

# Package ‘FeatureExtraction’

May 8, 2025

**Type** Package

**Title** Generating Features for a Cohort

**Version** 3.10.0

**Date** 2025-05-08

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**Description** An R interface for generating features for a cohort using data in the Common Data Model. Features can be constructed using default or custom made feature definitions. Furthermore it's possible to aggregate features and get the summary statistics.

**Depends** R (>= 3.2.2),  
DatabaseConnector (>= 3.0.0),  
Andromeda (>= 1.0.0)

**Imports** methods,  
dplyr,  
rJava,  
jsonlite,  
SqlRender (>= 1.18.0),  
ParallelLogger (>= 2.0.2),  
cli,  
pillar,  
readr,  
rlang,  
RSQLite,  
DBI,  
checkmate,  
vroom

**Suggests** testthat,  
knitr,  
rmarkdown,  
Eunomia (>= 2.0.0),  
withr,  
curl,  
http

**License** Apache License 2.0

**VignetteBuilder** knitr

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

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

**NeedsCompilation** no

**RoxygenNote** 7.3.2

**Encoding** UTF-8

**Language** en-US

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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.

---

```
.getDbLooCovariateData
```

*Get covariate information from the database*

---

**Description**

Get covariate information from the database

**Usage**

```
.getDbLooCovariateData(  
  connection,  
  tempEmulationSchema = NULL,  
  cdmDatabaseSchema,  
  cohortTable = "#cohort_person",  
  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. Either the connection or connectionDetails argument should be specified.
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.
cdmDatabaseSchema	The 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 (temp) table holding the cohort for which we want to construct covariates
cohortIds	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.
cdmVersion	Define the OMOP CDM version used: currently supported is "5".
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 createCovariate 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 binary 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.

---

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**

```
covariateData <- FeatureExtraction::createEmptyCovariateData(  
  cohortIds = 1,  
  aggregated = FALSE,  
  temporal = FALSE  
)  
aggregatedCovariateData <- aggregateCovariates(covariateData)
```

---

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

```
binaryCovDataFile <- system.file("testdata/binaryCovariateData.zip",
  package = "FeatureExtraction")
covariateData1 <- loadCovariateData(binaryCovDataFile)
covariateData2 <- loadCovariateData(binaryCovDataFile)
covDataDiff <- computeStandardizedDifference(
  covariateData1,
  covariateData2,
  cohortId1 = 1,
  cohortId2 = 2
)
```

---

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

```
covSettings <- createDefaultCovariateSettings()
detailedSettings <- convertPrespecSettingsToDetailedSettings(covariateSettings = covSettings)
```

---

CovariateData-class      *Covariate Data*


---

**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**

```

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

```

---

```
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 NULL, 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 NULL, 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: 'cohortId' and 'cohortName'. The cohort ID should correspond to the cohort_definition_id of the cohort to use for creating a covariate.

valueType	Either 'binary' or 'count'. When valueType = 'count', the covariate value will be the number of times the cohort was observed in the window.
startDay	What is the start day (relative to the index date) of the covariate window?
endDay	What is the end day (relative to the index date) of the covariate window?
includedCovariateIds	A list of covariate IDs that should be restricted to.
warnOnAnalysisIdOverlap	Warn if the provided 'analysisId' overlaps with any predefined analysis as available in the 'createCovariateSettings()' 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

analysisId	A unique identifier for this analysis.
covariateCohortDatabaseSchema	The database schema where the cohorts used to define the covariates can be found. If set to NULL, the database schema will be guessed, for example using the same one as for the main cohorts.
covariateCohortTable	The table where the cohorts used to define the covariates can be found. If set to NULL, the table will be guessed, for example using the same one as for the main cohorts.

