Package 'Strategus'

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Type Package

Title Coordinate and Execute OHDSI HADES Modules

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Description Coordinate and execute large scale analytics using OHDSI Health Analytics Data-to-Evidence Suite (HADES) (<https://ohdsi.github.io/Hades/>) modules.

Depends R (>= 4.2.0),
CohortGenerator (>= 0.11.0),
DatabaseConnector (>= 6.2.3),
R6

Imports checkmate,
cli,
digest,
dplyr,
methods,
ParallelLogger (>= 3.1.0),
purrr,
ResultModelManager (>= 0.5.8),
rlang,
SqlRender (>= 1.18.0)

Suggests Characterization,
CirceR,
CohortDiagnostics,
CohortIncidence,
CohortMethod,
Cyclops,
Eunomia,
EvidenceSynthesis,
FeatureExtraction,
fs,
knitr,
PatientLevelPrediction,
readr,
rmarkdown,
RSQLite,
SelfControlledCaseSeries,

testthat (>= 3.0.0),
TreatmentPatterns,
withr

Remotes ohdsi/Characterization,
ohdsi/CohortDiagnostics,
ohdsi/CohortGenerator,
ohdsi/CohortIncidence,
ohdsi/CohortMethod,
ohdsi/PatientLevelPrediction,
ohdsi/ResultModelManager,
ohdsi/SelfControlledCaseSeries

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VignetteBuilder knitr

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`addCharacterizationModuleSpecifications` *Add Characterization module specifications to analysis specifications*

Description

Add Characterization module specifications to analysis specifications

Usage

```
addCharacterizationModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

`analysisSpecifications`
: An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`

`moduleSpecifications`
: Created by the `CharacterizationModule$createModuleSpecifications()` function.

Value

Returns the `analysisSpecifications` object with the module specifications added.

`addCohortDiagnosticsModuleSpecifications` *Add Cohort Diagnostics module specifications to analysis specifications*

Description

Add Cohort Diagnostics module specifications to analysis specifications

Usage

```
addCohortDiagnosticsModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

analysisSpecifications	An object of type AnalysisSpecifications as created by createEmptyAnalysisSpecificiations
moduleSpecifications	Created by the CohortDiagnosticsModule$createModuleSpecifications() function.

Value

Returns the analysisSpecifications object with the module specifications added.

---

addCohortGeneratorModuleSpecifications

Add Cohort Generator module specifications to analysis specifications

---

Description

Add Cohort Generator module specifications to analysis specifications

Usage

```
addCohortGeneratorModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

analysisSpecifications	An object of type AnalysisSpecifications as created by createEmptyAnalysisSpecificiations
moduleSpecifications	Created by the CohortGeneratorModule$createModuleSpecifications() function.

Value

Returns the analysisSpecifications object with the module specifications added.

addCohortIncidenceModuleSpecifications

Add Cohort Incidence module specifications to analysis specifications

Description

Add Cohort Incidence module specifications to analysis specifications

Usage

```
addCohortIncidenceModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

analysisSpecifications	An object of type AnalysisSpecifications as created by createEmptyAnalysisSpecificiations
moduleSpecifications	Created by the CohortIncidenceModule$createModuleSpecifications() function.

Value

Returns the analysisSpecifications object with the module specifications added.

addCohortMethodeModuleSpecifications

Add Cohort Method module specifications to analysis specifications

Description

Add Cohort Method module specifications to analysis specifications

Usage

```
addCohortMethodeModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

analysisSpecifications	An object of type AnalysisSpecifications as created by createEmptyAnalysisSpecificiations
moduleSpecifications	Created by the CohortMethodModule$createModuleSpecifications() function.

Value

Returns the `analysisSpecifications` object with the module specifications added.

`addEvidenceSynthesisModuleSpecifications` *Add Evidence Synthesis module specifications to analysis specifications*

Description

Add Evidence Synthesis module specifications to analysis specifications

Usage

```
addEvidenceSynthesisModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

`analysisSpecifications`	An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`
`moduleSpecifications`	Created by the `EvidenceSynthesisModule$createModuleSpecifications()` function.

Value

Returns the `analysisSpecifications` object with the module specifications added.

`addModuleSpecifications` *Add generic module specifications to analysis specifications*

Description

Add generic module specifications to analysis specifications

Usage

```
addModuleSpecifications(analysisSpecifications, moduleSpecifications)
```

Arguments

`analysisSpecifications`	An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`
`moduleSpecifications`	An object of type `ModuleSpecifications`

Value

Returns the `analysisSpecifications` object with the module specifications added.

`addPatientLevelPredictionModuleSpecifications` *Add Patient Level Prediction module specifications to analysis specifications*

Description

Add Patient Level Prediction module specifications to analysis specifications

Usage

```
addPatientLevelPredictionModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

`analysisSpecifications`
: An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`

`moduleSpecifications`
: Created by the `PatientLevelPredictionModule$createModuleSpecifications()` function.

Value

Returns the `analysisSpecifications` object with the module specifications added.

`addPatientLevelPredictionValidationModuleSpecifications` *Add Patient Level Prediction Validation Module module specifications to analysis specifications*

Description

Add Patient Level Prediction Validation Module module specifications to analysis specifications

Usage

```
addPatientLevelPredictionValidationModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

`analysisSpecifications`
: An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`

`moduleSpecifications`
: Created by the `PatientLevelPredictionValidationModule$createModuleSpecifications()` function.

Value

Returns the `analysisSpecifications` object with the module specifications added.

`addSelfControlledCaseSeriesModuleSpecifications` *Add Self Controlled Case Series Module module specifications to analysis specifications*

Description

Add Self Controlled Case Series Module module specifications to analysis specifications

Usage

```
addSelfControlledCaseSeriesModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

`analysisSpecifications`
: An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`

`moduleSpecifications`
: Created by the `SelfControlledCaseSeriesModule$createModuleSpecifications()` function.

Value

Returns the `analysisSpecifications` object with the module specifications added.

addSharedResources *Add shared resources (i.e. cohorts) to analysis specifications*

Description

Add shared resources (i.e. cohorts) to analysis specifications

Usage

```
addSharedResources(analysisSpecifications, sharedResources)
```

Arguments

analysisSpecifications	An object of type AnalysisSpecifications as created by createEmptyAnalysisSpecificiations
sharedResources	An object of type SharedResources.

Value

Returns the analysisSpecifications object with the module specifications added.

addTreatmentPatternsModuleSpecifications *Add Treatment Patterns Module specifications to analysis specifications*

Description

Add Treatment Patterns Module specifications to analysis specifications

Usage

