

# Package ‘FeatureExtraction’

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**Type** Package

**Title** Generating Features for a Cohort

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**Description** An R package for generating features (covariates) for a cohort using data in the Common Data Model.

**Depends** R (>= 3.2.2),  
DatabaseConnector (>= 3.0.0),  
Andromeda

**Imports** methods,  
dplyr,  
rJava,  
jsonlite,  
SqlRender (>= 1.6.0),  
ParallelLogger (>= 2.0.2),  
cli,  
pillar,  
readr,  
rlang,  
RSQLite,  
DBI,  
checkmate

**Suggests** testthat,  
knitr,  
rmarkdown,  
Eunomia,  
withr

**Remotes** ohdsi/Eunomia

**License** Apache License 2.0

**VignetteBuilder** knitr

**URL** <https://github.com/OHDSI/FeatureExtraction>

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

**NeedsCompilation** no

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**Encoding** UTF-8**Language** en-US**R topics documented:**

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`.createLooCovariateSettings`*Get covariate settings***Description**

Get covariate settings

**Usage**

```
.createLooCovariateSettings(useLengthOfObs = TRUE)
```

**Arguments**

`useLengthOfObs` if length of observations should be used

**Value**

Returns an object of type `covariateSettings`, containing settings for the covariates.

**Examples**

```
## Not run:  
looCovariateSettings <- .createLooCovariateSettings(useLengthOfObs = TRUE)  
  
## End(Not run)
```

---

`.getDbLooCovariateData`

*Get covariate information from the database*

---

**Description**

Get covariate information from the database

**Usage**

```
.getDbLooCovariateData(  
  connection,  
  oracleTempSchema = NULL,  
  cdmDatabaseSchema,  
  cohortTable = "#cohort_person",  
  cohortIds = c(-1),  
  cdmVersion = "5",  
  rowIdField = "subject_id",  
  covariateSettings,  
  aggregated = FALSE,  
  minCharacterizationMean = 0  
)
```

**Arguments**

<code>connection</code>	A connection to the server containing the schema as created using the <code>connect</code> function in the <code>DatabaseConnector</code> package. Either the connection or <code>connectionDetails</code> argument should be specified.
<code>oracleTempSchema</code>	A schema where temp tables can be created in Oracle.

<code>cdmDatabaseSchema</code>	The name of the database schema that contains the OMOP CDM instance. Requires read permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.
<code>cohortTable</code>	Name of the (temp) table holding the cohort for which we want to construct covariates
<code>cohortIds</code>	For which cohort ID(s) should covariates be constructed? If set to -1, covariates will be constructed for all cohorts in the specified cohort table.
<code>cdmVersion</code>	Define the OMOP CDM version used: currently supported is "5".
<code>rowIdField</code>	The name of the field in the cohort table that is to be used as the row_id field in the output table. This can be especially usefull if there is more than one period per person.
<code>covariateSettings</code>	Either an object of type <code>covariateSettings</code> as created using one of the create-Covariate functions, or a list of such objects.
<code>aggregated</code>	Should aggregate statistics be computed instead of covariates per cohort entry?
<code>minCharacterizationMean</code>	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.

## Value

Returns an object of type `covariateData`, containing information on the covariates.

## Examples

```
## Not run:
eunomiaConnectionDetails <- Eunomia::getEunomiaConnectionDetails()
covSettings <- .createLooCovariateSettings(useLengthOfObs = TRUE)
Eunomia::createCohorts(
  connectionDetails = eunomiaConnectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
connection <- DatabaseConnector::connect(connectionDetails)
loocovariateData <- .getDbLooCovariateData(connection,
  oracleTempSchema = NULL,
  cdmDatabaseSchema = "main",
  cohortTable = "cohort",
  cohortId = 1,
  cdmVersion = "5",
  rowIdField = "subject_id",
  covariateSettings = covSettings,
  aggregated = FALSE
)

## End(Not run)
```

---

aggregateCovariates	<i>Aggregate covariate data</i>
---------------------	---------------------------------

---

**Description**

Aggregate covariate data

**Usage**

```
aggregateCovariates(covariateData)
```

**Arguments**

`covariateData` An object of type `covariateData` as generated using `getDbCovariateData`.

**Value**

An object of class `covariateData`.

**Examples**

```
## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)
aggregatedCovariateData <- aggregateCovariates(covariateData)

## End(Not run)
```

---

computeStandardizedDifference
-------------------------------

---

*Compute standardized difference of mean for all covariates.*

---

**Description**

Computes the standardized difference for all covariates between two cohorts. The standardized difference is defined as the difference between the mean divided by the overall standard deviation.

**Usage**

```
computeStandardizedDifference(
  covariateData1,
  covariateData2,
  cohortId1 = NULL,
  cohortId2 = NULL
)
```

**Arguments**

- covariateData1 The covariate data of the first cohort. Needs to be in aggregated format.
- covariateData2 The covariate data of the second cohort. Needs to be in aggregated format.
- cohortId1 If provided, covariateData1 will be restricted to this cohort. If not provided, covariateData1 is assumed to contain data on only 1 cohort.
- cohortId2 If provided, covariateData2 will be restricted to this cohort. If not provided, covariateData2 is assumed to contain data on only 1 cohort.

**Value**

A data frame with means and standard deviations per cohort as well as the standardized difference of mean.

**Examples**

```
## Not run:
binaryCovDataFile <- system.file("testdata/binaryCovariateData.zip",
  package = "FeatureExtraction"
)
covariateData1 <- loadCovariateData(binaryCovDataFile)
covariateData2 <- loadCovariateData(binaryCovDataFile)
covDataDiff <- computeStandardizedDifference(
  covariateData1,
  covariateData2,
  cohortId1 = 1,
  cohortId2 = 2
)

## End(Not run)
```

---

convertPrespecSettingsToDetailedSettings

*Convert prespecified covariate settings into detailed covariate settings*

---

**Description**

Convert prespecified covariate settings into detailed covariate settings

**Usage**

```
convertPrespecSettingsToDetailedSettings(covariateSettings)
```

**Arguments**

- covariateSettings
- An object of type covariateSettings as created for example by the [createCovariateSettings](#) function.

**Details**

For advanced users only.

**Value**

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

**Examples**

```
## Not run:
covSettings <- createDefaultCovariateSettings()
detailedSettings <- convertPrespecSettingsToDetailedSettings(covariateSettings = covSettings)

## End(Not run)
```

---

CovariateData-class	<i>Covariate Data</i>
---------------------	-----------------------

---

**Description**

CovariateData is an S4 class that inherits from [Andromeda](#). It contains information on covariates, which can be either captured on a per-person basis, or aggregated across the cohort(s).

By default covariates refer to a specific time period, with for example different covariate IDs for whether a diagnosis code was observed in the year before and month before index date. However, a CovariateData can also be temporal, meaning that next to a covariate ID there is also a time ID, which identifies the (user specified) time window the covariate was captured.

A CovariateData object is typically created using [getDbCovariateData](#), can only be saved using [saveCovariateData](#), and loaded using [loadCovariateData](#).

**Usage**

```
## S4 method for signature 'CovariateData'
show(object)

## S4 method for signature 'CovariateData'
summary(object)
```

**Arguments**

object	An object of class ‘CovariateData’.
--------	-------------------------------------

**See Also**

[isCovariateData](#), [isAggregatedCovariateData](#), [isTemporalCovariateData](#)

---

createAnalysisDetails *Create detailed covariate settings*

---

## Description

Create detailed covariate settings

## Usage

```
createAnalysisDetails(
  analysisId,
  sqlFileName,
  parameters,
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c()
)
```

## Arguments

analysisId	An integer between 0 and 999 that uniquely identifies this analysis.
sqlFileName	The name of the parameterized SQL file embedded in the featureExtraction package.
parameters	The list of parameter values used to render the template SQL.
includedCovariateConceptIds	A list of concept IDs that should be used to construct covariates.
addDescendantsToInclude	Should descendant concept IDs be added to the list of concepts to include?
excludedCovariateConceptIds	A list of concept IDs that should NOT be used to construct covariates.
addDescendantsToExclude	Should descendant concept IDs be added to the list of concepts to exclude?
includedCovariateIds	A list of covariate IDs that should be restricted to.

## Details

creates an object specifying in detail how covariates should be constructed from data in the CDM model. Warning: this function is for advanced users only.

## Value

An object of type analysisDetail, to be used in [createDetailedCovariateSettings](#) or [createDetailedTemporalC](#)



**Examples**

```
analysisDetails <- createAnalysisDetails(
  analysisId = 1,
  sqlFileName = "DemographicsGender.sql",
  parameters = list(
    analysisId = 1,
    analysisName = "Gender",
    domainId = "Demographics"
  ),
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c()
)
```

---

```
createCohortAttrCovariateSettings
```

*Create cohort attribute covariate settings*

---

**Description**

Create cohort attribute covariate settings

**Usage**

```
createCohortAttrCovariateSettings(
  analysisId = -1,
  attrDatabaseSchema,
  attrDefinitionTable = "attribute_definition",
  cohortAttrTable = "cohort_attribute",
  includeAttrIds = c(),
  isBinary = FALSE,
  missingMeansZero = FALSE
)
```

**Arguments**

analysisId	A unique identifier for this analysis.
attrDatabaseSchema	The database schema where the attribute definition and cohort attribute table can be found.
attrDefinitionTable	The name of the attribute definition table.
cohortAttrTable	The name of the cohort attribute table.
includeAttrIds	(optional) A list of attribute definition IDs to restrict to.
isBinary	Needed for aggregation: Are these binary variables? Binary variables should only have the values 0 or 1.
missingMeansZero	Needed for aggregation: For continuous values, should missing values be interpreted as 0?