covariateCohorts	A data frame with at least two columns: 'cohortId' and 'cohortName'. The cohort ID should correspond to the cohort_definition_id of the cohort to use for creating a covariate.
valueType	Either 'binary' or 'count'. When valueType = 'count', the covariate value will be the number of times the cohort was observed in the window.
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.
includedCovariateIds	A list of covariate IDs that should be restricted to.
warnOnAnalysisIdOverlap	Warn if the provided 'analysisId' overlaps with any predefined analysis as available in the 'createTemporalCovariateSettings()' 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,
useMeasurementValueAsConceptAnyTimePrior = FALSE,
useMeasurementValueAsConceptLongTerm = FALSE,
useMeasurementValueAsConceptMediumTerm = FALSE,
useMeasurementValueAsConceptShortTerm = FALSE,
useObservationAnyTimePrior = FALSE,
useObservationLongTerm = FALSE,
useObservationMediumTerm = FALSE,
useObservationShortTerm = FALSE,
useObservationValueAsConceptAnyTimePrior = FALSE,
useObservationValueAsConceptLongTerm = FALSE,
useObservationValueAsConceptMediumTerm = FALSE,
useObservationValueAsConceptShortTerm = 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 term 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 short term 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)
useMeasurementRangeGroupShortTerm	Covariates indicating whether measurements are below, within, or above normal range in the short term window. (analysis ID 712)
useMeasurementValueAsConceptAnyTimePrior	One covariate per measurement-value concept combination any time prior to index. (analysis ID 713)
useMeasurementValueAsConceptLongTerm	One covariate per measurement-value concept combination in the long term window. (analysis ID 714)
useMeasurementValueAsConceptMediumTerm	One covariate per measurement-value concept combination in the medium term window. (analysis ID 715)
useMeasurementValueAsConceptShortTerm	One covariate per measurement-value concept combination in the short term window. (analysis ID 716)
useObservationAnyTimePrior	One covariate per observation in the observation table any time prior to index. (analysis ID 801)
useObservationLongTerm	One covariate per observation in the observation table in the long term window. (analysis ID 802)

useObservationMediumTerm	One covariate per observation in the observation table in the medium term window. (analysis ID 803)
useObservationShortTerm	One covariate per observation in the observation table in the short term window. (analysis ID 804)
useObservationValueAsConceptAnyTimePrior	One covariate per observation-value concept combination any time prior to index. (analysis ID 805)
useObservationValueAsConceptLongTerm	One covariate per observation-value concept combination in the long term window. (analysis ID 806)
useObservationValueAsConceptMediumTerm	One covariate per observation-value concept combination in the medium term window. (analysis ID 807)
useObservationValueAsConceptShortTerm	One covariate per observation-value concept combination in the short term window. (analysis ID 808)
useCharlsonIndex	The Charlson comorbidity index (Romano adaptation) using all conditions prior to the window end. (analysis ID 901)
useDcsi	The Diabetes Comorbidity Severity Index (DCSI) using all conditions prior to the window end. (analysis ID 902)
useChads2	The CHADS2 score using all conditions prior to the window end. (analysis ID 903)
useChads2Vasc	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)
useDistinctConditionCountLongTerm	The number of distinct condition concepts observed in the long term window. (analysis ID 905)
useDistinctConditionCountMediumTerm	The number of distinct condition concepts observed in the medium term window. (analysis ID 906)
useDistinctConditionCountShortTerm	The number of distinct condition concepts observed in the short term window. (analysis ID 907)
useDistinctIngredientCountLongTerm	The number of distinct ingredients observed in the long term window. (analysis ID 908)
useDistinctIngredientCountMediumTerm	The number of distinct ingredients observed in the medium term window. (analysis ID 909)
useDistinctIngredientCountShortTerm	The number of distinct ingredients observed in the short term window. (analysis ID 910)
useDistinctProcedureCountLongTerm	The number of distinct procedures observed in the long term window. (analysis ID 911)