```
addTreatmentPatternsModuleSpecifications(
  analysisSpecifications,
  moduleSpecifications
)
```

Arguments

analysisSpecifications	An object of type AnalysisSpecifications as created by createEmptyAnalysisSpecificiations
moduleSpecifications	Created by the "tbd"

Value

Returns the analysisSpecifications object with the module specifications added

CharacterizationModule

Characterize cohorts with the Rhref*https://ohdsi.github.io/Characterization/HADES Characterization Package*

Description

Computes cohort characterization information against the OMOP Common Data Model

Super class

`Strategus::StrategusModule` -> `CharacterizationModule`

Public fields

`tablePrefix` The table prefix to append to the results tables

Methods

Public methods:

- `CharacterizationModule$new()`
- `CharacterizationModule$execute()`
- `CharacterizationModule$createResultsDataModel()`
- `CharacterizationModule$getResultsDataModelSpecification()`
- `CharacterizationModule$uploadResults()`
- `CharacterizationModule$createModuleSpecifications()`
- `CharacterizationModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
CharacterizationModule$new()
```

Method `execute()`**:** Execute characterization

Usage:

```
CharacterizationModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
CharacterizationModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = self$tablePrefix
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
CharacterizationModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
CharacterizationModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Creates the CharacterizationModule Specifications

Usage:

```
CharacterizationModule$createModuleSpecifications(
  targetIds,
  outcomeIds,
```

```
  outcomeWashoutDays = c(365),
  minPriorObservation = 365,
  dechallengeStopInterval = 30,
  dechallengeEvaluationWindow = 30,
  riskWindowStart = c(1, 1),
  startAnchor = c("cohort start", "cohort start"),
  riskWindowEnd = c(0, 365),
  endAnchor = c("cohort end", "cohort end"),
  minCharacterizationMean = 0.01,
 covariateSettings = FeatureExtraction::createCovariateSettings(useDemographicsGender =
  T, useDemographicsAge = T, useDemographicsAgeGroup = T, useDemographicsRace = T,
  useDemographicsEthnicity = T, useDemographicsIndexYear = T, useDemographicsIndexMonth
  = T, useDemographicsTimeInCohort = T, useDemographicsPriorObservationTime = T,
    useDemographicsPostObservationTime = T, useConditionGroupEraLongTerm = T,
    useDrugGroupEraOverlapping = T, useDrugGroupEraLongTerm = T,
    useProcedureOccurrenceLongTerm = T, useMeasurementLongTerm = T,

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

Arguments:

`targetIds` A vector of cohort IDs to use as the target(s) for the characterization

`outcomeIds` A vector of cohort IDs to use as the outcome(s) for the characterization

`outcomeWashoutDays` A vector of integers specifying the washout days for each outcome (same length as the outcomeIds)

`minPriorObservation` The number of days of minimum observation a patient in the target populations must have

`dechallengeStopInterval` description

`dechallengeEvaluationWindow` description

`riskWindowStart` The number of days after start anchor to start the time-at-risk (can be a vector for multiple TARS)

`startAnchor` The TAR starts relative to this either cohort start or cohort end (can be a vector for multiple TARS)

`riskWindowEnd` The number of days after end anchor to end the time-at-risk (can be a vector for multiple TARS)

`endAnchor` The TAR ends relative to this either cohort start or cohort end (can be a vector for multiple TARS)

`minCharacterizationMean` The minimum fraction patients in the target have a covariate for it to be included

`covariateSettings` Covariates for the database, cohort and risk factor characterization
`caseCovariateSettings` Covariates for the case-series characterization
`casePreTargetDuration` The number of days before target start to use for case-series
`casePostOutcomeDuration` The number of days after outcome start to use for case-series

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
CharacterizationModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`CohortDiagnosticsModule`

Evaluate phenotypes with the R*hrefhttps://ohdsi.github.io/CohortDiagnostics/HADES CohortDiagnostics Package*

Description

Development and evaluation of phenotype algorithms against the OMOP Common Data Model.

Super class

`Strategus::StrategusModule` -> `CohortDiagnosticsModule`

Public fields

`tablePrefix` The table prefix to append to results tables

Methods

Public methods:

- `CohortDiagnosticsModule$new()`
- `CohortDiagnosticsModule$execute()`
- `CohortDiagnosticsModule$createResultsDataModel()`
- `CohortDiagnosticsModule$getResultsDataModelSpecification()`
- `CohortDiagnosticsModule$uploadResults()`
- `CohortDiagnosticsModule$createModuleSpecifications()`
- `CohortDiagnosticsModule$validateModuleSpecifications()`
- `CohortDiagnosticsModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
CohortDiagnosticsModule$new()
```

Method `execute()`**:** Executes the CohortDiagnostics package

Usage:

```
CohortDiagnosticsModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
CohortDiagnosticsModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = self$tablePrefix
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
CohortDiagnosticsModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
CohortDiagnosticsModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Creates the CohortDiagnostics Module Specifications

Usage:

```
CohortDiagnosticsModule$createModuleSpecifications(
  cohortIds = NULL,
  runInclusionStatistics = TRUE,
  runIncludedSourceConcepts = TRUE,
  runOrphanConcepts = TRUE,
  runTimeSeries = FALSE,
  runVisitContext = TRUE,
  runBreakdownIndexEvents = TRUE,
  runIncidenceRate = TRUE,
  runCohortRelationship = TRUE,
  runTemporalCohortCharacterization = TRUE,
  temporalCovariateSettings = private$.getDefaultCovariateSettings(),
  minCharacterizationMean = 0.01,
  irWashoutPeriod = 0
)
```

Arguments:

`cohortIds` A list of cohort IDs to use when running the CohortDiagnostics. Default is NULL which will use all cohorts present in the cohort definition set in the analysis specification

`runInclusionStatistics` Generate and export statistic on the cohort inclusion rules?

`runIncludedSourceConcepts` Generate and export the source concepts included in the cohorts?

`runOrphanConcepts` Generate and export potential orphan concepts?

`runTimeSeries` Generate and export the time series diagnostics?

`runVisitContext` Generate and export index-date visit context?

`runBreakdownIndexEvents` Generate and export the breakdown of index events?

`runIncidenceRate` Generate and export the cohort incidence rates?

`runCohortRelationship` Generate and export the cohort relationship? Cohort relationship checks the temporal relationship between two or more cohorts.

`runTemporalCohortCharacterization` Generate and export the temporal cohort characterization? Only records with values greater than 0.001 are returned.

`temporalCovariateSettings` Either an object of type `covariateSettings` as created using one of the createTemporalCovariateSettings function in the FeatureExtraction package, or a list of such objects.