**Details**

Creates an object specifying where the cohort attributes can be found to construct covariates. The attributes should be defined in a table with the same structure as the `attribute_definition` table in the Common Data Model. It should at least have these columns:

**attribute\_definition\_id** A unique identifier of type integer.

**attribute\_name** A short description of the attribute.

The cohort attributes themselves should be stored in a table with the same format as the `cohort_attribute` table in the Common Data Model. It should at least have these columns:

**cohort\_definition\_id** A key to link to the cohort table.

**subject\_id** A key to link to the cohort table.

**cohort\_start\_date** A key to link to the cohort table.

**attribute\_definition\_id** An foreign key linking to the attribute definition table.

**value\_as\_number** A real number.

**Value**

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

**Examples**

```
## Not run:
covariateSettings <- createCohortAttrCovariateSettings(
  analysisId = 1,
  attrDatabaseSchema = "main",
  attrDefinitionTable = "attribute_definition",
  cohortAttrTable = "cohort_attribute",
  includeAttrIds = c(1),
  isBinary = FALSE,
  missingMeansZero = FALSE
)

## End(Not run)
```

---

```
createCohortBasedCovariateSettings
```

*Create settings for covariates based on other cohorts*

---

**Description**

Create settings for covariates based on other cohorts

**Usage**

```
createCohortBasedCovariateSettings(
  analysisId,
  covariateCohortDatabaseSchema = NULL,
  covariateCohortTable = NULL,
  covariateCohorts,
  valueType = "binary",
  startDay = -365,
  endDay = 0,
  includedCovariateIds = c(),
  warnOnAnalysisIdOverlap = TRUE
)
```

**Arguments**

<code>analysisId</code>	A unique identifier for this analysis.
<code>covariateCohortDatabaseSchema</code>	The database schema where the cohorts used to define the covariates can be found. If set to <code>NULL</code> , the database schema will be guessed, for example using the same one as for the main cohorts.
<code>covariateCohortTable</code>	The table where the cohorts used to define the covariates can be found. If set to <code>NULL</code> , the table will be guessed, for example using the same one as for the main cohorts.
<code>covariateCohorts</code>	A data frame with at least two columns: <code>'cohortId'</code> and <code>'cohortName'</code> . The cohort ID should correspond to the <code>cohort_definition_id</code> of the cohort to use for creating a covariate.
<code>valueType</code>	Either <code>'binary'</code> or <code>'count'</code> . When <code>valueType = 'count'</code> , the covariate value will be the number of times the cohort was observed in the window.
<code>startDay</code>	What is the start day (relative to the index date) of the covariate window?
<code>endDay</code>	What is the end day (relative to the index date) of the covariate window?
<code>includedCovariateIds</code>	A list of covariate IDs that should be restricted to.
<code>warnOnAnalysisIdOverlap</code>	Warn if the provided <code>'analysisId'</code> overlaps with any predefined analysis as available in the <code>'createCovariateSettings()'</code> function.

**Details**

Creates an object specifying covariates to be constructed based on the presence of other cohorts.

**Value**

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

---

```
createCohortBasedTemporalCovariateSettings
```

*Create settings for temporal covariates based on other cohorts*

---

## Description

Create settings for temporal covariates based on other cohorts

## Usage

```
createCohortBasedTemporalCovariateSettings(
  analysisId,
  covariateCohortDatabaseSchema = NULL,
  covariateCohortTable = NULL,
  covariateCohorts,
  valueType = "binary",
  temporalStartDays = -365:-1,
  temporalEndDays = -365:-1,
  includedCovariateIds = c(),
  warnOnAnalysisIdOverlap = TRUE
)
```

## Arguments

<code>analysisId</code>	A unique identifier for this analysis.
<code>covariateCohortDatabaseSchema</code>	The database schema where the cohorts used to define the covariates can be found. If set to <code>NULL</code> , the database schema will be guessed, for example using the same one as for the main cohorts.
<code>covariateCohortTable</code>	The table where the cohorts used to define the covariates can be found. If set to <code>NULL</code> , the table will be guessed, for example using the same one as for the main cohorts.
<code>covariateCohorts</code>	A data frame with at least two columns: <code>'cohortId'</code> and <code>'cohortName'</code> . The cohort ID should correspond to the <code>cohort_definition_id</code> of the cohort to use for creating a covariate.
<code>valueType</code>	Either <code>'binary'</code> or <code>'count'</code> . When <code>valueType = 'count'</code> , the covariate value will be the number of times the cohort was observed in the window.
<code>temporalStartDays</code>	A list of integers representing the start of a time period, relative to the index date. 0 indicates the index date, -1 indicates the day before the index date, etc. The start day is included in the time period.
<code>temporalEndDays</code>	A list of integers representing the end of a time period, relative to the index date. 0 indicates the index date, -1 indicates the day before the index date, etc. The end day is included in the time period.
<code>includedCovariateIds</code>	A list of covariate IDs that should be restricted to.
<code>warnOnAnalysisIdOverlap</code>	Warn if the provided <code>'analysisId'</code> overlaps with any predefined analysis as available in the <code>'createTemporalCovariateSettings()'</code> function.

**Details**

Creates an object specifying temporal covariates to be constructed based on the presence of other cohorts.

**Value**

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

---

```
createCovariateSettings
```

*Create covariate settings*

---

**Description**

Create covariate settings

**Usage**

```
createCovariateSettings(
  useDemographicsGender = FALSE,
  useDemographicsAge = FALSE,
  useDemographicsAgeGroup = FALSE,
  useDemographicsRace = FALSE,
  useDemographicsEthnicity = FALSE,
  useDemographicsIndexYear = FALSE,
  useDemographicsIndexMonth = FALSE,
  useDemographicsPriorObservationTime = FALSE,
  useDemographicsPostObservationTime = FALSE,
  useDemographicsTimeInCohort = FALSE,
  useDemographicsIndexYearMonth = FALSE,
  useCareSiteId = FALSE,
  useConditionOccurrenceAnyTimePrior = FALSE,
  useConditionOccurrenceLongTerm = FALSE,
  useConditionOccurrenceMediumTerm = FALSE,
  useConditionOccurrenceShortTerm = FALSE,
  useConditionOccurrencePrimaryInpatientAnyTimePrior = FALSE,
  useConditionOccurrencePrimaryInpatientLongTerm = FALSE,
  useConditionOccurrencePrimaryInpatientMediumTerm = FALSE,
  useConditionOccurrencePrimaryInpatientShortTerm = FALSE,
  useConditionEraAnyTimePrior = FALSE,
  useConditionEraLongTerm = FALSE,
  useConditionEraMediumTerm = FALSE,
  useConditionEraShortTerm = FALSE,
  useConditionEraOverlapping = FALSE,
  useConditionEraStartLongTerm = FALSE,
  useConditionEraStartMediumTerm = FALSE,
  useConditionEraStartShortTerm = FALSE,
  useConditionGroupEraAnyTimePrior = FALSE,
  useConditionGroupEraLongTerm = FALSE,
  useConditionGroupEraMediumTerm = FALSE,
  useConditionGroupEraShortTerm = FALSE,
```

```
useConditionGroupEraOverlapping = FALSE,
useConditionGroupEraStartLongTerm = FALSE,
useConditionGroupEraStartMediumTerm = FALSE,
useConditionGroupEraStartShortTerm = FALSE,
useDrugExposureAnyTimePrior = FALSE,
useDrugExposureLongTerm = FALSE,
useDrugExposureMediumTerm = FALSE,
useDrugExposureShortTerm = FALSE,
useDrugEraAnyTimePrior = FALSE,
useDrugEraLongTerm = FALSE,
useDrugEraMediumTerm = FALSE,
useDrugEraShortTerm = FALSE,
useDrugEraOverlapping = FALSE,
useDrugEraStartLongTerm = FALSE,
useDrugEraStartMediumTerm = FALSE,
useDrugEraStartShortTerm = FALSE,
useDrugGroupEraAnyTimePrior = FALSE,
useDrugGroupEraLongTerm = FALSE,
useDrugGroupEraMediumTerm = FALSE,
useDrugGroupEraShortTerm = FALSE,
useDrugGroupEraOverlapping = FALSE,
useDrugGroupEraStartLongTerm = FALSE,
useDrugGroupEraStartMediumTerm = FALSE,
useDrugGroupEraStartShortTerm = FALSE,
useProcedureOccurrenceAnyTimePrior = FALSE,
useProcedureOccurrenceLongTerm = FALSE,
useProcedureOccurrenceMediumTerm = FALSE,
useProcedureOccurrenceShortTerm = FALSE,
useDeviceExposureAnyTimePrior = FALSE,
useDeviceExposureLongTerm = FALSE,
useDeviceExposureMediumTerm = FALSE,
useDeviceExposureShortTerm = FALSE,
useMeasurementAnyTimePrior = FALSE,
useMeasurementLongTerm = FALSE,
useMeasurementMediumTerm = FALSE,
useMeasurementShortTerm = FALSE,
useMeasurementValueAnyTimePrior = FALSE,
useMeasurementValueLongTerm = FALSE,
useMeasurementValueMediumTerm = FALSE,
useMeasurementValueShortTerm = FALSE,
useMeasurementRangeGroupAnyTimePrior = FALSE,
useMeasurementRangeGroupLongTerm = FALSE,
useMeasurementRangeGroupMediumTerm = FALSE,
useMeasurementRangeGroupShortTerm = FALSE,
useObservationAnyTimePrior = FALSE,
useObservationLongTerm = FALSE,
useObservationMediumTerm = FALSE,
useObservationShortTerm = FALSE,
useCharlsonIndex = FALSE,
useDcsi = FALSE,
useChads2 = FALSE,
useChads2Vasc = FALSE,
```

```

useHfrs = FALSE,
useDistinctConditionCountLongTerm = FALSE,
useDistinctConditionCountMediumTerm = FALSE,
useDistinctConditionCountShortTerm = FALSE,
useDistinctIngredientCountLongTerm = FALSE,
useDistinctIngredientCountMediumTerm = FALSE,
useDistinctIngredientCountShortTerm = FALSE,
useDistinctProcedureCountLongTerm = FALSE,
useDistinctProcedureCountMediumTerm = FALSE,
useDistinctProcedureCountShortTerm = FALSE,
useDistinctMeasurementCountLongTerm = FALSE,
useDistinctMeasurementCountMediumTerm = FALSE,
useDistinctMeasurementCountShortTerm = FALSE,
useDistinctObservationCountLongTerm = FALSE,
useDistinctObservationCountMediumTerm = FALSE,
useDistinctObservationCountShortTerm = FALSE,
useVisitCountLongTerm = FALSE,
useVisitCountMediumTerm = FALSE,
useVisitCountShortTerm = FALSE,
useVisitConceptCountLongTerm = FALSE,
useVisitConceptCountMediumTerm = FALSE,
useVisitConceptCountShortTerm = FALSE,
longTermStartDays = -365,
mediumTermStartDays = -180,
shortTermStartDays = -30,
endDays = 0,
includedCovariateConceptIds = c(),
addDescendantsToInclude = FALSE,
excludedCovariateConceptIds = c(),
addDescendantsToExclude = FALSE,
includedCovariateIds = c()
)

```

## Arguments

```

useDemographicsGender
    Gender of the subject. (analysis ID 1)
useDemographicsAge
    Age of the subject on the index date (in years). (analysis ID 2)
useDemographicsAgeGroup
    Age of the subject on the index date (in 5 year age groups) (analysis ID 3)
useDemographicsRace
    Race of the subject. (analysis ID 4)
useDemographicsEthnicity
    Ethnicity of the subject. (analysis ID 5)
useDemographicsIndexYear
    Year of the index date. (analysis ID 6)
useDemographicsIndexMonth
    Month of the index date. (analysis ID 7)
useDemographicsPriorObservationTime
    Number of continuous days of observation time preceding the index date. (analysis ID 8)

