# Package 'SelfControlledCaseSeries'

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**Type** Package

**Title** Self-Controlled Case Series

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**Description** SelfControlledCaseSeries is an R package for performing self-controlled case series (SCCS) analyses in an observational database in the OMOP Common Data Model.

**VignetteBuilder** knitr

**Depends** R (>= 3.2.2),
Cyclops (>= 1.2.0),
DatabaseConnector (>= 1.11.4)

**Imports** RJDBC,
SqlRender (>= 1.1.1),
bit,
ff,
ffbase (>= 0.12.1),
Rcpp (>= 0.11.2),
OhdsiRTools (>= 1.1.1),
splines,
ggplot2

**Suggests** testthat,
knitr,
rmarkdown,
EmpiricalCalibration

**License** Apache License 2.0

**LinkingTo** Rcpp

**NeedsCompilation** yes

**RoxygenNote** 6.0.1

# R topics documented:

computeMdrr                *Compute the minimum detectable relative risk*

### Description

Compute the minimum detectable relative risk

### Usage

```
computeMdrr(sccsEraData, exposureCovariateId, alpha = 0.05, power = 0.8,
  twoSided = TRUE, method = "binomial")
```

### Arguments

sccsEraData       An object containing study population observation time, outcomesa and covari-
                  ates as created using the [createSccsEraData](#) function. This should include the
                  following dataframes: outcomes, covariates, and covariateRef.

exposureCovariateId
                  Covariate Id for the health exposure of interest.

alpha             Type I error.

| power | 1 - beta, where beta is the type II error. |
|---|---|
| twoSided | Consider a two-sided test? |
| method | The type of sample size formula that will be used. Allowable values are "proportion", "binomial", "SRL1", "SRL2", or "ageEffects". Currently "ageEffects" is not supported. |

## Details

Compute the minimum detectable relative risk (MDRR) for a given study population, using the observerd time at risk and total time in days and number of events. Five sample size formulas are implemented: sampling proportion, binomial proportion, 2 signed root likelihood ratio methods, and likelihood extension for age effects. The expressions by Musonda (2006) are used.

## Value

A data frame with the MDRR, number of events, time at risk, and total time.

## References

Musonda P, Farrington CP, Whitaker HJ (2006) Samples sizes for self-controlled case series studies, Statistics in Medicine, 15;25(15):2618-31

---

createAgeSettings *Create age settings*

---

## Description

Create age settings

## Usage

```
createAgeSettings(includeAge = FALSE, ageKnots = 5,
  allowRegularization = FALSE, minAge = NULL, maxAge = NULL)
```

## Arguments

| includeAge | Should age be included in the model? |
|---|---|
| ageKnots | If a single number is provided this is assumed to indicate the number of knots to use for the spline, and the knots are automatically spaced according to equal percentiles of the data. If more than one number is provided these are assumed to be the exact location of the knots in age-days |
| allowRegularization | |
| | When fitting the model, should the covariates defined here be allowed to be regularized? |
| minAge | Minimum age at which patient time will be included in the analysis. Note that information prior to the min age is still used to determine exposure status after the minimum age (e.g. when a prescription was started just prior to reaching the minimum age). Also, outcomes occurring before the minimum age is reached will be considered as prior outcomes when using first outcomes only. Age should be specified in years, but non-integer values are allowed. If not specified, no age restriction will be applied. |

maxAge          Maximum age at which patient time will be included in the analysis. Age should
                be specified in years, but non-integer values are allowed. If not specified, no age
                restriction will be applied.

## Details

Create an object specifing whether and how age should be included in the model. Age can be
included by splitting patient time into calendar months. During a month, the relative risk attributed
to age is assumed to be constant, and the risk from month to month is modeled using a cubic spline.

## Value

An object of type `ageSettings`.

