE,
  useConditionOccurrencePrimaryInpatientDuring = FALSE,
  useConditionEraDuring = FALSE,
  useConditionGroupEraDuring = FALSE
)

duringData <- getDbDuringCovariateData(
  connection <- connection,
  cdmDatabaseSchema = 'main',
  cohortIds = 1,
  covariateSettings = settings,
  cohortTable = 'cohort'
)
```

insertResultsToDatabase

Upload the results into a result database

Description

This function uploads results in csv format into a result database

Usage

```
insertResultsToDatabase(
  connectionDetails,
  schema,
  resultsFolder,
  tablePrefix = "",
  csvTablePrefix = "c_"
)
```

Arguments

connectionDetails	The connection details to the result database
schema	The schema for the result database
resultsFolder	The folder containing the csv results

tablePrefix A prefix to append to the result tables for the characterization results
 csvTablePrefix The prefix added to the csv results - default is 'c_'

Details

Calls ResultModelManager uploadResults function to upload the csv files

Value

Returns the connection to the sqlite database

See Also

Other Database: [createCharacterizationTables\(\)](#), [createSqliteDatabase\(\)](#)

Examples

```
# generate results into resultsFolder
conDet <- exampleOmopConnectionDetails()

drSet <- createDechallengeRechallengeSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)

cSet <- createCharacterizationSettings(
  dechallengeRechallengeSettings = drSet
)

runCharacterizationAnalyses(
  connectionDetails = conDet,
  targetDatabaseSchema = 'main',
  targetTable = 'cohort',
  outcomeDatabaseSchema = 'main',
  outcomeTable = 'cohort',
  cdmDatabaseSchema = 'main',
  characterizationSettings = cSet,
  outputDirectory = tempdir()
)

# create sqlite database
charResultDbCD <- createSqliteDatabase()

# create database results tables
createCharacterizationTables(
  connectionDetails = charResultDbCD,
  resultSchema = 'main'
)

# insert results
insertResultsToDatabase(
  connectionDetails = charResultDbCD,
```

```
    schema = 'main',  
    resultsFolder = tempdir()  
  )
```

loadCharacterizationSettings

Load the characterization settings previously saved as a json file

Description

This function converts the json file back into an R object

Usage

```
loadCharacterizationSettings(fileName)
```

Arguments

fileName The location of the the json settings

Details

Input the directory containing the 'characterizationSettings.json' file and load the settings into R

Value

Returns the json settings as an R object

See Also

Other LargeScale: [createCharacterizationSettings\(\)](#), [runCharacterizationAnalyses\(\)](#), [saveCharacterizationSettings\(\)](#)

Examples

```
# example code  
  
setPath <- file.path(tempdir(), 'charSet.json')  
  
drSet <- createDechallengeRechallengeSettings(  
  targetIds = c(1,2),  
  outcomeIds = 3  
)  
  
cSet <- createCharacterizationSettings(  
  dechallengeRechallengeSettings = drSet  
)
```

```
saveCharacterizationSettings(  
  settings = cSet,  
  fileName = setPath  
)  
  
setting <- loadCharacterizationSettings(setPath)
```

```
runCharacterizationAnalyses
```

execute a large-scale characterization study

Description

Specify the database connection containing the CDM data, the cohort database schemas/tables, the characterization settings and the directory to save the results to

Usage