`minCharacterizationMean` The minimum mean value for characterization output. Values below this will be cut off from output. This will help reduce the file size of the characterization output, but will remove information on covariates that have very low values. The default is 0.001 (i.e. 0.1 percent)

`irWashoutPeriod` Number of days washout to include in calculation of incidence rates - default is 0

Method `validateModuleSpecifications()`**:** Validate the module specifications

Usage:

```
CohortDiagnosticsModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` The CohortIncidence module specifications

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
CohortDiagnosticsModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`CohortGeneratorModule` *Generate cohorts with the* R*hrefhttps://ohdsi.github.io/CohortGenerator/HADES CohortGenerator Package*

Description

Generates cohorts against the OMOP Common Data Model

Super class

`Strategus::StrategusModule` -> `CohortGeneratorModule`

Public fields

`cohortDefinitionSharedResourcesClassName` A constant for the name of the cohort definition shared resources section of the analysis specification

`negativeControlOutcomeSharedResourcesClassName` A constant for the name of the negative control outcome shared resources section of the analysis specification

Methods

Public methods:

- `CohortGeneratorModule$new()`
- `CohortGeneratorModule$execute()`
- `CohortGeneratorModule$createResultsDataModel()`
- `CohortGeneratorModule$getResultsDataModelSpecification()`
- `CohortGeneratorModule$uploadResults()`
- `CohortGeneratorModule$createModuleSpecifications()`
- `CohortGeneratorModule$createCohortSharedResourceSpecifications()`
- `CohortGeneratorModule$createNegativeControlOutcomeCohortSharedResourceSpecifications()`
- `CohortGeneratorModule$validateModuleSpecifications()`
- `CohortGeneratorModule$validateCohortSharedResourceSpecifications()`

- CohortGeneratorModule$validateNegativeControlOutcomeCohortSharedResourceSpecifications()
- CohortGeneratorModule$clone()

Method `new()`**:** Initialize the module

Usage:

```
CohortGeneratorModule$new()
```

Method `execute()`**:** Generates the cohorts

Usage:

```
CohortGeneratorModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the DatabaseConnector::createConne function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by createEmptyAnalysisSpec

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by createEmptyAnalysisSpec

`executionSettings` An object of type `ExecutionSettings` as created by createCdmExecutionSettings() or createResultsExecutionSettings().

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
CohortGeneratorModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = ""
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the DatabaseConnector::createConnectionDetails() function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the DatabaseConnector::createConnectionDetails() function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
CohortGeneratorModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
CohortGeneratorModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`: Creates the CohortGenerator Module Specifications

Usage:

```
CohortGeneratorModule$createModuleSpecifications(generateStats = TRUE)
```

Arguments:

`generateStats` When TRUE, the Circe cohort definition SQL will include steps to compute inclusion rule statistics.

Method `createCohortSharedResourceSpecifications()`: Create shared specifications for the cohort definition set

Usage:

```
CohortGeneratorModule$createCohortSharedResourceSpecifications(
  cohortDefinitionSet
)
```

Arguments:

`cohortDefinitionSet` The cohort definition set to include in the specification. See the CohortGenerator package for details on how to build this object.

Method `createNegativeControlOutcomeCohortSharedResourceSpecifications()`: Create shared specifications for the negative control outcomes cohort set

Usage:

```
CohortGeneratorModule$createNegativeControlOutcomeCohortSharedResourceSpecifications(
  negativeControlOutcomeCohortSet,
  occurrenceType,
  detectOnDescendants
)
```

Arguments:

`negativeControlOutcomeCohortSet` The negative control outcome cohort definition set defines the concepts to use to construct negative control outcome cohorts. See the CohortGenerator package for more details.

`occurrenceType` Either "first" or "all

detectOnDescendants When TRUE, the concept ID for the negative control will use the concept_ancestor table and will detect descendant concepts when constructing the cohort.

Method `validateModuleSpecifications()`: Validate the module specifications

Usage:

```
CohortGeneratorModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

moduleSpecifications The CohortGenerator module specifications

Method `validateCohortSharedResourceSpecifications()`: Validate the cohort shared resource specifications

Usage:

```
CohortGeneratorModule$validateCohortSharedResourceSpecifications(
  cohortSharedResourceSpecifications
)
```

Arguments:

cohortSharedResourceSpecifications The cohort shared resource specifications

Method `validateNegativeControlOutcomeCohortSharedResourceSpecifications()`: Validate the cohort shared resource specifications

Usage:

```
CohortGeneratorModule$validateNegativeControlOutcomeCohortSharedResourceSpecifications(
  negativeControlOutcomeCohortSharedResourceSpecifications
)
```

Arguments:

negativeControlOutcomeCohortSharedResourceSpecifications The cohort shared resource specifications

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
CohortGeneratorModule$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

`CohortIncidenceModule` *Compute incidence with the* R*hrefhttps://ohdsi.github.io/CohortIncidence/HADES CohortIncidence Package*

Description

Computes incidence rates for cohorts against the OMOP Common Data Model

Super class

`Strategus::StrategusModule` -> `CohortIncidenceModule`

Public fields

`tablePrefix` The table prefix to append to results tables

Methods

Public methods:

- `CohortIncidenceModule$new()`
- `CohortIncidenceModule$execute()`
- `CohortIncidenceModule$createResultsDataModel()`
- `CohortIncidenceModule$getResultsDataModelSpecification()`
- `CohortIncidenceModule$uploadResults()`
- `CohortIncidenceModule$createModuleSpecifications()`
- `CohortIncidenceModule$validateModuleSpecifications()`
- `CohortIncidenceModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
CohortIncidenceModule$new()
```

Method `execute()`**:** Execute the CohortIncidence package

Usage:

```
CohortIncidenceModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
CohortIncidenceModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = ""
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
CohortIncidenceModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
CohortIncidenceModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Creates the CohortIncidence Module Specifications

Usage:

```
CohortIncidenceModule$createModuleSpecifications(irDesign = NULL)
```

Arguments:

`irDesign` The incidence rate design created from the CohortIncidence package

Method `validateModuleSpecifications()`**:** Validate the module specifications

Usage:

```
CohortIncidenceModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` The CohortIncidence module specifications

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
CohortIncidenceModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

CohortMethodModule *New-user cohort studies with the* R*hrefhttps://ohdsi.github.io/CohortMethod/HADES CohortMethod Package*

Description

Module for performing new-user cohort studies against the OMOP Common Data Model

Super class

`Strategus::StrategusModule` -> `CohortMethodModule`

Methods

Public methods:

- `CohortMethodModule$new()`
- `CohortMethodModule$execute()`
- `CohortMethodModule$createResultsDataModel()`
- `CohortMethodModule$getResultsDataModelSpecification()`
- `CohortMethodModule$uploadResults()`
- `CohortMethodModule$createModuleSpecifications()`
- `CohortMethodModule$validateModuleSpecifications()`
- `CohortMethodModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
CohortMethodModule$new()
```

Method `execute()`**:** Executes the CohortMethod package

Usage:

```
CohortMethodModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` The analysis specifications for the study

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
CohortMethodModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = ""
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
CohortMethodModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
CohortMethodModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Creates the CohortMethod Module Specifications

Usage:

```
CohortMethodModule$createModuleSpecifications(
  cmAnalysisList,
  targetComparatorOutcomesList,
  analysesToExclude = NULL,
  refitPsForEveryOutcome = FALSE,
  refitPsForEveryStudyPopulation = TRUE,
  cmDiagnosticThresholds = CohortMethod::createCmDiagnosticThresholds()
)
```

Arguments:

`cmAnalysisList` A list of objects of type `cmAnalysis` as created using the 'CohortMethod::createCmAnalysis function.

`targetComparatorOutcomesList` A list of objects of type `targetComparatorOutcomes` as created using the CohortMethod::createTargetComparatorOutcomes function.

`analysesToExclude` Analyses to exclude. See the Analyses to Exclude section for details.

`refitPsForEveryOutcome` Should the propensity model be fitted for every outcome (i.e. after people who already had the outcome are removed)? If false, a single propensity model will be fitted, and people who had the outcome previously will be removed afterwards.

`refitPsForEveryStudyPopulation` Should the propensity model be fitted for every study population definition? If false, a single propensity model will be fitted, and the study population criteria will be applied afterwards.

`cmDiagnosticThresholds` An object of type `CmDiagnosticThresholds` as created using `CohortMethod::createC`

Details: Run a list of analyses for the target-comparator-outcomes of interest. This function will run all specified analyses against all hypotheses of interest, meaning that the total number of outcome models is `length(cmAnalysisList) * length(targetComparatorOutcomesList)` (if all analyses specify an outcome model should be fitted). When you provide several analyses it will determine whether any of the analyses have anything in common, and will take advantage of this fact. For example, if we specify several analyses that only differ in the way the outcome model is fitted, then this function will extract the data and fit the propensity model only once, and re-use this in all the analysis.
After completion, a tibble containing references to all generated files can be obtained using the `CohortMethod::getFileReference()` function. A summary of the analysis results can be obtained using the `CohortMethod::getResultsSummary()` function.

Analyses to Exclude:
Normally, `runCmAnalyses` will run all combinations of target-comparator-outcome-analyses settings. However, sometimes we may not need all those combinations. Using the `analysesToExclude` argument, we can remove certain items from the full matrix. This argument should be a data frame with at least one of the following columns:

Method `validateModuleSpecifications()`**:** Validate the module specifications

Usage:

```
CohortMethodModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` The CohortMethod module specifications

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
CohortMethodModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

createCdmExecutionSettings *Create CDM execution settings*

Description

Create CDM execution settings

Usage

```
createCdmExecutionSettings(
  workDatabaseSchema,
  cdmDatabaseSchema,
 cohortTableNames = CohortGenerator::getCohortTableNames(cohortTable = "cohort"),
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema"),
  workFolder,
  resultsFolder,
  logFileName = file.path(resultsFolder, "strategus-log.txt"),
  minCellCount = 5,
  incremental = TRUE,
  maxCores = parallel::detectCores(),
  modulesToExecute = c()
)
```

Arguments

workDatabaseSchema	A database schema where intermediate data can be stored. The user (as identified in the connection details) will need to have write access to this database schema.
cdmDatabaseSchema	The database schema containing the data in CDM format. The user (as identified in the connection details) will need to have read access to this database schema.
cohortTableNames	An object identifying the various cohort table names that will be created in the workDatabaseSchema. This object can be created using the CohortGenerator::getCohortTableNa function.
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.
workFolder	A folder in the local file system where intermediate results can be written.
resultsFolder	The root folder holding the study results.
logFileName	Logging information from Strategus and all modules will be located in this file. Individual modules will continue to have their own module-specific logs. By default this will be written to the root of the resultsFolder
minCellCount	The minimum number of subjects contributing to a count before it can be included in results.

incremental	This value will be passed to each module that supports execution in an incremental manner. Modules and their underlying packages may use the workFolder contents to determine their state of execution and attempt to pick up where they left off when this value is set to TRUE.
maxCores	The maximum number of processing cores to use for execution. The default is to use all available cores on the machine.
modulesToExecute	(Optional) A vector with the list of modules to execute. When an empty vector/NULL is supplied (default), all modules in the analysis specification are executed.

Value

An object of type ExecutionSettings.

---

createEmptyAnalysisSpecificiations *Create an empty analysis specifications object.*

Description

Create an empty analysis specifications object.

Usage

```
createEmptyAnalysisSpecificiations()
```

Value

An object of type AnalysisSpecifications.

---

createResultDataModel *Create Result Data Model*

Description

Use this at the study design stage to create data models for modules This functions loads modules and executes any custom code to create the results data model in the specified schema in the results database.

Usage

```
createResultDataModel(
  analysisSpecifications,
  resultsDataModelSettings,
  resultsConnectionDetails
)
```

Arguments

`analysisSpecifications`
: An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`

`resultsDataModelSettings`
: The results data model settings as created using [@seealso `createResultsDataModelSettings()`]

`resultsConnectionDetails`
: The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`createResultsDataModelSettings`
Create Results Data Model Settings

Description

The results data model settings are used to create the results data model and to upload results.

Usage

```
createResultsDataModelSettings(
  resultsDatabaseSchema,
  resultsFolder,
 logFileName = file.path(resultsFolder, "strategus-results-data-model-log.txt"),
  modulesToExecute = c()
)
```

Arguments

`resultsDatabaseSchema`
: The schema in the results database that holds the results data model.

`resultsFolder`
: The root folder holding the study results.

`logFileName`
: Log location for data model operations

`modulesToExecute`
: (Optional) A vector with the list of modules to execute. When an empty vector/NULL is supplied (default), all modules in the analysis specification are executed.

Value

An object of type `ResultsDataModelSettings`

`createResultsExecutionSettings` *Create Results execution settings*

Description

Create Results execution settings

Usage