useDistinctProcedureCountMediumTerm	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 = TRUE,
useMeasurementValueAsConceptAnyTimePrior = FALSE,
useMeasurementValueAsConceptLongTerm = TRUE,
useMeasurementValueAsConceptMediumTerm = FALSE,
useMeasurementValueAsConceptShortTerm = TRUE,
useObservationAnyTimePrior = FALSE,
useObservationLongTerm = TRUE,
useObservationMediumTerm = FALSE,
useObservationShortTerm = TRUE,
useObservationValueAsConceptAnyTimePrior = FALSE,
useObservationValueAsConceptLongTerm = TRUE,
useObservationValueAsConceptMediumTerm = FALSE,
useObservationValueAsConceptShortTerm = 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**

```
covSettings <- createDefaultCovariateSettings(  
  includedCovariateConceptIds = c(1),  
  addDescendantsToInclude = FALSE,  
  excludedCovariateConceptIds = c(2),  
  addDescendantsToExclude = FALSE,  
  includedCovariateIds = c(1)  
)
```

---

`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**

```
covSettings <- createDefaultTemporalCovariateSettings(
  includedCovariateConceptIds = c(1),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(2),
  addDescendantsToExclude = FALSE,
  includedCovariateIds = c(1)
)
```

---

```
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**

```
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)
```

---

```
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**

```
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
)
```

---

```
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**

an empty object of class CovariateData

## Examples

```
covariateData <- FeatureExtraction::createEmptyCovariateData(
  cohortIds = 1,
  aggregated = FALSE,
  temporal = FALSE
)
```

---

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**

```
eunomiaConnectionDetails <- Eunomia::getEunomiaConnectionDetails()
covSettings <- createDefaultCovariateSettings()
Eunomia::createCohorts(
  connectionDetails = eunomiaConnectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
covData1 <- getDbCovariateData(
  connectionDetails = eunomiaConnectionDetails,
  tempEmulationSchema = NULL,
  cdmDatabaseSchema = "main",
  cdmVersion = "5",
  cohortTable = "cohort",
  cohortDatabaseSchema = "main",
  cohortTableIsTemp = FALSE,
  cohortId = 1,
  rowIdField = "subject_id",
  covariateSettings = covSettings,
  aggregated = TRUE
)
covData2 <- getDbCovariateData(
  connectionDetails = eunomiaConnectionDetails,
  tempEmulationSchema = 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
)
```

---

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

```
table1CovSettings <- createTable1CovariateSettings(
  specifications = getDefaultTable1Specifications(),
  covariateSettings = createDefaultCovariateSettings(),
  includedCovariateConceptIds = c(),
  addDescendantsToInclude = FALSE,
  excludedCovariateConceptIds = c(),
  addDescendantsToExclude = FALSE,
```

```

    includedCovariateIds = c()
  )

```

---

```
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,
  useMeasurementValueAsConcept = FALSE,
  useObservation = FALSE,
  useObservationValueAsConcept = 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)

<code>useConditionEraStart</code>	One covariate per condition in the <code>condition_era</code> 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 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>useMeasurementRangeGroup</code>	Covariates indicating whether measurements are below, within, or above normal range within the time period. (analysis ID 703)
<code>useMeasurementValueAsConcept</code>	One covariate per measurement-value concept combination within the time period. (analysis ID 704)
<code>useObservation</code>	One covariate per observation in the observation table in the time window. (analysis ID 801)
<code>useObservationValueAsConcept</code>	One covariate per observation-value concept combination within the time period. (analysis ID 802)

useCharlsonIndex	The Charlson comorbidity index (Romano adaptation) using all conditions prior to the window end. (analysis ID 901)
useDcsi	The Diabetes Comorbidity Severity Index (DCSI) using all conditions prior to the window end. (analysis ID 902)
useChads2	The CHADS2 score using all conditions prior to the window end. (analysis ID 903)
useChads2Vasc	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,
  useMeasurementValueAsConcept = TRUE,
  useObservation = TRUE,
  useObservationValueAsConcept = 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)