```
runCharacterizationAnalyses(  
  connectionDetails,  
  targetDatabaseSchema,  
  targetTable,  
  outcomeDatabaseSchema,  
  outcomeTable,  
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),  
  cdmDatabaseSchema,  
  characterizationSettings,  
  outputDirectory,  
  executionPath = file.path(outputDirectory, "execution"),  
  csvFilePrefix = "c_",  
  databaseId = "1",  
  showSubjectId = FALSE,  
  minCellCount = 0,  
  incremental = TRUE,  
  threads = 1,  
  minCharacterizationMean = 0.01  
)
```

Arguments

connectionDetails

The connection details to the database containing the OMOP CDM data

targetDatabaseSchema

Schema name where your target cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.

targetTable	Name of the target cohort table.
outcomeDatabaseSchema	Schema name where your outcome cohort table resides. Note that for SQL Server, this should include both the database and schema name, for example 'scratch.dbo'.
outcomeTable	Name of the outcome cohort table.
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created
cdmDatabaseSchema	The schema with the OMOP CDM data
characterizationSettings	The study settings created using createCharacterizationSettings
outputDirectory	The location to save the final csv files to
executionPath	The location where intermediate results are saved to
csvFilePrefix	A string to append the csv files in the outputDirectory
databaseId	The unique identifier for the cdm database
showSubjectId	Whether to include subjectId of failed rechallenger case series or hide
minCellCount	The minimum count value that is calculated
incremental	If TRUE then skip previously executed analyses that completed
threads	The number of threads to use when running aggregate covariates
minCharacterizationMean	The minimum mean threshold to extract when running aggregate covariates

Details

The results of the characterization will be saved into an sqlite database inside the specified saveDirectory

Value

Multiple csv files in the outputDirectory.

See Also

Other LargeScale: [createCharacterizationSettings\(\)](#), [loadCharacterizationSettings\(\)](#), [saveCharacterizationSettings\(\)](#)

Examples

```
conDet <- exampleOmopConnectionDetails()

drSet <- createDechallengeRechallengerSettings(
  targetIds = c(1,2),
```



```
    outcomeIds = 3
  )

  cSet <- createCharacterizationSettings(
    dechallengeRechallengeSettings = drSet
  )

  runCharacterizationAnalyses(
    connectionDetails = conDet,
    targetDatabaseSchema = 'main',
    targetTable = 'cohort',
    outcomeDatabaseSchema = 'main',
    outcomeTable = 'cohort',
    cdmDatabaseSchema = 'main',
    characterizationSettings = cSet,
    outputDirectory = tempdir()
  )
```

`saveCharacterizationSettings`*Save the characterization settings as a json*

Description

This function converts the settings into a json object and saves it

Usage

```
saveCharacterizationSettings(settings, fileName)
```

Arguments

<code>settings</code>	An object of class <code>characterizationSettings</code> created using <code>createCharacterizationSettings</code>
<code>fileName</code>	The location to save the json settings

Details

Input the characterization settings and output a json file to a file named 'characterizationSettings.json' inside the `saveDirectory`

Value

Returns the location of the directory containing the json settings

See Also

Other LargeScale: [createCharacterizationSettings\(\)](#), [loadCharacterizationSettings\(\)](#), [runCharacterizationAnalyses\(\)](#)

Examples

```

drSet <- createDechallengeRechallengeSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)

cSet <- createCharacterizationSettings(
  dechallengeRechallengeSettings = drSet
)

saveCharacterizationSettings(
  settings = cSet,
  fileName = file.path(tempdir(), 'cSet.json')
)

```

viewCharacterization *viewCharacterization - Interactively view the characterization results*

Description

This is a shiny app for viewing interactive plots and tables

Usage

```
viewCharacterization(resultFolder, cohortDefinitionSet = NULL)
```

Arguments

resultFolder The location of the csv results
 cohortDefinitionSet
 The cohortDefinitionSet extracted using webAPI

Details

Input is the output of ...

Value

Opens a shiny app for interactively viewing the results

Examples

```

conDet <- exampleOmopConnectionDetails()

drSet <- createDechallengeRechallengeSettings(
  targetIds = c(1,2),
  outcomeIds = 3
)

```

```
cSet <- createCharacterizationSettings(  
  dechallengeRechallengeSettings = drSet  
)  
  
runCharacterizationAnalyses(  
  connectionDetails = conDet,  
  targetDatabaseSchema = 'main',  
  targetTable = 'cohort',  
  outcomeDatabaseSchema = 'main',  
  outcomeTable = 'cohort',  
  cdmDatabaseSchema = 'main',  
  characterizationSettings = cSet,  
  outputDirectory = file.path(tempdir(),'view')  
)  
  
viewCharacterization(  
  resultFolder = file.path(tempdir(),'view')  
)
```

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