---

createCovariateSettings

*Create covariate settings*

---

## Description

Create covariate settings

## Usage

```
createCovariateSettings(includeCovariateIds = NULL,
  excludeCovariateIds = NULL, label = "Covariates", stratifyById = TRUE,
  start = 0, addExposedDaysToStart = FALSE, end = 0,
  addExposedDaysToEnd = FALSE, firstOccurrenceOnly = FALSE,
  splitPoints = c(), allowRegularization = FALSE)
```

## Arguments

includeCovariateIds
                One or more IDs of variables in the `sccsData` object that should be used to
                construct this covariate. If no IDs are specified, all variables will be used.

excludeCovariateIds
                One or more IDs of variables in the `sccsData` object that should not be used to
                construct this covariate.

label           A label used to identify the covariates created using these settings.

stratifyById    Should a single covariate be created for every ID in the `sccsData` object, or
                should a single covariate be constructed? For example, if the IDs identify ex-
                posures to different drugs, should a covariate be constructed for every drug, or
                a single covariate for exposure to any of these drugs. Note that overlap will be
                considered a single exposure.

start           The start of the risk window in days, relative to the exposure start date.

addExposedDaysToStart
                Should the length of exposure be added to the start date?

end             The start of the risk window in days, relative to the exposure start date.

addExposedDaysToEnd
                Should the length of exposure be added to the end date?

firstOccurrenceOnly
:   Should only the first occurrence of the exposure be used?

splitPoints
:   To split the risk window into several smaller windows, specify the end of each sub- window relative to the start of the main risk window. If addExposed- DaysToStart is TRUE, the split points will be considered to be relative to the end of the main risk window instead.

allowRegularization
:   When fitting the model, should the covariates defined here be allowed to be regularized?

## Details

Create an object specifying how to create a (set of) covariates.

## Value

An object of type covariateSettings.

---

createCreateSccsEraDataArgs

*Create a parameter object for the function createSccsEraData*

---

## Description

Create a parameter object for the function createSccsEraData

## Usage

```
createCreateSccsEraDataArgs(naivePeriod = 0, firstOutcomeOnly = FALSE,
  covariateSettings, ageSettings = createAgeSettings(includeAge = FALSE),
  seasonalitySettings = createSeasonalitySettings(includeSeasonality = FALSE),
  eventDependentObservation = FALSE)
```

## Arguments

naivePeriod
:   The number of days at the start of a patient's observation periodthat should not be included in the risk calculations. Note thatthe naive period can be used to determine current covariatestatus right after the naive period, and whether an outcome isthe first one.

firstOutcomeOnly
:   Whether only the first occurrence of an outcome should beconsidered.

covariateSettings
:   Either an object of type covariateSettings as createdusing the createCovariate- Settings function, or alist of such objects.

ageSettings
:   An object of type ageSettings as created using thecreateAgeSettings function.

seasonalitySettings
:   An object of type seasonalitySettings as created using thecreateSeasonalitySet- tings function.

eventDependentObservation
:   Should the extension proposed by Farrington et al. be used toadjust for event- dependent observation time?

## Details

Create an object defining the parameter values.

---

createExposureOutcome     *Create a exposure-outcome combination.*

---

## Description

Create a exposure-outcome combination.

## Usage

    createExposureOutcome(exposureId, outcomeId, ...)

## Arguments

exposureId     A concept ID indentifying the target drug in the exposure table. If multiple
               strategies for picking the exposure will be tested in the analysis, a named list
               of numbers can be provided instead. In the analysis, the name of the num-
               ber to be used can be specified using the #' exposureType parameter in the
               createSccsAnalysis function.

outcomeId      A concept ID indentifying the outcome in the outcome table.

...            Custom variables, to be used in the analyses.

## Details

Create a set of hypotheses of interest, to be used with the runSccsAnalyses function.

---

createFitSccsModelArgs

                           *Create a parameter object for the function fitSccsModel*

---

## Description

Create a parameter object for the function fitSccsModel

## Usage

    createFitSccsModelArgs(prior = createPrior("laplace", useCrossValidation =
      TRUE), control = createControl(cvType = "auto", selectorType = "byPid",
      startingVariance = 0.1, noiseLevel = "quiet"))

## Arguments

prior          The prior used to fit the model. See createPrior fordetails.

control        The control object used to control the cross-validation used to determine thehy-
               perparameters of the prior (if applicable). SeecreateControl for details.