<code>useDemographicsAge</code>	Age of the subject on the index date (in years). (analysis ID 2)
<code>useDemographicsAgeGroup</code>	Age of the subject on the index date (in 5 year age groups) (analysis ID 3)
<code>useDemographicsRace</code>	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 condition_occurrence 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 condition_occurrence table starting in the time window. (analysis ID 102)
<code>useConditionEraStart</code>	One covariate per condition in the condition_era table starting in the time window. (analysis ID 201)
<code>useConditionEraGroupStart</code>	One covariate per condition era rolled up to SNOMED groups in the condition_era table starting in the time window. (analysis ID 203)
<code>useDrugExposure</code>	One covariate per drug in the drug_exposure table starting in the time window. (analysis ID 301)
<code>useDrugEraStart</code>	One covariate per drug in the drug_era table starting in the time window. (analysis ID 401)
<code>useDrugEraGroupStart</code>	One covariate per drug rolled up to ATC groups in the drug_era table starting in the time window. (analysis ID 403)
<code>useProcedureOccurrence</code>	One covariate per procedure in the procedure_occurrence 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')

timeInterval	Fixed interval length for timeId using the 'timePart' scale. For example, a 'timePart' of DAY with 'timeInterval' 30 has timeIds where timeId 1 is day 0 to day 29, timeId 2 is day 30 to day 59, etc.
sequenceEndDay	What is the end day (relative to the index date) of the data extraction?
sequenceStartDay	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

```
covariateData <- FeatureExtraction::createEmptyCovariateData(  
  cohortIds = c(1, 2),  
  aggregated = TRUE,  
  temporal = FALSE  
)  
  
covData <- filterByCohortDefinitionId(  
  covariateData = covariateData,  
  cohortIds = c(1)  
)
```



---

filterByRowId	<i>Filter covariates by row ID</i>
---------------	------------------------------------

---

**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**

```
covariateData <- FeatureExtraction::createEmptyCovariateData(  
  cohortIds = 1,  
  aggregated = FALSE,  
  temporal = FALSE  
)  
  
covData <- filterByRowId(  
  covariateData = covariateData,  
  rowIds = 1  
)
```

---

`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,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema")
)
```

**Arguments**

connection	A connection to the server containing the schema as created using the connect function in the DatabaseConnector package.
oracleTempSchema	DEPRECATED: use tempEmulationSchema instead.
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?
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.

**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

```
connectionDetails <- Eunomia::getEunomiaConnectionDetails()
Eunomia::createCohorts(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
connection <- DatabaseConnector::connect(connectionDetails)
covariateSettings <- createCohortAttrCovariateSettings(
  attrDatabaseSchema = "main",
  cohortAttrTable = "cohort_attribute",
  attrDefinitionTable = "attribute_definition",
  includeAttrIds = c(1),
  isBinary = FALSE,
  missingMeansZero = FALSE
)

covData <- getDbCohortAttrCovariatesData(
  connection = connection,
  tempEmulationSchema = NULL,
  cdmDatabaseSchema = "main",
  cdmVersion = "5",
  cohortTable = "cohort",
  cohortIds = 1,
  rowIdField = "subject_id",
  covariateSettings = covariateSettings,
  aggregated = FALSE
)
```

---

```
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,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema")
)
```

## Arguments

connection	A connection to the server containing the schema as created using the connect function in the DatabaseConnector package.
oracleTempSchema	DEPRECATED: use tempEmulationSchema instead.
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 [createCohortBasedCovariateSettings](#) or [createCohortBasedTemporalCovariateSettings](#) functions.

**aggregated** Should aggregate statistics be computed instead of covariates per cohort entry?

**minCharacterizationMean**

The minimum mean value for binary 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.

**tempEmulationSchema**

Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.

**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 `ffdf` 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.

---

<code>getDbCovariateData</code>	<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,
    tempEmulationSchema = getOption("sqlRenderTempEmulationSchema")
  )

```

## 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

DEPRECATED: use `tempEmulationSchema` instead.

### 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 useful if there is more than one period per person.

### covariateSettings

Either an object of type `covariateSettings` as created using one of the `createCovariate` functions, or a list of such objects.

### aggregated

Should aggregate statistics be computed instead of covariates per cohort entry? If `aggregated` is set to `FALSE`, the results returned will be based on each `subject_id` and `cohort_start_date` in your cohort table. If your cohort contains multiple entries for the same `subject_id` (due to different `cohort_start_date` values),

you must carefully set the `rowIdField` so you can identify the patients properly. See issue #229 for more discussion on this parameter.