```

`useDemographicsPostObservationTime`  
 Number of continuous days of observation time following the index date. (analysis ID 9)

`useDemographicsTimeInCohort`  
 Number of days of observation time during cohort period. (analysis ID 10)

`useDemographicsIndexYearMonth`  
 Both calendar year and month of the index date in a single variable. (analysis ID 11)

`useCareSiteId` Care site associated with the cohort start, pulled from the `visit_detail`, `visit_occurrence`, or `person` table, in that order. (analysis ID 12)

`useConditionOccurrenceAnyTimePrior`  
 One covariate per condition in the `condition_occurrence` table starting any time prior to index. (analysis ID 101)

`useConditionOccurrenceLongTerm`  
 One covariate per condition in the `condition_occurrence` table starting in the long term window. (analysis ID 102)

`useConditionOccurrenceMediumTerm`  
 One covariate per condition in the `condition_occurrence` table starting in the medium term window. (analysis ID 103)

`useConditionOccurrenceShortTerm`  
 One covariate per condition in the `condition_occurrence` table starting in the short term window. (analysis ID 104)

`useConditionOccurrencePrimaryInpatientAnyTimePrior`  
 One covariate per condition observed as a primary diagnosis in an inpatient setting in the `condition_occurrence` table starting any time prior to index. (analysis ID 105)

`useConditionOccurrencePrimaryInpatientLongTerm`  
 One covariate per condition observed as a primary diagnosis in an inpatient setting in the `condition_occurrence` table starting in the long term window. (analysis ID 106)

`useConditionOccurrencePrimaryInpatientMediumTerm`  
 One covariate per condition observed as a primary diagnosis in an inpatient setting in the `condition_occurrence` table starting in the medium term window. (analysis ID 107)

`useConditionOccurrencePrimaryInpatientShortTerm`  
 One covariate per condition observed as a primary diagnosis in an inpatient setting in the `condition_occurrence` table starting in the short term window. (analysis ID 108)

`useConditionEraAnyTimePrior`  
 One covariate per condition in the `condition_era` table overlapping with any time prior to index. (analysis ID 201)

`useConditionEraLongTerm`  
 One covariate per condition in the `condition_era` table overlapping with any part of the long term window. (analysis ID 202)

`useConditionEraMediumTerm`  
 One covariate per condition in the `condition_era` table overlapping with any part of the medium term window. (analysis ID 203)

`useConditionEraShortTerm`  
 One covariate per condition in the `condition_era` table overlapping with any part of the short term window. (analysis ID 204)



useConditionEraOverlapping	One covariate per condition in the condition_era table overlapping with the end of the risk window. (analysis ID 205)
useConditionEraStartLongTerm	One covariate per condition in the condition_era table starting in the long term window. (analysis ID 206)
useConditionEraStartMediumTerm	One covariate per condition in the condition_era table starting in the medium term window. (analysis ID 207)
useConditionEraStartShortTerm	One covariate per condition in the condition_era table starting in the short term window. (analysis ID 208)
useConditionGroupEraAnyTimePrior	One covariate per condition era rolled up to groups in the condition_era table overlapping with any time prior to index. (analysis ID 209)
useConditionGroupEraLongTerm	One covariate per condition era rolled up to groups in the condition_era table overlapping with any part of the long term window. (analysis ID 210)
useConditionGroupEraMediumTerm	One covariate per condition era rolled up to groups in the condition_era table overlapping with any part of the medium term window. (analysis ID 211)
useConditionGroupEraShortTerm	One covariate per condition era rolled up to groups in the condition_era table overlapping with any part of the short term window. (analysis ID 212)
useConditionGroupEraOverlapping	One covariate per condition era rolled up to groups in the condition_era table overlapping with the end of the risk window. (analysis ID 213)
useConditionGroupEraStartLongTerm	One covariate per condition era rolled up to groups in the condition_era table starting in the long term window. (analysis ID 214)
useConditionGroupEraStartMediumTerm	One covariate per condition era rolled up to groups in the condition_era table starting in the medium term window. (analysis ID 215)
useConditionGroupEraStartShortTerm	One covariate per condition era rolled up to groups in the condition_era table starting in the short term window. (analysis ID 216)
useDrugExposureAnyTimePrior	One covariate per drug in the drug_exposure table starting any time prior to index. (analysis ID 301)
useDrugExposureLongTerm	One covariate per drug in the drug_exposure table starting in the long term window. (analysis ID 302)
useDrugExposureMediumTerm	One covariate per drug in the drug_exposure table starting in the medium term window. (analysis ID 303)
useDrugExposureShortTerm	One covariate per drug in the drug_exposure table starting in the short term window. (analysis ID 304)
useDrugEraAnyTimePrior	One covariate per drug in the drug_era table overlapping with any time prior to index. (analysis ID 401)

`useDrugEraLongTerm`  
One covariate per drug in the `drug_era` table overlapping with any part of the long term window. (analysis ID 402)

`useDrugEraMediumTerm`  
One covariate per drug in the `drug_era` table overlapping with any part of the medium term window. (analysis ID 403)

`useDrugEraShortTerm`  
One covariate per drug in the `drug_era` table overlapping with any part of the short window. (analysis ID 404)

`useDrugEraOverlapping`  
One covariate per drug in the `drug_era` table overlapping with the end of the risk window. (analysis ID 405)

`useDrugEraStartLongTerm`  
One covariate per drug in the `drug_era` table starting in the long term window. (analysis ID 406)

`useDrugEraStartMediumTerm`  
One covariate per drug in the `drug_era` table starting in the medium term window. (analysis ID 407)

`useDrugEraStartShortTerm`  
One covariate per drug in the `drug_era` table starting in the long short window. (analysis ID 408)

`useDrugGroupEraAnyTimePrior`  
One covariate per drug rolled up to ATC groups in the `drug_era` table overlapping with any time prior to index. (analysis ID 409)

`useDrugGroupEraLongTerm`  
One covariate per drug rolled up to ATC groups in the `drug_era` table overlapping with any part of the long term window. (analysis ID 410)

`useDrugGroupEraMediumTerm`  
One covariate per drug rolled up to ATC groups in the `drug_era` table overlapping with any part of the medium term window. (analysis ID 411)

`useDrugGroupEraShortTerm`  
One covariate per drug rolled up to ATC groups in the `drug_era` table overlapping with any part of the short term window. (analysis ID 412)

`useDrugGroupEraOverlapping`  
One covariate per drug rolled up to ATC groups in the `drug_era` table overlapping with the end of the risk window. (analysis ID 413)

`useDrugGroupEraStartLongTerm`  
One covariate per drug rolled up to ATC groups in the `drug_era` table starting in the long term window. (analysis ID 414)

`useDrugGroupEraStartMediumTerm`  
One covariate per drug rolled up to ATC groups in the `drug_era` table starting in the medium term window. (analysis ID 415)

`useDrugGroupEraStartShortTerm`  
One covariate per drug rolled up to ATC groups in the `drug_era` table starting in the short term window. (analysis ID 416)

`useProcedureOccurrenceAnyTimePrior`  
One covariate per procedure in the `procedure_occurrence` table any time prior to index. (analysis ID 501)

`useProcedureOccurrenceLongTerm`  
One covariate per procedure in the `procedure_occurrence` table in the long term window. (analysis ID 502)

useProcedureOccurrenceMediumTerm	One covariate per procedure in the procedure_occurrence table in the medium term window. (analysis ID 503)
useProcedureOccurrenceShortTerm	One covariate per procedure in the procedure_occurrence table in the short term window. (analysis ID 504)
useDeviceExposureAnyTimePrior	One covariate per device in the device exposure table starting any time prior to index. (analysis ID 601)
useDeviceExposureLongTerm	One covariate per device in the device exposure table starting in the long term window. (analysis ID 602)
useDeviceExposureMediumTerm	One covariate per device in the device exposure table starting in the medium term window. (analysis ID 603)
useDeviceExposureShortTerm	One covariate per device in the device exposure table starting in the short term window. (analysis ID 604)
useMeasurementAnyTimePrior	One covariate per measurement in the measurement table any time prior to index. (analysis ID 701)
useMeasurementLongTerm	One covariate per measurement in the measurement table in the long term window. (analysis ID 702)
useMeasurementMediumTerm	One covariate per measurement in the measurement table in the medium term window. (analysis ID 703)
useMeasurementShortTerm	One covariate per measurement in the measurement table in the short term window. (analysis ID 704)
useMeasurementValueAnyTimePrior	One covariate containing the value per measurement-unit combination any time prior to index. (analysis ID 705)
useMeasurementValueLongTerm	One covariate containing the value per measurement-unit combination in the long term window. (analysis ID 706)
useMeasurementValueMediumTerm	One covariate containing the value per measurement-unit combination in the medium term window. (analysis ID 707)
useMeasurementValueShortTerm	One covariate containing the value per measurement-unit combination in the short term window. (analysis ID 708)
useMeasurementRangeGroupAnyTimePrior	Covariates indicating whether measurements are below, within, or above normal range any time prior to index. (analysis ID 709)
useMeasurementRangeGroupLongTerm	Covariates indicating whether measurements are below, within, or above normal range in the long term window. (analysis ID 710)
useMeasurementRangeGroupMediumTerm	Covariates indicating whether measurements are below, within, or above normal range in the medium term window. (analysis ID 711)