```
createResultsExecutionSettings(
  resultsDatabaseSchema,
  workFolder,
  resultsFolder,
  logFileName = file.path(resultsFolder, "strategus-log.txt"),
  minCellCount = 5,
  maxCores = parallel::detectCores(),
  modulesToExecute = c()
)
```

Arguments

`resultsDatabaseSchema`	The schema in the results database that holds the results data model.
`workFolder`	A folder in the local file system where intermediate results can be written.
`resultsFolder`	The root folder holding the study results.
`logFileName`	Logging information from Strategus and all modules will be located in this file. Individual modules will continue to have their own module-specific logs. By default this will be written to the root of the `resultsFolder`
`minCellCount`	The minimum number of subjects contributing to a count before it can be included in results.
`maxCores`	The maximum number of processing cores to use for execution. The default is to use all available cores on the machine.
`modulesToExecute`	(Optional) A vector with the list of modules to execute. When an empty vector/NULL is supplied (default), all modules in the analysis specification are executed.

Value

An object of type `ExecutionSettings`.

EvidenceSynthesisModule

Meta-analysis with the R*hrefhttps://ohdsi.github.io/EvidenceSynthesis/HADES EvidenceSynthesis Package*

Description

Module for for combining causal effect estimates and study diagnostics across multiple data sites in a distributed study. This includes functions for performing meta-analysis and forest plots

Super class

`Strategus::StrategusModule` -> `EvidenceSynthesisModule`

Methods

Public methods:

- `EvidenceSynthesisModule$new()`
- `EvidenceSynthesisModule$execute()`
- `EvidenceSynthesisModule$createResultsDataModel()`
- `EvidenceSynthesisModule$getResultsDataModelSpecification()`
- `EvidenceSynthesisModule$uploadResults()`
- `EvidenceSynthesisModule$validateModuleSpecifications()`
- `EvidenceSynthesisModule$createEvidenceSynthesisSource()`
- `EvidenceSynthesisModule$createRandomEffectsMetaAnalysis()`
- `EvidenceSynthesisModule$createFixedEffectsMetaAnalysis()`
- `EvidenceSynthesisModule$createBayesianMetaAnalysis()`
- `EvidenceSynthesisModule$createEsDiagnosticThresholds()`
- `EvidenceSynthesisModule$createModuleSpecifications()`
- `EvidenceSynthesisModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
EvidenceSynthesisModule$new()
```

Method `execute()`**:** Executes the EvidenceSynthesis package

Usage:

```
EvidenceSynthesisModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

executionSettings An object of type ExecutionSettings as created by createCdmExecutionSettings() or createResultsExecutionSettings().

Method createResultsDataModel(): Create the results data model for the module

Usage:

```
EvidenceSynthesisModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = ""
)
```

Arguments:

resultsConnectionDetails The connection details to the results database which is an object of class connectionDetails as created by the DatabaseConnector::createConnectionDetails() function.

resultsConnectionDetails The connection details to the results database which is an object of class connectionDetails as created by the DatabaseConnector::createConnectionDetails() function.

resultsDatabaseSchema The schema in the results database that holds the results data model.

tablePrefix A prefix to apply to the database table names (optional).

tablePrefix A prefix to apply to the database table names (optional).

Method getResultsDataModelSpecification(): Get the results data model specification for the module

Usage:

```
EvidenceSynthesisModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

tablePrefix A prefix to apply to the database table names (optional).

tablePrefix A prefix to apply to the database table names (optional).

Method uploadResults(): Upload the results for the module

Usage:

```
EvidenceSynthesisModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

resultsConnectionDetails The connection details to the results database which is an object of class connectionDetails as created by the DatabaseConnector::createConnectionDetails() function.

resultsConnectionDetails The connection details to the results database which is an object of class connectionDetails as created by the DatabaseConnector::createConnectionDetails() function.

analysisSpecifications An object of type AnalysisSpecifications as created by createEmptyAnalysisSpec

analysisSpecifications An object of type AnalysisSpecifications as created by createEmptyAnalysisSpec

resultsDataModelSettings The results data model settings as created using [@seealso createResultsDataModel

Method validateModuleSpecifications(): Validate the module specifications

Usage:

```
EvidenceSynthesisModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` The EvidenceSynthesis module specifications Create an evidence synthesis source

Method `createEvidenceSynthesisSource()`**:**

Usage:

```
EvidenceSynthesisModule$createEvidenceSynthesisSource(
  sourceMethod = "CohortMethod",
  databaseIds = NULL,
  analysisIds = NULL,
  likelihoodApproximation = "adaptive grid"
)
```

Arguments:

`sourceMethod` The source method generating the estimates to synthesize. Can be "CohortMethod" or "SelfControlledCaseSeries"

`databaseIds` The database IDs to include. Use `databaseIds = NULL` to include all database IDs.

`analysisIds` The source method analysis IDs to include. Use `analysisIds = NULL` to include all analysis IDs.

`likelihoodApproximation` The type of likelihood approximation. Can be "adaptive grid" or "normal".

Returns: An object of type `EvidenceSynthesisSource`. Create parameters for a random-effects meta-analysis

Method `createRandomEffectsMetaAnalysis()`**:**

Usage:

```
EvidenceSynthesisModule$createRandomEffectsMetaAnalysis(
  alpha = 0.05,
  evidenceSynthesisAnalysisId = 1,
  evidenceSynthesisDescription = "Random-effects",
  evidenceSynthesisSource = NULL,
  controlType = "outcome"
)
```

Arguments:

`alpha` The alpha (expected type I error) used for the confidence intervals.

`evidenceSynthesisAnalysisId` description

`evidenceSynthesisDescription` description

`evidenceSynthesisSource` description

`controlType` description Create a parameter object for the function computeFixedEffectMeta-Analysis

Details: Use DerSimonian-Laird meta-analysis

Method `createFixedEffectsMetaAnalysis()`**:**

Usage:

```
EvidenceSynthesisModule$createFixedEffectsMetaAnalysis(
  alpha = 0.05,
  evidenceSynthesisAnalysisId = 1,
  evidenceSynthesisDescription = "Fixed-effects",
  evidenceSynthesisSource = NULL,
  controlType = "outcome"
)
```

Arguments:

`alpha` The alpha (expected type I error) used for the confidence intervals.

`evidenceSynthesisAnalysisId` description

`evidenceSynthesisDescription` description

`evidenceSynthesisSource` description

`controlType` description Create a parameter object for the function computeBayesianMeta-Analysis

Details: Create an object defining the parameter values.

Method `createBayesianMetaAnalysis()`**:**

Usage:

```
EvidenceSynthesisModule$createBayesianMetaAnalysis(
  chainLength = 1100000,
  burnIn = 1e+05,
  subSampleFrequency = 100,
  priorSd = c(2, 0.5),
  alpha = 0.05,
  robust = FALSE,
  df = 4,
  seed = 1,
  evidenceSynthesisAnalysisId = 1,
  evidenceSynthesisDescription = "Bayesian random-effects",
  evidenceSynthesisSource = NULL,
  controlType = "outcome"
)
```

Arguments:

`chainLength` Number of MCMC iterations.

