

# 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,  
readr,  
ResultModelManager (>= 0.5.8),  
rlang,  
SqlRender (>= 1.18.0)

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

testthat (>= 3.0.0),  
withr

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

**License** Apache License 2.0

**VignetteBuilder** knitr

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

**BugReports** <https://github.com/OHDSI/Strategus/issues>

**NeedsCompilation** no

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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 `createEmptyAnalysisSpecifications`

## 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 [createEmptyAnalysisSpecifications\(\)](#)

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 [createEmptyAnalysisSpecifications\(\)](#)

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 [createEmptyAnalysisSpecifications](#)

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 [createEmptyAnalysisSpecifications](#)

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 [createEmptyAnalysisSpecifications](#)

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 [createEmptyAnalysisSpecifications](#)

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 [createEmptyAnalysisSpecifications](#)

moduleSpecifications

Created by the [PatientLevelPredictionModule\\$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 [createEmptyAnalysisSpecifications](#)

moduleSpecifications

Created by the [SelfControlledCaseSeriesModule\\$createModuleSpecifications\(\)](#) function.

**Value**

Returns the analysisSpecifications object with the module specifications added.

---

addSharedResources	<i>Add shared resources (i.e. cohorts) to analysis specifications</i>
--------------------	---

---

**Description**

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

**Usage**

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

**Arguments**

analysisSpecifications

An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications](#)

sharedResources

An object of type SharedResources.

**Value**

Returns the analysisSpecifications object with the module specifications added.

---

CharacterizationModule

*Characterize cohorts with the R*  
*<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::createConnectionDetails\(\)](#) function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by [createEmptyAnalysisSpecifications\(\)](#)

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by [createEmptyAnalysisSpecifications\(\)](#)

`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* [href=https://ohdsi.github.io/CohortDiagnostics/HADES](https://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::createConnectionDetails\(\)](#) function.

analysisSpecifications An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications\(\)](#)

analysisSpecifications An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications\(\)](#)

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](https://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::createConnectionDetails\(\)](#) function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by [createEmptyAnalysisSpecifications\(\)](#)

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by [createEmptyAnalysisSpecifications\(\)](#)

`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*[href="https://ohdsi.github.io/CohortIncidence/HADES"](https://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::createConnectionDetails` 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	<i>New-user</i>	<i>cohort</i>	<i>studies</i>	<i>with</i>	<i>the</i>
	<a href="https://ohdsi.github.io/CohortMethod/HADES">Rhrefhttps://ohdsi.github.io/CohortMethod/HADES</a>				
	<i>Package CohortMethod</i>				

---

## 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::createConnectionDetails\(\)](#) 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.

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::createCmDiagnosticThresholds`

*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::getCohortTableNames](#) 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.

---

createEmptyAnalysisSpecifications

*Create an empty analysis specifications object.*

---

**Description**

Create an empty analysis specifications object.

**Usage**

```
createEmptyAnalysisSpecifications()
```

**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 [createEmptyAnalysisSpecifications\(\)](#)

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")
)
```

**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

**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*  
*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::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecifications()`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecifications()`

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 "Cohort-Method" 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 computeFixedEffectMetaAnalysis

*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 computeBayesianMetaAnalysis

*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(
  mdrThreshold = 10,
  easeThreshold = 0.25,
  i2Threshold = 0.4,
  tauThreshold = log(2)
)
```

*Arguments:*

`mdrThreshold` 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 [createEmptyAnalysisSpecifications\(\)](#).

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*  
<https://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::createConnectionDetails()` function.

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecifications()`

`analysisSpecifications` An object of type `AnalysisSpecifications` as created by `createEmptyAnalysisSpecifications()`

`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.

---

SelfControlledCaseSeriesModule

*Self-Controlled Case Series design with the  
Rhref<https://ohdsi.github.io/SelfControlledCaseSeries/HADES>  
SelfControlledCaseSeries Package*

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**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::createConnectionDetails\(\)](#) function.

analysisSpecifications An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications\(\)](#)

analysisSpecifications An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications\(\)](#)

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.

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StrategusModule	<i>StrategusModule defines the base class for each HADES module</i>
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## 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::createConnectionDetails\(\)](#) function.

analysisSpecifications An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications\(\)](#)

analysisSpecifications An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications\(\)](#)

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 [createEmptyAnalysisSpecifications\(\)](#)

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.



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uploadResults	<i>Upload results</i>
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**Description**

Upload the results for a given analysis

**Usage**

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

**Arguments**

analysisSpecifications

An object of type AnalysisSpecifications as created by [createEmptyAnalysisSpecifications\(\)](#)

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.

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zipResults	<i>Create a zip file with all study results for sharing with study coordinator</i>
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**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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