<code>useMeasurementRangeGroupShortTerm</code>	Covariates indicating whether measurements are below, within, or above normal range in the short term window. (analysis ID 712)
<code>useObservationAnyTimePrior</code>	One covariate per observation in the observation table any time prior to index. (analysis ID 801)
<code>useObservationLongTerm</code>	One covariate per observation in the observation table in the long term window. (analysis ID 802)
<code>useObservationMediumTerm</code>	One covariate per observation in the observation table in the medium term window. (analysis ID 803)
<code>useObservationShortTerm</code>	One covariate per observation in the observation table in the short term window. (analysis ID 804)
<code>useCharlsonIndex</code>	The Charlson comorbidity index (Romano adaptation) using all conditions prior to the window end. (analysis ID 901)
<code>useDcsi</code>	The Diabetes Comorbidity Severity Index (DCSI) using all conditions prior to the window end. (analysis ID 902)
<code>useChads2</code>	The CHADS2 score using all conditions prior to the window end. (analysis ID 903)
<code>useChads2Vasc</code>	The CHADS2VAsC score using all conditions prior to the window end. (analysis ID 904)
<code>useHfrs</code>	The Hospital Frailty Risk Score score using all conditions prior to the window end. (analysis ID 926)
<code>useDistinctConditionCountLongTerm</code>	The number of distinct condition concepts observed in the long term window. (analysis ID 905)
<code>useDistinctConditionCountMediumTerm</code>	The number of distinct condition concepts observed in the medium term window. (analysis ID 906)
<code>useDistinctConditionCountShortTerm</code>	The number of distinct condition concepts observed in the short term window. (analysis ID 907)
<code>useDistinctIngredientCountLongTerm</code>	The number of distinct ingredients observed in the long term window. (analysis ID 908)
<code>useDistinctIngredientCountMediumTerm</code>	The number of distinct ingredients observed in the medium term window. (analysis ID 909)
<code>useDistinctIngredientCountShortTerm</code>	The number of distinct ingredients observed in the short term window. (analysis ID 910)
<code>useDistinctProcedureCountLongTerm</code>	The number of distinct procedures observed in the long term window. (analysis ID 911)
<code>useDistinctProcedureCountMediumTerm</code>	The number of distinct procedures observed in the medium term window. (analysis ID 912)

useDistinctProcedureCountShortTerm  
 The number of distinct procedures observed in the short term window. (analysis ID 913)

useDistinctMeasurementCountLongTerm  
 The number of distinct measurements observed in the long term window. (analysis ID 914)

useDistinctMeasurementCountMediumTerm  
 The number of distinct measurements observed in the medium term window. (analysis ID 915)

useDistinctMeasurementCountShortTerm  
 The number of distinct measurements observed in the short term window. (analysis ID 916)

useDistinctObservationCountLongTerm  
 The number of distinct observations observed in the long term window. (analysis ID 917)

useDistinctObservationCountMediumTerm  
 The number of distinct observations observed in the medium term window. (analysis ID 918)

useDistinctObservationCountShortTerm  
 The number of distinct observations observed in the short term window. (analysis ID 919)

useVisitCountLongTerm  
 The number of visits observed in the long term window. (analysis ID 920)

useVisitCountMediumTerm  
 The number of visits observed in the medium term window. (analysis ID 921)

useVisitCountShortTerm  
 The number of visits observed in the short term window. (analysis ID 922)

useVisitConceptCountLongTerm  
 The number of visits observed in the long term window, stratified by visit concept ID. (analysis ID 923)

useVisitConceptCountMediumTerm  
 The number of visits observed in the medium term window, stratified by visit concept ID. (analysis ID 924)

useVisitConceptCountShortTerm  
 The number of visits observed in the short term window, stratified by visit concept ID. (analysis ID 925)

longTermStartDays  
 What is the start day (relative to the index date) of the long-term window?

mediumTermStartDays  
 What is the start day (relative to the index date) of the medium-term window?

shortTermStartDays  
 What is the start day (relative to the index date) of the short-term window?

endDays  
 What is the end day (relative to the index date) of the window?

includedCovariateConceptIds  
 A list of concept IDs that should be used to construct covariates.

addDescendantsToInclude  
 Should descendant concept IDs be added to the list of concepts to include?

excludedCovariateConceptIds  
 A list of concept IDs that should NOT be used to construct covariates.

addDescendantsToExclude

Should descendant concept IDs be added to the list of concepts to exclude?

includedCovariateIds

A list of covariate IDs that should be restricted to.

## Details

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

## Value

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

## Examples

```
settings <- createCovariateSettings(
  useDemographicsGender = TRUE,
  useDemographicsAge = FALSE,
  useDemographicsAgeGroup = TRUE,
  useDemographicsRace = TRUE,
  useDemographicsEthnicity = TRUE,
  useDemographicsIndexYear = TRUE,
  useDemographicsIndexMonth = TRUE,
  useDemographicsPriorObservationTime = FALSE,
  useDemographicsPostObservationTime = FALSE,
  useDemographicsTimeInCohort = FALSE,
  useDemographicsIndexYearMonth = FALSE,
  useCareSiteId = FALSE,
  useConditionOccurrenceAnyTimePrior = FALSE,
  useConditionOccurrenceLongTerm = FALSE,
  useConditionOccurrenceMediumTerm = FALSE,
  useConditionOccurrenceShortTerm = FALSE,
  useConditionOccurrencePrimaryInpatientAnyTimePrior = FALSE,
  useConditionOccurrencePrimaryInpatientLongTerm = FALSE,
  useConditionOccurrencePrimaryInpatientMediumTerm = FALSE,
  useConditionOccurrencePrimaryInpatientShortTerm = FALSE,
  useConditionEraAnyTimePrior = FALSE,
  useConditionEraLongTerm = FALSE,
  useConditionEraMediumTerm = FALSE,
  useConditionEraShortTerm = FALSE,
  useConditionEraOverlapping = FALSE,
  useConditionEraStartLongTerm = FALSE,
  useConditionEraStartMediumTerm = FALSE,
  useConditionEraStartShortTerm = FALSE,
  useConditionGroupEraAnyTimePrior = FALSE,
  useConditionGroupEraLongTerm = TRUE,
  useConditionGroupEraMediumTerm = FALSE,
  useConditionGroupEraShortTerm = TRUE,
  useConditionGroupEraOverlapping = FALSE,
  useConditionGroupEraStartLongTerm = FALSE,
  useConditionGroupEraStartMediumTerm = FALSE,
  useConditionGroupEraStartShortTerm = FALSE,
  useDrugExposureAnyTimePrior = FALSE,
  useDrugExposureLongTerm = FALSE,
  useDrugExposureMediumTerm = FALSE,
  useDrugExposureShortTerm = FALSE,
  useDrugEraAnyTimePrior = FALSE,
```

```
useDrugEraLongTerm = FALSE,
useDrugEraMediumTerm = FALSE,
useDrugEraShortTerm = FALSE,
useDrugEraOverlapping = FALSE,
useDrugEraStartLongTerm = FALSE,
useDrugEraStartMediumTerm = FALSE,
useDrugEraStartShortTerm = FALSE,
useDrugGroupEraAnyTimePrior = FALSE,
useDrugGroupEraLongTerm = TRUE,
useDrugGroupEraMediumTerm = FALSE,
useDrugGroupEraShortTerm = TRUE,
useDrugGroupEraOverlapping = TRUE,
useDrugGroupEraStartLongTerm = FALSE,
useDrugGroupEraStartMediumTerm = FALSE,
useDrugGroupEraStartShortTerm = FALSE,
useProcedureOccurrenceAnyTimePrior = FALSE,
useProcedureOccurrenceLongTerm = TRUE,
useProcedureOccurrenceMediumTerm = FALSE,
useProcedureOccurrenceShortTerm = TRUE,
useDeviceExposureAnyTimePrior = FALSE,
useDeviceExposureLongTerm = TRUE,
useDeviceExposureMediumTerm = FALSE,
useDeviceExposureShortTerm = TRUE,
useMeasurementAnyTimePrior = FALSE,
useMeasurementLongTerm = TRUE,
useMeasurementMediumTerm = FALSE,
useMeasurementShortTerm = TRUE,
useMeasurementValueAnyTimePrior = FALSE,
useMeasurementValueLongTerm = FALSE,
useMeasurementValueMediumTerm = FALSE,
useMeasurementValueShortTerm = FALSE,
useMeasurementRangeGroupAnyTimePrior = FALSE,
useMeasurementRangeGroupLongTerm = TRUE,
useMeasurementRangeGroupMediumTerm = FALSE,
useMeasurementRangeGroupShortTerm = FALSE,
useObservationAnyTimePrior = FALSE,
useObservationLongTerm = TRUE,
useObservationMediumTerm = FALSE,
useObservationShortTerm = TRUE,
useCharlsonIndex = TRUE,
useDcsi = TRUE,
useChads2 = TRUE,
useChads2Vasc = TRUE,
useHfrs = FALSE,
useDistinctConditionCountLongTerm = FALSE,
useDistinctConditionCountMediumTerm = FALSE,
useDistinctConditionCountShortTerm = FALSE,
useDistinctIngredientCountLongTerm = FALSE,
useDistinctIngredientCountMediumTerm = FALSE,
useDistinctIngredientCountShortTerm = FALSE,
useDistinctProcedureCountLongTerm = FALSE,
useDistinctProcedureCountMediumTerm = FALSE,
useDistinctProcedureCountShortTerm = FALSE,
useDistinctMeasurementCountLongTerm = FALSE,
useDistinctMeasurementCountMediumTerm = FALSE,
useDistinctMeasurementCountShortTerm = FALSE,
useDistinctObservationCountLongTerm = FALSE,
```

```

useDistinctObservationCountMediumTerm = FALSE,
useDistinctObservationCountShortTerm = FALSE,
useVisitCountLongTerm = FALSE,
useVisitCountMediumTerm = FALSE,
useVisitCountShortTerm = FALSE,
useVisitConceptCountLongTerm = FALSE,
useVisitConceptCountMediumTerm = FALSE,
useVisitConceptCountShortTerm = FALSE,
longTermStartDays = -365,
mediumTermStartDays = -180,
shortTermStartDays = -30,
endDays = 0,
includedCovariateConceptIds = c(),
addDescendantsToInclude = FALSE,
excludedCovariateConceptIds = c(),
addDescendantsToExclude = FALSE,
includedCovariateIds = c()
)

```

---

```
createDefaultCovariateSettings
```

*Create default covariate settings*

---

## Description

Create default covariate settings

## Usage

```

createDefaultCovariateSettings(
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c()
)

```

## Arguments

**includedCovariateConceptIds**  
A list of concept IDs that should be used to construct covariates.

**addDescendantsToInclude**  
Should descendant concept IDs be added to the list of concepts to include?

**excludedCovariateConceptIds**  
A list of concept IDs that should NOT be used to construct covariates.

**addDescendantsToExclude**  
Should descendant concept IDs be added to the list of concepts to exclude?

**includedCovariateIds**  
A list of covariate IDs that should be restricted to.



**Value**

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

**Examples**

```
## Not run:
covSettings <- createDefaultCovariateSettings(
  includedCovariateConceptIds = c(1),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(2),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c(1)
)

## End(Not run)
```

---

```
createDefaultTemporalCovariateSettings
      Create default covariate settings
```

---

**Description**

Create default covariate settings

**Usage**

```
createDefaultTemporalCovariateSettings(
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c()
)
```

**Arguments**

```
includedCovariateConceptIds
      A list of concept IDs that should be used to construct covariates.
addDescendantsToInclude
      Should descendant concept IDs be added to the list of concepts to include?
excludedCovariateConceptIds
      A list of concept IDs that should NOT be used to construct covariates.
addDescendantsToExclude
      Should descendant concept IDs be added to the list of concepts to exclude?
includedCovariateIds
      A list of covariate IDs that should be restricted to.
```

**Value**

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

## Examples

```
## Not run:
covSettings <- createDefaultTemporalCovariateSettings(
  includedCovariateConceptIds = c(1),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(2),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c(1)
)

## End(Not run)
```

---

createDetailedCovariateSettings

*Create detailed covariate settings*

---

## Description

Create detailed covariate settings

## Usage

```
createDetailedCovariateSettings(analyses = list())
```

## Arguments

**analyses**            A list of analysisDetail objects as created using [createAnalysisDetails](#).

## Details

creates an object specifying in detail how covariates should be constructed from data in the CDM model. Warning: this function is for advanced users only.