`burnIn` Number of MCMC iterations to consider as burn in.

`subSampleFrequency` Subsample frequency for the MCMC.

`priorSd` A two-dimensional vector with the standard deviation of the prior for mu and tau, respectively.

`alpha` The alpha (expected type I error) used for the credible intervals.

`robust` Whether or not to use a t-distribution model; default: FALSE.

`df` Degrees of freedom for the t-model, only used if robust is TRUE.

`seed` The seed for the random number generator.

`evidenceSynthesisAnalysisId` description

`evidenceSynthesisDescription` description

`evidenceSynthesisSource` description

`controlType` description Create EvidenceSynthesis diagnostics thresholds

Details: Create an object defining the parameter values.

Method `createEsDiagnosticThresholds()`: Threshold used to determine if we pass or fail diagnostics.

Usage:

```
EvidenceSynthesisModule$createEsDiagnosticThresholds(
  mdrrThreshold = 10,
  easeThreshold = 0.25,
  i2Threshold = 0.4,
  tauThreshold = log(2)
)
```

Arguments:

`mdrrThreshold` What is the maximum allowed minimum detectable relative risk (MDRR)?

`easeThreshold` What is the maximum allowed expected absolute systematic error (EASE).

`i2Threshold` What is the maximum allowed I^2 (measure of between-database heterogeneity in random-effects models)?

`tauThreshold` What is the maximum allowed tau (measure of between-database heterogeneity in Bayesian random-effects models)?

Returns: An object of type `EsDiagnosticThresholds`.

Method `createModuleSpecifications()`: Creates the module Specifications

Usage:

```
EvidenceSynthesisModule$createModuleSpecifications(
  evidenceSynthesisAnalysisList,
  esDiagnosticThresholds = self$createEsDiagnosticThresholds()
)
```

Arguments:

`evidenceSynthesisAnalysisList` A list of objects of type `EvidenceSynthesisAnalysis` as generated by either the `EvidenceSynthesisModule$createFixedEffectsMetaAnalysis()` or `EvidenceSynthesisModule$createBayesianMetaAnalysis()` function.

`esDiagnosticThresholds` An object of type`EsDiagnosticThresholds` as generated by the `EvidenceSynthesisModule$createEsDiagnosticThresholds()` function.

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
EvidenceSynthesisModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`execute` *Execute analysis specifications.*

Description

Execute analysis specifications.

Usage

```
execute(analysisSpecifications, executionSettings, connectionDetails)
```

Arguments

`analysisSpecifications`
: An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecificiations`

`executionSettings`
: An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

`connectionDetails`
: An object of class `connectionDetails` as created by the `DatabaseConnector::createConnection` function.

Value

Returns a list of lists that contains

- moduleName: The name of the module executed
- result: The result of the execution. See purrr::safely for details on this result.
- executionTime: The time for the module to execute

`getCdmDatabaseMetaData` *Gets the metadata for your OMOP CDM Database*

Description

This function is used to gather metadata about your OMOP CDM and inspect for informational purposes. This information will be saved with your results when executing an analysis specification.

Usage

```
getCdmDatabaseMetaData(cdmExecutionSettings, connectionDetails)
```

Arguments

`cdmExecutionSettings`
: An object of type `CdmExecutionSettings` as created `createCdmExecutionSettings()`.

`connectionDetails`
: An object of class `connectionDetails` as created by the `DatabaseConnector::createConnection` function.

PatientLevelPredictionModule *Patient-level prediction with the* R*hrefhttps://ohdsi.github.io/PatientLevelPrediction/HADES PatientLevelPrediction Package*

Description

Module for performing patient-level prediction in an observational database in the OMOP Common Data Model.

Super class

`Strategus::StrategusModule` -> `PatientLevelPredictionModule`

Public fields

`tablePrefix` The table prefix to append to the results tables

Methods

Public methods:

- `PatientLevelPredictionModule$new()`
- `PatientLevelPredictionModule$execute()`
- `PatientLevelPredictionModule$createResultsDataModel()`
- `PatientLevelPredictionModule$getResultsDataModelSpecification()`
- `PatientLevelPredictionModule$uploadResults()`
- `PatientLevelPredictionModule$createModuleSpecifications()`
- `PatientLevelPredictionModule$validateModuleSpecifications()`
- `PatientLevelPredictionModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
PatientLevelPredictionModule$new()
```

Method `execute()`**:** Executes the PatientLevelPrediction package

Usage:

```
PatientLevelPredictionModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
PatientLevelPredictionModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = self$tablePrefix
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
PatientLevelPredictionModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
PatientLevelPredictionModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Creates the PatientLevelPrediction Module Specifications

Usage:

```
PatientLevelPredictionModule$createModuleSpecifications(modelDesignList)
```

Arguments:

`modelDesignList` A list of model designs created using `PatientLevelPrediction::createModelDesign()`

Method `validateModuleSpecifications()`**:** Validate the module specifications

Usage:

```
PatientLevelPredictionModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` The PatientLevelPrediction module specifications

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
PatientLevelPredictionModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`PatientLevelPredictionValidationModule` *Module for performing validation of patient-level prediction models*

Description

Module for performing patient-level prediction model validation for models built using the PatientLevelPrediction package.

Super class

`Strategus::StrategusModule` -> `PatientLevelPredictionValidationModule`

Public fields

`tablePrefix` The table prefix to append to the results tables

Methods

Public methods:

- `PatientLevelPredictionValidationModule$new()`
- `PatientLevelPredictionValidationModule$execute()`
- `PatientLevelPredictionValidationModule$createResultsDataModel()`
- `PatientLevelPredictionValidationModule$uploadResults()`
- `PatientLevelPredictionValidationModule$createModuleSpecifications()`
- `PatientLevelPredictionValidationModule$validateModuleSpecifications()`
- `PatientLevelPredictionValidationModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
PatientLevelPredictionValidationModule$new()
```

Method `execute()`**:** Executes the PatientLevelPrediction package to validate a PLP model

Usage:

```
PatientLevelPredictionValidationModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
PatientLevelPredictionValidationModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = self$tablePrefix
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
PatientLevelPredictionValidationModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`: Creates the PatientLevelPredictionValidation Module Specifications

Usage:

```
PatientLevelPredictionValidationModule$createModuleSpecifications(
  validationList = list(PatientLevelPrediction::createValidationDesign(plpModelList =
    list(file.path("location_to_model")), targetId = 1, outcomeId = 3,
   restrictPlpDataSettings = PatientLevelPrediction::createRestrictPlpDataSettings(),
   populationSettings = NULL, recalibrate = "weakRecalibration", runCovariateSummary =
    TRUE), PatientLevelPrediction::createValidationDesign(plpModelList =
    list(file.path("location_to_model")), targetId = 4, outcomeId = 3,
   restrictPlpDataSettings = PatientLevelPrediction::createRestrictPlpDataSettings(),

     populationSettings = NULL, recalibrate = "weakRecalibration", runCovariateSummary
    = TRUE)),
  logLevel = "INFO"
)
```

Arguments:

`validationList` A list of validation designs from `PatientLevelPrediction::createValidationDesign`

`logLevel` The logging level while executing the model validation.

Method `validateModuleSpecifications()`: Validate the module specifications

Usage:

```
PatientLevelPredictionValidationModule$validateModuleSpecifications(
  moduleSpecifications
)
```

Arguments:

`moduleSpecifications` The PatientLevelPredictionValidation module specifications

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
PatientLevelPredictionValidationModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`SelfControlledCaseSeriesModule` *Self-Controlled Case Series design with the* R*hrefhttps://ohdsi.github.io/SelfControlledCaseSeries/HADES SelfControlledCaseSeries Package*

Description

Module for performing Self-Controlled Case Series (SCCS) analyses against the OMOP Common Data Model.

Super class

`Strategus::StrategusModule` -> `SelfControlledCaseSeriesModule`

Public fields

`tablePrefix` The table prefix for results tables

Methods

Public methods:

- `SelfControlledCaseSeriesModule$new()`
- `SelfControlledCaseSeriesModule$execute()`
- `SelfControlledCaseSeriesModule$createResultsDataModel()`
- `SelfControlledCaseSeriesModule$getResultsDataModelSpecification()`
- `SelfControlledCaseSeriesModule$uploadResults()`
- `SelfControlledCaseSeriesModule$createModuleSpecifications()`
- `SelfControlledCaseSeriesModule$validateModuleSpecifications()`
- `SelfControlledCaseSeriesModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
SelfControlledCaseSeriesModule$new()
```

Method `execute()`**:** Executes the SelfControlledCaseSeries package

Usage:

```
SelfControlledCaseSeriesModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
SelfControlledCaseSeriesModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = ""
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
SelfControlledCaseSeriesModule$getResultsDataModelSpecification(
  tablePrefix = ""
)
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for the module

Usage:

```
SelfControlledCaseSeriesModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Creates the SelfControlledCaseSeries Module Specifications

Usage:

```
SelfControlledCaseSeriesModule$createModuleSpecifications(
  sccsAnalysisList,
  exposuresOutcomeList,
  analysesToExclude = NULL,
  combineDataFetchAcrossOutcomes = FALSE,
 sccsDiagnosticThresholds = SelfControlledCaseSeries::createSccsDiagnosticThresholds()
)
```

Arguments:

`sccsAnalysisList` description

`exposuresOutcomeList` description

`analysesToExclude` description

`combineDataFetchAcrossOutcomes` description

`sccsDiagnosticThresholds` description

Method `validateModuleSpecifications()`: Validate the module specifications

Usage:

```
SelfControlledCaseSeriesModule$validateModuleSpecifications(
  moduleSpecifications
)
```

Arguments:

`moduleSpecifications` The SelfControlledCaseSeries module specifications

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
SelfControlledCaseSeriesModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`StrategusModule` *StrategusModule defines the base class for each HADES module*

Description

StrategusModule serves as an internal base class that defines the core functions and structure to be inherited and implemented by any specific HADES module. It provides a standardized framework for creating modular components within the Strategus pipeline.

Public fields

`moduleName` The name of the module taken from the class name. This is set in the constructor of the class.

`moduleClassName` The class name that identifies the module specifications in the overall analysis specification. This is set in the constructor of the class.

`internalModuleSpecificationClassName` A constant value. The base class name that identifies a module specification in the analysis specification.

`internalSharedResourcesClassName` A constant value. The class name that identifies the shared resources section in the overall analysis specification.

Methods

Public methods:

- `StrategusModule$new()`
- `StrategusModule$execute()`
- `StrategusModule$createResultsDataModel()`
- `StrategusModule$getResultsDataModelSpecification()`
- `StrategusModule$uploadResults()`
- `StrategusModule$createModuleSpecifications()`
- `StrategusModule$createSharedResourcesSpecifications()`
- `StrategusModule$validateModuleSpecifications()`
- `StrategusModule$validateSharedResourcesSpecifications()`
- `StrategusModule$clone()`

Method `new()`: Initialize the module

Usage:

```
StrategusModule$new()
```

Method `execute()`: Executes the module

Usage:

```
StrategusModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`: Create the results data model for the module

Usage:

```
StrategusModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = ""
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`: Get the results data model specification for the module

Usage:

```
StrategusModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`: Upload the results for the module

Usage:

```
StrategusModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Base function for creating the module settings object. Each module will have its own implementation and this base class method will be used to ensure the class of the specifications is set properly.

Usage:

```
StrategusModule$createModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` An object of type `ModuleSpecifications`

`moduleSpecifications` An object of type `ModuleSpecifications`

Method `createSharedResourcesSpecifications()`**:** Base function for creating the shared resources settings object. Each module will have its own implementation if it needs to create a shared resource.

Usage:

```
StrategusModule$createSharedResourcesSpecifications(
  className,
  sharedResourcesSpecifications
)
```

Arguments:

`className` The class name of the shared resources specifications

`sharedResourcesSpecifications` The shared resources specifications

Method `validateModuleSpecifications()`**:** Base function for validating the module settings object. Each module will have its own implementation and this base class method will be used to ensure the module specifications are valid ahead of execution

Usage:

```
StrategusModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` An object of type `ModuleSpecifications`

`moduleSpecifications` An object of type `ModuleSpecifications`

Method `validateSharedResourcesSpecifications()`**:** Base function for validating the shared resources specification settings object. Each module will have its own implementation and this base class method will be used to ensure the module specifications are valid ahead of execution

Usage:

```
StrategusModule$validateSharedResourcesSpecifications(
  className,
  sharedResourcesSpecifications
)
```

Arguments:

`className` The class name of the shared resources specifications

`sharedResourcesSpecifications` The shared resources specifications

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
StrategusModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`TreatmentPatternsModule` *Evaluate phenotypes with the* R*hrefhttps://github.com/darwin-eu/TreatmentPatterns/DARWIN TreatmentPatterns Package*

Description

Characterization and description of patterns of events (cohorts). against the OMOP Common Data Model.