`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.

`tempEmulationSchema`

Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.

## 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

```
eunomiaConnectionDetails <- Eunomia::getEunomiaConnectionDetails()
covSettings <- createDefaultCovariateSettings()
Eunomia::createCohorts(
  connectionDetails = eunomiaConnectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
covData <- getDbCovariateData(
  connectionDetails = eunomiaConnectionDetails,
  tempEmulationSchema = NULL,
  cdmDatabaseSchema = "main",
  cdmVersion = "5",
  cohortTable = "cohort",
  cohortDatabaseSchema = "main",
  cohortTableIsTemp = FALSE,
  cohortIds = -1,
  rowIdField = "subject_id",
  covariateSettings = covSettings,
  aggregated = FALSE
)
```

---

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,
  tempEmulationSchema = getOption("sqlRenderTempEmulationSchema")
)
```

## Arguments

connection	A connection to the server containing the schema as created using the connect function in the DatabaseConnector package.
oracleTempSchema	DEPRECATED: use tempEmulationSchema instead.
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 binary 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.
tempEmulationSchema	Some database platforms like Oracle and Impala do not truly support temp tables. To emulate temp tables, provide a schema with write privileges where temp tables can be created.

## 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 `ffdf` 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**

```

connectionDetails <- Eunomia::getEunomiaConnectionDetails()
Eunomia::createCohorts(
  connectionDetails = connectionDetails,
  cdmDatabaseSchema = "main",
  cohortDatabaseSchema = "main",
  cohortTable = "cohort"
)
connection <- DatabaseConnector::connect(connectionDetails)

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

```

---

```
getDefaultTable1Specifications
```

*Get the default table 1 specifications*

---

**Description**

Loads the default specifications for a table 1, to be used with the [createTable1](#) function.

**Usage**

```
getDefaultTable1Specifications()
```

**Value**

A specifications objects.

**Examples**

```
defaultTable1Specs <- getDefaultTable1Specifications()
```

---

```
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**

```
covariateData <- FeatureExtraction::createEmptyCovariateData(  
  cohortIds = 1,  
  aggregated = FALSE,  
  temporal = FALSE  
)  
isAggrCovData <- isAggregatedCovariateData(covariateData)
```

---

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**

```
binaryCovDataFile <- system.file("testdata/binaryCovariateData.zip",  
  package = "FeatureExtraction")  
covData <- loadCovariateData(binaryCovDataFile)  
isCovData <- isCovariateData(covData)
```

---

isTemporalCovariateData	<i>Check whether covariate data is temporal</i>
-------------------------	---

---

**Description**

Check whether covariate data is temporal

**Usage**

```
isTemporalCovariateData(x)
```

**Arguments**

x	The covariate data object to check.
---	-------------------------------------

**Value**

A logical value.

**Examples**

```
covariateData <- FeatureExtraction::createEmptyCovariateData(  
  cohortIds = 1,  
  aggregated = FALSE,  
  temporal = FALSE  
)  
isTempCovData <- isTemporalCovariateData(covariateData)
```

---

loadCovariateData	<i>Load the covariate data from a folder</i>
-------------------	--

---

**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**

```
binaryCovDataFile <- system.file("testdata/binaryCovariateData.zip",
  package = "FeatureExtraction")
covData <- loadCovariateData(binaryCovDataFile)
```

---

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.

**Value**

No return value, called for side effects.

**Examples**

```
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)
```

---

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.

## Value

An object of class CovariateData.

## Examples

```
covariateData <- FeatureExtraction::createEmptyCovariateData(  
  cohortIds = 1,  
  aggregated = FALSE,  
  temporal = FALSE  
)  
  
covData <- tidyCovariateData(  
  covariateData = covariateData,  
  minFraction = 0.001,  
  normalize = TRUE,  
  removeRedundancy = TRUE  
)
```

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