## Value

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

## Examples

```
## Not run:
analysisDetails <- createAnalysisDetails(
  analysisId = 1,
  sqlFileName = "DemographicsGender.sql",
  parameters = list(
    analysisId = 1,
    analysisName = "Gender",
    domainId = "Demographics"
  ),
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
```

```

    includedCovariateIds = c()
  )
  covSettings <- createDetailedCovariateSettings(analyses = analysisDetails)

## End(Not run)

```

---

```

createDetailedTemporalCovariateSettings
  Create detailed temporal covariate settings

```

---

## Description

Create detailed temporal covariate settings

## Usage

```

createDetailedTemporalCovariateSettings(
  analyses = list(),
  temporalStartDays = -365:-1,
  temporalEndDays = -365:-1
)

```

## Arguments

<code>analyses</code>	A list of analysis detail objects as created using <a href="#">createAnalysisDetails</a> .
<code>temporalStartDays</code>	A list of integers representing the start of a time period, relative to the index date. 0 indicates the index date, -1 indicates the day before the index date, etc. The start day is included in the time period.
<code>temporalEndDays</code>	A list of integers representing the end of a time period, relative to the index date. 0 indicates the index date, -1 indicates the day before the index date, etc. The end day is included in the time period.

## Details

creates an object specifying in detail how temporal covariates should be constructed from data in the CDM model. Warning: this function is for advanced users only.

## Value

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

## Examples

```

## Not run:
analysisDetails <- createAnalysisDetails(
  analysisId = 1,
  sqlFileName = "DemographicsGender.sql",
  parameters = list(
    analysisId = 1,

```

```

        analysisName = "Gender",
        domainId = "Demographics"
    ),
    includedCovariateConceptIds = c(),
    addDescendantsToInclude = FALSE,
    excludedCovariateConceptIds = c(),
    addDescendantsToExclude = FALSE,
    includedCovariateIds = c()
)
covSettings <- createDetailedTemporalCovariateSettings(
    analyses = analysisDetails,
    temporalStartDays = -365:-1,
    temporalEndDays = -365:-1
)

## End(Not run)

```

---

```
createEmptyCovariateData
```

*Creates an empty covariate data object*

---

## Description

Creates an empty covariate data object

## Usage

```
createEmptyCovariateData(cohortIds, aggregated, temporal)
```

## Arguments

cohortIds	For which cohort IDs should the covariate data be created?
aggregated	if the data should be aggregated
temporal	if the data is temporary

## Value

the empty CovariateData object

## Examples

```

## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
    cohortIds = 1,
    aggregated = FALSE,
    temporal = FALSE
)

## End(Not run)

```

---

createTable1

---

*Create a table 1*


---

## Description

Creates a formatted table of cohort characteristics, to be included in publications or reports. Allows for creating a table describing a single cohort, or a table comparing two cohorts.

## Usage

```
createTable1(
  covariateData1,
  covariateData2 = NULL,
  cohortId1 = NULL,
  cohortId2 = NULL,
  specifications = getDefaultTable1Specifications(),
  output = "two columns",
  showCounts = FALSE,
  showPercent = TRUE,
  percentDigits = 1,
  valueDigits = 1,
  stdDiffDigits = 2
)
```

## Arguments

covariateData1	The covariate data of the cohort to be included in the table.
covariateData2	The covariate data of the cohort to also be included, when comparing two cohorts.
cohortId1	If provided, covariateData1 will be restricted to this cohort. If not provided, covariateData1 is assumed to contain data on only 1 cohort.
cohortId2	If provided, covariateData2 will be restricted to this cohort. If not provided, covariateData2 is assumed to contain data on only 1 cohort.
specifications	Specifications of which covariates to display, and how.
output	The output format for the table. Options are output = "two columns", output = "one column", or output = "list".
showCounts	Show the number of cohort entries having the binary covariate?
showPercent	Show the percentage of cohort entries having the binary covariate?
percentDigits	Number of digits to be used for percentages.
valueDigits	Number of digits to be used for the values of continuous variables.
stdDiffDigits	Number of digits to be used for the standardized differences.

## Value

A data frame, or, when output = "list" a list of two data frames.

**Examples**

```
## Not run:
eunomiaConnectionDetails <- Eunomia::getEunomiaConnectionDetails()
covSettings <- createDefaultCovariateSettings()
Eunomia::createCohorts(
  connectionDetails = eunomiaConnectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
covData1 <- getDbCovariateData(
  connectionDetails = eunomiaConnectionDetails,
  oracleTempSchema = NULL,
  cdmDatabaseSchema = "main",
  cdmVersion = "5",
  cohortTable = "cohort",
  cohortDatabaseSchema = "main",
  cohortTableIsTemp = FALSE,
  cohortId = 1,
  rowIdField = "subject_id",
  covariateSettings = covSettings,
  aggregated = TRUE
)
covData2 <- getDbCovariateData(
  connectionDetails = eunomiaConnectionDetails,
  oracleTempSchema = NULL,
  cdmDatabaseSchema = "main",
  cdmVersion = "5",
  cohortTable = "cohort",
  cohortDatabaseSchema = "main",
  cohortTableIsTemp = FALSE,
  cohortId = 2,
  rowIdField = "subject_id",
  covariateSettings = covSettings,
  aggregated = TRUE
)
table1 <- createTable1(
  covariateData1 = covData1,
  covariateData2 = covData2,
  cohortId1 = 1,
  cohortId2 = 2,
  specifications = getDefaultTable1Specifications(),
  output = "one column",
  showCounts = FALSE,
  showPercent = TRUE,
  percentDigits = 1,
  valueDigits = 1,
  stdDiffDigits = 2
)

## End(Not run)
```

---

```
createTable1CovariateSettings
```

*Create covariate settings for a table 1*

---

## Description

Creates a covariate settings object for generating only those covariates that will be included in a table 1. This function works by filtering the covariateSettings object for the covariates in the specifications object.

## Usage

```
createTable1CovariateSettings(
  specifications = getDefaultTable1Specifications(),
  covariateSettings = createDefaultCovariateSettings(),
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c()
)
```

## Arguments

**specifications** A specifications object for generating a table using the [createTable1](#) function.

**covariateSettings** The covariate settings object to use as the basis for the filtered covariate settings.

**includedCovariateConceptIds** A list of concept IDs that should be used to construct covariates.

**addDescendantsToInclude** Should descendant concept IDs be added to the list of concepts to include?

**excludedCovariateConceptIds** A list of concept IDs that should NOT be used to construct covariates.

**addDescendantsToExclude** Should descendant concept IDs be added to the list of concepts to exclude?

**includedCovariateIds** A list of covariate IDs that should be restricted to.

## Value

A covariate settings object, for example to be used when calling the [getDbCovariateData](#) function.

## Examples

```
## Not run:
table1CovSettings <- createTable1CovariateSettings(
  specifications = getDefaultTable1Specifications(),
  covariateSettings = createDefaultCovariateSettings(),
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
```

```

    includedCovariateIds = c()
  )

## End(Not run)

```

---

```

createTemporalCovariateSettings
      Create covariate settings

```

---

## Description

Create covariate settings

## Usage

```

createTemporalCovariateSettings(
  useDemographicsGender = FALSE,
  useDemographicsAge = FALSE,
  useDemographicsAgeGroup = FALSE,
  useDemographicsRace = FALSE,
  useDemographicsEthnicity = FALSE,
  useDemographicsIndexYear = FALSE,
  useDemographicsIndexMonth = FALSE,
  useDemographicsPriorObservationTime = FALSE,
  useDemographicsPostObservationTime = FALSE,
  useDemographicsTimeInCohort = FALSE,
  useDemographicsIndexYearMonth = FALSE,
  useCareSiteId = FALSE,
  useConditionOccurrence = FALSE,
  useConditionOccurrencePrimaryInpatient = FALSE,
  useConditionEraStart = FALSE,
  useConditionEraOverlap = FALSE,
  useConditionEraGroupStart = FALSE,
  useConditionEraGroupOverlap = FALSE,
  useDrugExposure = FALSE,
  useDrugEraStart = FALSE,
  useDrugEraOverlap = FALSE,
  useDrugEraGroupStart = FALSE,
  useDrugEraGroupOverlap = FALSE,
  useProcedureOccurrence = FALSE,
  useDeviceExposure = FALSE,
  useMeasurement = FALSE,
  useMeasurementValue = FALSE,
  useMeasurementRangeGroup = FALSE,
  useObservation = FALSE,
  useCharlsonIndex = FALSE,
  useDcsi = FALSE,
  useChads2 = FALSE,
  useChads2Vasc = FALSE,
  useHfrs = FALSE,
  useDistinctConditionCount = FALSE,

```



```

    useDistinctIngredientCount = FALSE,
    useDistinctProcedureCount = FALSE,
    useDistinctMeasurementCount = FALSE,
    useDistinctObservationCount = FALSE,
    useVisitCount = FALSE,
    useVisitConceptCount = FALSE,
    temporalStartDays = -365:-1,
    temporalEndDays = -365:-1,
    includedCovariateConceptIds = c(),
    addDescendantsToInclude = FALSE,
    excludedCovariateConceptIds = c(),
    addDescendantsToExclude = FALSE,
    includedCovariateIds = c()
  )

```

## Arguments

`useDemographicsGender`  
Gender of the subject. (analysis ID 1)

`useDemographicsAge`  
Age of the subject on the index date (in years). (analysis ID 2)

`useDemographicsAgeGroup`  
Age of the subject on the index date (in 5 year age groups) (analysis ID 3)

`useDemographicsRace`  
Race of the subject. (analysis ID 4)

`useDemographicsEthnicity`  
Ethnicity of the subject. (analysis ID 5)

`useDemographicsIndexYear`  
Year of the index date. (analysis ID 6)

`useDemographicsIndexMonth`  
Month of the index date. (analysis ID 7)

`useDemographicsPriorObservationTime`  
Number of days of observation time preceding the index date. (analysis ID 8)

`useDemographicsPostObservationTime`  
Number of days of observation time preceding the index date. (analysis ID 9)

`useDemographicsTimeInCohort`  
Number of days of observation time preceding the index date. (analysis ID 10)

`useDemographicsIndexYearMonth`  
Calendar month of the index date. (analysis ID 11)

`useCareSiteId` Care site associated with the cohort start, pulled from the `visit_detail`, `visit_occurrence`, or `person` table, in that order. (analysis ID 12)