Super class

`Strategus::StrategusModule` -> `TreatmentPatternsModule`

Public fields

`tablePrefix` The table prefix to append to the results tables

Methods

Public methods:

- `TreatmentPatternsModule$new()`
- `TreatmentPatternsModule$execute()`
- `TreatmentPatternsModule$createResultsDataModel()`
- `TreatmentPatternsModule$getResultsDataModelSpecification()`
- `TreatmentPatternsModule$uploadResults()`
- `TreatmentPatternsModule$createModuleSpecifications()`
- `TreatmentPatternsModule$validateModuleSpecifications()`
- `TreatmentPatternsModule$clone()`

Method `new()`**:** Initialize the module

Usage:

```
TreatmentPatternsModule$new()
```

Method `execute()`**:** Execute Treatment Patterns

Usage:

```
TreatmentPatternsModule$execute(
  connectionDetails,
  analysisSpecifications,
  executionSettings
)
```

Arguments:

`connectionDetails` An object of class `connectionDetails` as created by the `DatabaseConnector::createConne` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`executionSettings` An object of type `ExecutionSettings` as created by `createCdmExecutionSettings()` or `createResultsExecutionSettings()`.

Method `createResultsDataModel()`**:** Create the results data model for the module

Usage:

```
TreatmentPatternsModule$createResultsDataModel(
  resultsConnectionDetails,
  resultsDatabaseSchema,
  tablePrefix = self$tablePrefix
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsDatabaseSchema` The schema in the results database that holds the results data model.

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `getResultsDataModelSpecification()`**:** Get the results data model specification for the module

Usage:

```
TreatmentPatternsModule$getResultsDataModelSpecification(tablePrefix = "")
```

Arguments:

`tablePrefix` A prefix to apply to the database table names (optional).

`tablePrefix` A prefix to apply to the database table names (optional).

Method `uploadResults()`**:** Upload the results for TreatmentPatterns

Usage:

```
TreatmentPatternsModule$uploadResults(
  resultsConnectionDetails,
  analysisSpecifications,
  resultsDataModelSettings
)
```

Arguments:

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`resultsConnectionDetails` The connection details to the results database which is an object of class `connectionDetails` as created by the `DatabaseConnector::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpec`

`resultsDataModelSettings` The results data model settings as created using [@seealso `createResultsDataModel`

Method `createModuleSpecifications()`**:** Creates the TreatmentPatternsnModule Specifications

Usage:

```
TreatmentPatternsModule$createModuleSpecifications(
  cohorts,
  includeTreatments = "startDate",
  indexDateOffset = 0,
  minEraDuration = 0,
  splitEventCohorts = NULL,
  splitTime = NULL,
  eraCollapseSize = 30,
  combinationWindow = 30,
  minPostCombinationDuration = 30,
  filterTreatments = "First",
  maxPathLength = 5,
  ageWindow = 5,
  minCellCount = 1,
  censorType = "minCellCount"
)
```

Arguments:

`cohorts (data.frame())`
Data frame containing the following columns and data types:

cohortId `numeric(1)` Cohort ID's of the cohorts to be used in the cohort table.

cohortName `character(1)` Cohort names of the cohorts to be used in the cohort table.

type `character(1)` **["target", "event', "exit"**] Cohort type, describing if the cohort is a target, event, or exit cohort

`includeTreatments (character(1): "startDate")`

`"startDate"` Include treatments after the target cohort start date and onwards.

`"endDate"` Include treatments before target cohort end date and before.

`indexDateOffset (integer(1): 0)`
Offset the index date of the `Target` cohort.

`minEraDuration (integer(1): 0)`
Minimum time an event era should last to be included in analysis

`splitEventCohorts (character(n): "")`
Specify event cohort to split in acute (< X days) and therapy (>= X days)

`splitTime (integer(1): 30)`
Specify number of days (X) at which each of the split event cohorts should be split in acute and therapy

`eraCollapseSize (integer(1): 30)`
Window of time between which two eras of the same event cohort are collapsed into one era

`combinationWindow (integer(1): 30)`
Window of time two event cohorts need to overlap to be considered a combination treatment

`minPostCombinationDuration (integer(1): 30)`
Minimum time an event era before or after a generated combination treatment should last to be included in analysis

`filterTreatments (character(1): "First" ["first", "Changes", "all"])`
Select first occurrence of ('First'); changes between ('Changes'); or all event cohorts ('All').

`maxPathLength (integer(1): 5)`
Maximum number of steps included in treatment pathway

`ageWindow (integer(n): 10)`
Number of years to bin age groups into. It may also be a vector of integers. I.e. `c(0, 18, 150)` which will results in age group `0-18` which includes subjects `< 19`. And age group `18-150` which includes subjects `> 18`.

`minCellCount (integer(1): 5)`
Minimum count required per pathway. Censors data below `x` as `<x`. This minimum value will carry over to the sankey diagram and sunburst plot.

`censorType (character(1))`

`"minCellCount"` Censors pathways `<minCellCount` to `minCellCount`.

`"remove"` Censors pathways `<minCellCount` by removing them completely.

`"mean"` Censors pathways `<minCellCount` to the mean of all frequencies below `minCellCount`

Method `validateModuleSpecifications()`**:** Validate the module specifications

Usage:

```
TreatmentPatternsModule$validateModuleSpecifications(moduleSpecifications)
```

Arguments:

`moduleSpecifications` The CohortMethod module specifications

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
TreatmentPatternsModule$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

`uploadResults` *Upload results*

Description

Upload the results for a given analysis

Usage

```
uploadResults(
  analysisSpecifications,
  resultsDataModelSettings,
  resultsConnectionDetails
)
```

Arguments

analysisSpecifications	An object of type AnalysisSpecifications as created by createEmptyAnalysisSpecificiations
resultsDataModelSettings	The results data model settings as created using [@seealso createResultsDataModelSettings()]
resultsConnectionDetails	The connection details to the results database which is an object of class connectionDetails as created by the DatabaseConnector::createConnectionDetails() function.

---

zipResults *Create a zip file with all study results for sharing with study coordinator*

Description

Create a zip file with all study results for sharing with study coordinator

Usage

```
zipResults(resultsFolder, zipFile)
```

Arguments

resultsFolder	The root folder holding the study results.
zipFile	The path to the zip file to be created.

Details

Creates a .zip file of the .csv files found in the resultsFolder. The resulting .zip file will have relative paths to the root of the resultsFolder which is generally found in executionSettings$resultsFolder.

Value

Does not return anything. Is called for the side-effect of creating the zip file with results.

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