`useConditionOccurrence`  
One covariate per condition in the `condition_occurrence` table starting in the time window. (analysis ID 101)

`useConditionOccurrencePrimaryInpatient`  
One covariate per condition observed as a primary diagnosis in an inpatient setting in the `condition_occurrence` table starting in the time window. (analysis ID 102)

`useConditionEraStart`  
One covariate per condition in the `condition_era` table starting in the time window. (analysis ID 201)

<code>useConditionEraOverlap</code>	One covariate per condition in the <code>condition_era</code> table overlapping with any part of the time window. (analysis ID 202)
<code>useConditionEraGroupStart</code>	One covariate per condition era rolled up to SNOMED groups in the <code>condition_era</code> table starting in the time window. (analysis ID 203)
<code>useConditionEraGroupOverlap</code>	One covariate per condition era rolled up to SNOMED groups in the <code>condition_era</code> table overlapping with any part of the time window. (analysis ID 204)
<code>useDrugExposure</code>	One covariate per drug in the <code>drug_exposure</code> table starting in the time window. (analysis ID 301)
<code>useDrugEraStart</code>	One covariate per drug in the <code>drug_era</code> table starting in the time window. (analysis ID 401)
<code>useDrugEraOverlap</code>	One covariate per drug in the <code>drug_era</code> table overlapping with any part of the time window. (analysis ID 402)
<code>useDrugEraGroupStart</code>	One covariate per drug rolled up to ATC groups in the <code>drug_era</code> table starting in the time window. (analysis ID 403)
<code>useDrugEraGroupOverlap</code>	One covariate per drug rolled up to ATC groups in the <code>drug_era</code> table overlapping with any part of the time window. (analysis ID 404)
<code>useProcedureOccurrence</code>	One covariate per procedure in the <code>procedure_occurrence</code> table in the time window. (analysis ID 501)
<code>useDeviceExposure</code>	One covariate per device in the <code>device exposure</code> table starting in the timewindow. (analysis ID 601)
<code>useMeasurement</code>	One covariate per measurement in the <code>measurement</code> table in the time window. (analysis ID 701)
<code>useMeasurementValue</code>	One covariate containing the value per measurement-unit combination in the time window. If multiple values are found, the last is taken. (analysis ID 702)
<code>useMeasurementRangeGroup</code>	Covariates indicating whether measurements are below, within, or above normal range within the time period. (analysis ID 703)
<code>useObservation</code>	One covariate per observation in the <code>observation</code> table in the time window. (analysis ID 801)
<code>useCharlsonIndex</code>	The Charlson comorbidity index (Romano adaptation) using all conditions prior to the window end. (analysis ID 901)
<code>useDcsi</code>	The Diabetes Comorbidity Severity Index (DCSI) using all conditions prior to the window end. (analysis ID 902)
<code>useChads2</code>	The CHADS2 score using all conditions prior to the window end. (analysis ID 903)
<code>useChads2Vasc</code>	The CHADS2VASc score using all conditions prior to the window end. (analysis ID 904)

useHfrs	The Hospital Frailty Risk Score score using all conditions prior to the window end. (analysis ID 926)
useDistinctConditionCount	The number of distinct condition concepts observed in the time window. (analysis ID 905)
useDistinctIngredientCount	The number of distinct ingredients observed in the time window. (analysis ID 906)
useDistinctProcedureCount	The number of distinct procedures observed in the time window. (analysis ID 907)
useDistinctMeasurementCount	The number of distinct measurements observed in the time window. (analysis ID 908)
useDistinctObservationCount	The number of distinct observations in the time window. (analysis ID 909)
useVisitCount	The number of visits observed in the time window. (analysis ID 910)
useVisitConceptCount	The number of visits observed in the time window, stratified by visit concept ID. (analysis ID 911)
temporalStartDays	A list of integers representing the start of a time period, relative to the index date. 0 indicates the index date, -1 indicates the day before the index date, etc. The start day is included in the time period.
temporalEndDays	A list of integers representing the end of a time period, relative to the index date. 0 indicates the index date, -1 indicates the day before the index date, etc. The end day is included in the time period.
includedCovariateConceptIds	A list of concept IDs that should be used to construct covariates.
addDescendantsToInclude	Should descendant concept IDs be added to the list of concepts to include?
excludedCovariateConceptIds	A list of concept IDs that should NOT be used to construct covariates.
addDescendantsToExclude	Should descendant concept IDs be added to the list of concepts to exclude?
includedCovariateIds	A list of covariate IDs that should be restricted to.

### Details

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

### Value

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

**Examples**

```

settings <- createTemporalCovariateSettings(
  useDemographicsGender = TRUE,
  useDemographicsAge = FALSE,
  useDemographicsAgeGroup = TRUE,
  useDemographicsRace = TRUE,
  useDemographicsEthnicity = TRUE,
  useDemographicsIndexYear = TRUE,
  useDemographicsIndexMonth = TRUE,
  useDemographicsPriorObservationTime = FALSE,
  useDemographicsPostObservationTime = FALSE,
  useDemographicsTimeInCohort = FALSE,
  useDemographicsIndexYearMonth = FALSE,
  useCareSiteId = FALSE,
  useConditionOccurrence = FALSE,
  useConditionOccurrencePrimaryInpatient = FALSE,
  useConditionEraStart = FALSE,
  useConditionEraOverlap = FALSE,
  useConditionEraGroupStart = FALSE,
  useConditionEraGroupOverlap = TRUE,
  useDrugExposure = FALSE,
  useDrugEraStart = FALSE,
  useDrugEraOverlap = FALSE,
  useDrugEraGroupStart = FALSE,
  useDrugEraGroupOverlap = TRUE,
  useProcedureOccurrence = TRUE,
  useDeviceExposure = TRUE,
  useMeasurement = TRUE,
  useMeasurementValue = FALSE,
  useMeasurementRangeGroup = TRUE,
  useObservation = TRUE,
  useCharlsonIndex = TRUE,
  useDcsi = TRUE,
  useChads2 = TRUE,
  useChads2Vasc = TRUE,
  useHfrs = FALSE,
  useDistinctConditionCount = FALSE,
  useDistinctIngredientCount = FALSE,
  useDistinctProcedureCount = FALSE,
  useDistinctMeasurementCount = FALSE,
  useDistinctObservationCount = FALSE,
  useVisitCount = FALSE,
  useVisitConceptCount = FALSE,
  temporalStartDays = -365:-1,
  temporalEndDays = -365:-1,
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c()
)

```

---

```
createTemporalSequenceCovariateSettings  
  Create covariate settings
```

---

## Description

Create covariate settings

## Usage

```
createTemporalSequenceCovariateSettings(  
  useDemographicsGender = FALSE,  
  useDemographicsAge = FALSE,  
  useDemographicsAgeGroup = FALSE,  
  useDemographicsRace = FALSE,  
  useDemographicsEthnicity = FALSE,  
  useDemographicsIndexYear = FALSE,  
  useDemographicsIndexMonth = FALSE,  
  useConditionOccurrence = FALSE,  
  useConditionOccurrencePrimaryInpatient = FALSE,  
  useConditionEraStart = FALSE,  
  useConditionEraGroupStart = FALSE,  
  useDrugExposure = FALSE,  
  useDrugEraStart = FALSE,  
  useDrugEraGroupStart = FALSE,  
  useProcedureOccurrence = FALSE,  
  useDeviceExposure = FALSE,  
  useMeasurement = FALSE,  
  useMeasurementValue = FALSE,  
  useObservation = FALSE,  
  timePart = "month",  
  timeInterval = 1,  
  sequenceEndDay = -1,  
  sequenceStartDay = -730,  
  includedCovariateConceptIds = c(),  
  addDescendantsToInclude = FALSE,  
  excludedCovariateConceptIds = c(),  
  addDescendantsToExclude = FALSE,  
  includedCovariateIds = c()  
)
```

## Arguments

```
useDemographicsGender  
  Gender of the subject. (analysis ID 1)  
useDemographicsAge  
  Age of the subject on the index date (in years). (analysis ID 2)  
useDemographicsAgeGroup  
  Age of the subject on the index date (in 5 year age groups) (analysis ID 3)  
useDemographicsRace  
  Race of the subject. (analysis ID 4)
```

<code>useDemographicsEthnicity</code>	Ethnicity of the subject. (analysis ID 5)
<code>useDemographicsIndexYear</code>	Year of the index date. (analysis ID 6)
<code>useDemographicsIndexMonth</code>	Month of the index date. (analysis ID 7)
<code>useConditionOccurrence</code>	One covariate per condition in the <code>condition_occurrence</code> table starting in the time window. (analysis ID 101)
<code>useConditionOccurrencePrimaryInpatient</code>	One covariate per condition observed as a primary diagnosis in an inpatient setting in the <code>condition_occurrence</code> table starting in the time window. (analysis ID 102)
<code>useConditionEraStart</code>	One covariate per condition in the <code>condition_era</code> table starting in the time window. (analysis ID 201)
<code>useConditionEraGroupStart</code>	One covariate per condition era rolled up to SNOMED groups in the <code>condition_era</code> table starting in the time window. (analysis ID 203)
<code>useDrugExposure</code>	One covariate per drug in the <code>drug_exposure</code> table starting in the time window. (analysis ID 301)
<code>useDrugEraStart</code>	One covariate per drug in the <code>drug_era</code> table starting in the time window. (analysis ID 401)
<code>useDrugEraGroupStart</code>	One covariate per drug rolled up to ATC groups in the <code>drug_era</code> table starting in the time window. (analysis ID 403)
<code>useProcedureOccurrence</code>	One covariate per procedure in the <code>procedure_occurrence</code> table in the time window. (analysis ID 501)
<code>useDeviceExposure</code>	One covariate per device in the device exposure table starting in the timewindow. (analysis ID 601)
<code>useMeasurement</code>	One covariate per measurement in the measurement table in the time window. (analysis ID 701)
<code>useMeasurementValue</code>	One covariate containing the value per measurement-unit combination in the time window. If multiple values are found, the last is taken. (analysis ID 702)
<code>useObservation</code>	One covariate per observation in the observation table in the time window. (analysis ID 801)
<code>timePart</code>	The interval scale ('DAY', 'MONTH', 'YEAR')
<code>timeInterval</code>	Fixed interval length for <code>timeId</code> using the 'timePart' scale. For example, a 'timePart' of DAY with 'timeInterval' 30 has <code>timeIds</code> where <code>timeId</code> 1 is day 0 to day 29, <code>timeId</code> 2 is day 30 to day 59, etc.
<code>sequenceEndDay</code>	What is the end day (relative to the index date) of the data extraction?
<code>sequenceStartDay</code>	What is the start day (relative to the index date) of the data extraction?

includedCovariateConceptIds  
A list of concept IDs that should be used to construct covariates.

addDescendantsToInclude  
Should descendant concept IDs be added to the list of concepts to include?

excludedCovariateConceptIds  
A list of concept IDs that should NOT be used to construct covariates.

addDescendantsToExclude  
Should descendant concept IDs be added to the list of concepts to exclude?

includedCovariateIds  
A list of covariate IDs that should be restricted to.

### Details

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

### Value

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

### Examples

```
settings <- createTemporalSequenceCovariateSettings(  
  useDemographicsGender = TRUE,  
  useDemographicsAge = FALSE,  
  useDemographicsAgeGroup = TRUE,  
  useDemographicsRace = TRUE,  
  useDemographicsEthnicity = TRUE,  
  useDemographicsIndexYear = TRUE,  
  useDemographicsIndexMonth = TRUE,  
  useConditionOccurrence = FALSE,  
  useConditionOccurrencePrimaryInpatient = FALSE,  
  useConditionEraStart = FALSE,  
  useConditionEraGroupStart = FALSE,  
  useDrugExposure = FALSE,  
  useDrugEraStart = FALSE,  
  useDrugEraGroupStart = FALSE,  
  useProcedureOccurrence = TRUE,  
  useDeviceExposure = TRUE,  
  useMeasurement = TRUE,  
  useMeasurementValue = FALSE,  
  useObservation = TRUE,  
  timePart = "DAY",  
  timeInterval = 1,  
  sequenceEndDay = -1,  
  sequenceStartDay = -730,  
  includedCovariateConceptIds = c(),  
  addDescendantsToInclude = FALSE,  
  excludedCovariateConceptIds = c(),  
  addDescendantsToExclude = FALSE,  
  includedCovariateIds = c()  
)
```

---

`filterByCohortDefinitionId`  
*Filter covariates by cohort definition IDs*

---

### Description

Filter covariates by cohort definition IDs

### Usage

```
filterByCohortDefinitionId(covariateData, cohortId = 1, cohortIds = c(1))
```

### Arguments

`covariateData` An object of type `CovariateData`  
`cohortId` DEPRECATED The cohort definition IDs to keep.  
`cohortIds` The cohort definition IDs to keep.

### Value

An object of type `covariateData`.

### Examples

```
## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)

covData <- filterByCohortDefinitionId(
  covariateData = covariateData,
  cohortIds = c(1)
)

## End(Not run)
```

---

`filterByRowId` *Filter covariates by row ID*

---

### Description

Filter covariates by row ID

### Usage

```
filterByRowId(covariateData, rowIds)
```



**Arguments**

covariateData    An object of type CovariateData  
 rowIds            A vector containing the rowIds to keep.

**Value**

An object of type covariateData.

**Examples**

```
## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)

covData <- filterByRowId(
  covariateData = covariateData,
  rowIds = 1
)

## End(Not run)
```

---

filterCovariateDataCovariates

*Filters the covariateData covariates based on the given characterization mean value.*

---

**Description**

Filters the covariateData covariates based on the given characterization mean value.

**Usage**

```
filterCovariateDataCovariates(
  covariateData,
  covariatesName,
  minCharacterizationMean = 0
)
```

**Arguments**

covariateData    The covariate data  
 covariatesName    The name of the covariates object inside the covariateData  
 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.

---

```
getDbCohortAttrCovariatesData
```

*Getcovariate information from the database through the cohort\_attribute table*

---

## Description

Constructs covariates using the cohort\_attribute table.

## Usage

```
getDbCohortAttrCovariatesData(
  connection,
  oracleTempSchema = NULL,
  cdmDatabaseSchema,
  cohortTable = "#cohort_person",
  cohortId = -1,
  cohortIds = c(-1),
  cdmVersion = "5",
  rowIdField = "subject_id",
  covariateSettings,
  aggregated = FALSE
)
```

## Arguments

connection	A connection to the server containing the schema as created using the connect function in the DatabaseConnector package.
oracleTempSchema	A schema where temp tables can be created in Oracle.
cdmDatabaseSchema	The name of the database schema that contains the OMOP CDM instance. Requires read permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.
cohortTable	Name of the table holding the cohort for which we want to construct covariates. If it is a temp table, the name should have a hash prefix, e.g. '#temp_table'. If it is a non-temp table, it should include the database schema, e.g. 'cdm_database.cohort'.
cohortId	DEPRECATED:For which cohort ID should covariates be constructed? If set to -1, covariates will be constructed for all cohorts in the specified cohort table.
cohortIds	For which cohort ID(s) should covariates be constructed? If set to c(-1), covariates will be constructed for all cohorts in the specified cohort table.
cdmVersion	The version of the Common Data Model used. Currently only cdmVersion = "5" is supported.
rowIdField	The name of the field in the cohort temp table that is to be used as the row_id field in the output table. This can be especially usefull if there is more than one period per person.
covariateSettings	An object of type covariateSettings as created using the <a href="#">createCohortAttrCovariateSettings</a> function.
aggregated	Should aggregate statistics be computed instead of covariates per cohort entry?

## Details

This function uses the data in the CDM to construct a large set of covariates for the provided cohort. The cohort is assumed to be in an existing temp table with these fields: 'subject\_id', 'cohort\_definition\_id', 'cohort\_start\_date'. Optionally, an extra field can be added containing the unique identifier that will be used as rowID in the output. Typically, users don't call this function directly but rather use the [getDbCovariateData](#) function instead.

## Value

Returns an object of type `CovariateData`, which is an Andromeda object containing information on the baseline covariates. Information about multiple outcomes can be captured at once for efficiency reasons. This object is a list with the following components:

**covariates** An ffdi object listing the baseline covariates per person in the cohorts. This is done using a sparse representation: covariates with a value of 0 are omitted to save space. The covariates object will have three columns: rowId, covariateId, and covariateValue. The rowId is usually equal to the person\_id, unless specified otherwise in the rowIdField argument.

**covariateRef** A table describing the covariates that have been extracted.

. The CovariateData object will also have a metaData attribute, a list of objects with information on how the covariateData object was constructed.

## Examples

```
## Not run:
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
Eunomia::createCohorts(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
connection <- DatabaseConnector::connect(connectionDetails)
sql <- "SELECT 1 AS attribute_definition_id, 'Length of observation in days' AS attribute_name
      INTO @cohort_database_schema.@attribute_definition_table;"
sql <- SqlRender::render(
  sql,
  cohort_database_schema = "main",
  attribute_definition_table = "attribute_definition"
)
sql <- SqlRender::translate(
  sql = sql,
  targetDialect = attr(connection, "dbms")
)
DatabaseConnector::executeSql(connection, sql)
covariateSettings <- createCohortAttrCovariateSettings(
  attrDatabaseSchema = "main",
  cohortAttrTable = "cohort_attribute",
  attrDefinitionTable = "attribute_definition",
  includeAttrIds = c(1),
  isBinary = FALSE,
  missingMeansZero = FALSE
)

covData <- getDbCohortAttrCovariatesData(
```

```

connection = connection,
oracleTempSchema = NULL,
cdmDatabaseSchema = "main",
cdmVersion = "5",
cohortTable = "cohort",
cohortIds = 1,
rowIdField = "subject_id",
covariateSettings = covariateSettings,
aggregated = FALSE
)

## End(Not run)

```

---

getDbCohortBasedCovariatesData

*Get covariate information from the database based on other cohorts*

---

## Description

Constructs covariates using other cohorts.

## Usage

```

getDbCohortBasedCovariatesData(
  connection,
  oracleTempSchema = NULL,
  cdmDatabaseSchema,
  cohortTable = "#cohort_person",
  cohortId = -1,
  cohortIds = c(-1),
  cdmVersion = "5",
  rowIdField = "subject_id",
  covariateSettings,
  aggregated = FALSE,
  minCharacterizationMean = 0
)

```

## Arguments

connection	A connection to the server containing the schema as created using the connect function in the DatabaseConnector package.
oracleTempSchema	A schema where temp tables can be created in Oracle.
cdmDatabaseSchema	The name of the database schema that contains the OMOP CDM instance. Requires read permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.
cohortTable	Name of the table holding the cohort for which we want to construct covariates. If it is a temp table, the name should have a hash prefix, e.g. '#temp_table'. If it is a non-temp table, it should include the database schema, e.g. 'cdm_database.cohort'.

cohortId	DEPRECATED:For which cohort ID should covariates be constructed? If set to -1, covariates will be constructed for all cohorts in the specified cohort table.
cohortIds	For which cohort ID(s) should covariates be constructed? If set to c(-1), covariates will be constructed for all cohorts in the specified cohort table.
cdmVersion	The version of the Common Data Model used. Currently only cdmVersion = "5" is supported.
rowIdField	The name of the field in the cohort temp table that is to be used as the row_id field in the output table. This can be especially usefull if there is more than one period per person.
covariateSettings	An object of type covariateSettings as created using the <a href="#">createCohortBasedCovariateSettings</a> or <a href="#">createCohortBasedTemporalCovariateSettings</a> functions.
aggregated	Should aggregate statistics be computed instead of covariates per cohort entry?
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.

## Details

This function uses the data in the CDM to construct a large set of covariates for the provided cohort. The cohort is assumed to be in an existing temp table with these fields: 'subject\_id', 'cohort\_definition\_id', 'cohort\_start\_date'. Optionally, an extra field can be added containing the unique identifier that will be used as rowID in the output. Typically, users don't call this function directly but rather use the [getDbCovariateData](#) function instead.

## Value

Returns an object of type CovariateData, which is an Andromeda object containing information on the baseline covariates. Information about multiple outcomes can be captured at once for efficiency reasons. This object is a list with the following components:

**covariates** An ffdi object listing the baseline covariates per person in the cohorts. This is done using a sparse representation: covariates with a value of 0 are omitted to save space. The covariates object will have three columns: rowId, covariateId, and covariateValue. The rowId is usually equal to the person\_id, unless specified otherwise in the rowIdField argument.

**covariateRef** A table describing the covariates that have been extracted.

. The CovariateData object will also have a metaData attribute, a list of objects with information on how the covariateData object was constructed.

---

getDbCovariateData	<i>Get covariate information from the database</i>
--------------------	--

---

## Description

Uses one or several covariate builder functions to construct covariates.

**Usage**

```
getDbCovariateData(
  connectionDetails = NULL,
  connection = NULL,
  oracleTempSchema = NULL,
  cdmDatabaseSchema,
  cdmVersion = "5",
  cohortTable = "cohort",
  cohortDatabaseSchema = cdmDatabaseSchema,
  cohortTableIsTemp = FALSE,
  cohortId = -1,
  cohortIds = c(-1),
  rowIdField = "subject_id",
  covariateSettings,
  aggregated = FALSE,
  minCharacterizationMean = 0
)
```

**Arguments**

connectionDetails	An R object of type connectionDetails created using the function createConnectionDetails in the DatabaseConnector package. Either the connection or connectionDetails argument should be specified.
connection	A connection to the server containing the schema as created using the connect function in the DatabaseConnector package. Either the connection or connectionDetails argument should be specified.
oracleTempSchema	A schema where temp tables can be created in Oracle.
cdmDatabaseSchema	The name of the database schema that contains the OMOP CDM instance. Requires read permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.
cdmVersion	Define the OMOP CDM version used: currently supported is "5".
cohortTable	Name of the (temp) table holding the cohort for which we want to construct covariates
cohortDatabaseSchema	If the cohort table is not a temp table, specify the database schema where the cohort table can be found. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.
cohortTableIsTemp	Is the cohort table a temp table?
cohortId	DEPRECATED: For which cohort ID(s) should covariates be constructed? If set to -1, covariates will be constructed for all cohorts in the specified cohort table.
cohortIds	For which cohort ID(s) should covariates be constructed? If set to c(-1), covariates will be constructed for all cohorts in the specified cohort table.
rowIdField	The name of the field in the cohort table that is to be used as the row_id field in the output table. This can be especially usefull if there is more than one period per person.

covariateSettings	Either an object of type covariateSettings as created using one of the create-Covariate functions, or a list of such objects.
aggregated	Should aggregate statistics be computed instead of covariates per cohort entry?
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.

## Details

This function uses the data in the CDM to construct a large set of covariates for the provided cohort. The cohort is assumed to be in an existing table with these fields: 'subject\_id', 'cohort\_definition\_id', 'cohort\_start\_date'. Optionally, an extra field can be added containing the unique identifier that will be used as rowID in the output.

## Value

Returns an object of type covariateData, containing information on the covariates.

## Examples

```
## Not run:
eunomiaConnectionDetails <- Eunomia::getEunomiaConnectionDetails()
covSettings <- createDefaultCovariateSettings()
Eunomia::createCohorts(
  connectionDetails = eunomiaConnectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
covData <- getDbCovariateData(
  connectionDetails = eunomiaConnectionDetails,
  oracleTempSchema = NULL,
  cdmDatabaseSchema = "main",
  cdmVersion = "5",
  cohortTable = "cohort",
  cohortDatabaseSchema = "main",
  cohortTableIsTemp = FALSE,
  cohortIds = -1,
  rowIdField = "subject_id",
  covariateSettings = covSettings,
  aggregated = FALSE
)

## End(Not run)
```

---

getDbDefaultCovariateData

*Get default covariate information from the database*


---

## Description

Constructs a large default set of covariates for one or more cohorts using data in the CDM schema. Includes covariates for all drugs, drug classes, condition, condition classes, procedures, observations, etc.

## Usage

```
getDbDefaultCovariateData(
  connection,
  oracleTempSchema = NULL,
  cdmDatabaseSchema,
  cohortTable = "#cohort_person",
  cohortId = -1,
  cohortIds = c(-1),
  cdmVersion = "5",
  rowIdField = "subject_id",
  covariateSettings,
  targetDatabaseSchema,
  targetCovariateTable,
  targetCovariateRefTable,
  targetAnalysisRefTable,
  aggregated = FALSE,
  minCharacterizationMean = 0
)
```

## Arguments

connection	A connection to the server containing the schema as created using the connect function in the DatabaseConnector package.
oracleTempSchema	A schema where temp tables can be created in Oracle.
cdmDatabaseSchema	The name of the database schema that contains the OMOP CDM instance. Requires read permissions to this database. On SQL Server, this should specify both the database and the schema, so for example 'cdm_instance.dbo'.
cohortTable	Name of the table holding the cohort for which we want to construct covariates. If it is a temp table, the name should have a hash prefix, e.g. '#temp_table'. If it is a non-temp table, it should include the database schema, e.g. 'cdm_database.cohort'.
cohortId	DEPRECATED:For which cohort ID should covariates be constructed? If set to -1, covariates will be constructed for all cohorts in the specified cohort table.
cohortIds	For which cohort ID(s) should covariates be constructed? If set to c(-1), covariates will be constructed for all cohorts in the specified cohort table.
cdmVersion	The version of the Common Data Model used. Currently only cdmVersion = "5" is supported.



rowIdField	The name of the field in the cohort temp table that is to be used as the row_id field in the output table. This can be especially usefull if there is more than one period per person.
covariateSettings	Either an object of type covariateSettings as created using one of the create-Covariate functions, or a list of such objects.
targetDatabaseSchema	(Optional) The name of the database schema where the resulting covariates should be stored.
targetCovariateTable	(Optional) The name of the table where the resulting covariates will be stored. If not provided, results will be fetched to R. The table can be a permanent table in the targetDatabaseSchema or a temp table. If it is a temp table, do not specify targetDatabaseSchema.
targetCovariateRefTable	(Optional) The name of the table where the covariate reference will be stored.
targetAnalysisRefTable	(Optional) The name of the table where the analysis reference will be stored.
aggregated	Should aggregate statistics be computed instead of covariates per cohort entry?
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.

## Details

This function uses the data in the CDM to construct a large set of covariates for the provided cohort. The cohort is assumed to be in an existing temp table with these fields: 'subject\_id', 'cohort\_definition\_id', 'cohort\_start\_date'. Optionally, an extra field can be added containing the unique identifier that will be used as rowID in the output. Typically, users don't call this function directly but rather use the [getDbCovariateData](#) function instead.

## Value

Returns an object of type CovariateData, which is an Andromeda object containing information on the baseline covariates. Information about multiple outcomes can be captured at once for efficiency reasons. This object is a list with the following components:

**covariates** An ffdp object listing the baseline covariates per person in the cohorts. This is done using a sparse representation: covariates with a value of 0 are omitted to save space. The covariates object will have three columns: rowId, covariateId, and covariateValue. The rowId is usually equal to the person\_id, unless specified otherwise in the rowIdField argument.

**covariateRef** A table describing the covariates that have been extracted.

. The CovariateData object will also have a metaData attribute, a list of objects with information on how the covariateData object was constructed.

## Examples

```
## Not run:
connection <- DatabaseConnector::connect(connectionDetails)
```

```

Eunomia::createCohorts(connectionDetails)

results <- getDbDefaultCovariateData(
  connection = connection,
  cdmDatabaseSchema = "main",
  cohortTable = "cohort",
  covariateSettings = createDefaultCovariateSettings(),
  targetDatabaseSchema = "main",
  targetCovariateTable = "ut_cov",
  targetCovariateRefTable = "ut_cov_ref",
  targetAnalysisRefTable = "ut_cov_analysis_ref"
)

## End(Not run)

```

---

```

getDbDefaultTable1Specifications
  Get the default table 1 specifications

```

---

### Description

Loads the default specifications for a table 1, to be used with the `createTable1` function.

### Usage

```
getDbDefaultTable1Specifications()
```

### Value

A specifications objects.

### Examples

```

## Not run:
defaultTable1Specs <- getDbDefaultTable1Specifications()

## End(Not run)

```

---

```

isAggregatedCovariateData
  Check whether covariate data is aggregated

```

---

### Description

Check whether covariate data is aggregated

### Usage

```
isAggregatedCovariateData(x)
```

**Arguments**

x                      The covariate data object to check.

**Value**

A logical value.

**Examples**

```
## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)
isAggrCovData <- isAggregatedCovariateData(covariateData)

## End(Not run)
```

---

isCovariateData	<i>Check whether an object is a CovariateData object</i>
-----------------	--

---

**Description**

Check whether an object is a CovariateData object

**Usage**

```
isCovariateData(x)
```

**Arguments**

x                      The object to check.

**Value**

A logical value.

**Examples**

```
## Not run:
binaryCovDataFile <- system.file("testdata/binaryCovariateData.zip",
  package = "FeatureExtraction"
)
covData <- loadCovariateData(binaryCovDataFile)
isCovData <- isCovariateData(covData)

## End(Not run)
```

---

```
isTemporalCovariateData
```

*Check whether covariate data is temporal*

---

### Description

Check whether covariate data is temporal

### Usage

```
isTemporalCovariateData(x)
```

### Arguments

x                      The covariate data object to check.

### Value

A logical value.

### Examples

```
## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)
isTempCovData <- isTemporalCovariateData(covariateData)

## End(Not run)
```

---

```
loadCovariateData
```

*Load the covariate data from a folder*

---

### Description

loadCovariateData loads an object of type covariateData from a folder in the file system.

### Usage

```
loadCovariateData(file, readOnly)
```

### Arguments

file                      The name of the folder containing the data.  
readOnly                  DEPRECATED: If true, the data is opened read only.

**Details**

The data will be written to a set of files in the folder specified by the user.

**Value**

An object of class CovariateData.

**Examples**

```
## Not run:
binaryCovDataFile <- system.file("testdata/binaryCovariateData.zip",
  package = "FeatureExtraction"
)
covData <- loadCovariateData(binaryCovDataFile)

## End(Not run)
```

---

saveCovariateData	<i>Save the covariate data to folder</i>
-------------------	--

---

**Description**

saveCovariateData saves an object of type covariateData to folder.

**Usage**

```
saveCovariateData(covariateData, file)
```

**Arguments**

covariateData	An object of type covariateData as generated using getDbCovariateData.
file	The name of the folder where the data will be written. The folder should not yet exist.

**Details**

The data will be written to a set of files in the folder specified by the user.

**Examples**

```
## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)
# For this example we'll use a temporary file location:
fileName <- tempfile()
saveCovariateData(covariateData = covariateData, file = fileName)
# Cleaning up the file used in this example:
unlink(fileName)
```

```
## End(Not run)
```

---

tidyCovariateData	<i>Tidy covariate data</i>
-------------------	----------------------------

---

## Description

Tidy covariate data

## Usage

```
tidyCovariateData(
  covariateData,
  minFraction = 0.001,
  normalize = TRUE,
  removeRedundancy = TRUE
)
```

## Arguments

covariateData	An object as generated using the <a href="#">getDbCovariateData</a> function.
minFraction	Minimum fraction of the population that should have a non-zero value for a covariate for that covariate to be kept. Set to 0 to don't filter on frequency.
normalize	Normalize the covariates? (dividing by the max).
removeRedundancy	Should redundant covariates be removed?

## Details

Normalize covariate values by dividing by the max and/or remove redundant covariates and/or remove infrequent covariates. For temporal covariates, redundancy is evaluated per time ID.

## Examples

```
## Not run:
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)

covData <- tidyCovariateData(
  covariateData = covariateData,
  minFraction = 0.001,
  normalize = TRUE,
  removeRedundancy = TRUE
)

## End(Not run)
```

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