## Details

Create an object defining the parameter values.

---

createGetDbSccsDataArgs

*Create a parameter object for the function getDbSccsData*

---

## Description

Create a parameter object for the function getDbSccsData

## Usage

```
createGetDbSccsDataArgs(useCustomCovariates = FALSE,
  deleteCovariatesSmallCount = 100, studyStartDate = "",
  studyEndDate = "", exposureIds = "exposureId", customCovariateIds = "")
```

## Arguments

useCustomCovariates

        Create covariates from a custom table?

deleteCovariatesSmallCount

        The minimum count for a covariate to appear in the data to bekept.

studyStartDate  A calendar date specifying the minimum date where data isused. Date format is 'yyyymmdd'.

studyEndDate  A calendar date specifying the maximum date where data isused. Date format is 'yyyymmdd'.

exposureIds  A list of identifiers to define the exposures of interest. IfexposureTable = DRUG_ERA, exposureIds should be CONCEPT_ID.If exposureTable <> DRUG_ERA, exposureIds is used to selectthe cohort_concept_id in the cohort-like table. If noexposureIds are provided, all drugs or cohorts in theexposureTable are included as exposures.

customCovariateIds

        A list of cohort definition IDS identifying the records inthe customCovariateTable to use for building customcovariates.

## Details

Create an object defining the parameter values.

---

createSccsAnalysis     *Create a SelfControlledCaseSeries analysis specification*

---

## Description

Create a SelfControlledCaseSeries analysis specification

## Usage

```
createSccsAnalysis(analysisId = 1, description = "", exposureType = NULL,
  outcomeType = NULL, getDbSccsDataArgs, createSccsEraDataArgs,
  fitSccsModelArgs)
```

## Arguments

| | |
|---|---|
| analysisId | An integer that will be used later to refer to this specific set of analysis choices. |
| description | A short description of the analysis. |
| exposureType | If more than one exposure is provided for each exposureOutcome, this field should be used to select the specific exposure to use in this analysis. |
| outcomeType | If more than one outcome is provided for each exposureOutcome, this field should be used to select the specific outcome to use in this analysis. |
| getDbSccsDataArgs | |
| | An object representing the arguments to be used when calling the [getDbSccsData](#) function. |
| createSccsEraDataArgs | |
| | An object representing the arguments to be used when calling the [createSccsEraData](#) function. |
| fitSccsModelArgs | |
| | An object representing the arguments to be used when calling the [fitSccsModel](#) function. |

## Details

Create a set of analysis choices, to be used with the [runSccsAnalyses](#) function.

---

createSccsEraData            *Create SCCS era data*

---

## Description

Create SCCS era data

## Usage

```
createSccsEraData(sccsData, outcomeId = NULL, naivePeriod = 0,
  firstOutcomeOnly = FALSE, covariateSettings,
  ageSettings = createAgeSettings(includeAge = FALSE),
  seasonalitySettings = createSeasonalitySettings(includeSeasonality = FALSE),
  eventDependentObservation = FALSE)
```

## Arguments

| | |
|---|---|
| sccsData | An object of type sccsData as created using the [getDbSccsData](#) function. |
| outcomeId | The outcome to create the era data for. If not specified it is assumed to be the one outcome for which the data was loaded from the database. |
| naivePeriod | The number of days at the start of a patient's observation period that should not be included in the risk calculations. Note that the naive period can be used to determine current covariate status right after the naive period, and whether an outcome is the first one. |
| firstOutcomeOnly | |
| | Whether only the first occurrence of an outcome should be considered. |
| covariateSettings | |
| | Either an object of type covariateSettings as created using the [createCovariateSettings](#) function, or a list of such objects. |

| ageSettings | An object of type ageSettings as created using the createAgeSettings function. |
| seasonalitySettings | |
| | An object of type seasonalitySettings as created using the createSeasonalitySettings function. |
| eventDependentObservation | |
| | Should the extension proposed by Farrington et al. be used to adjust for event-dependent observation time? |

## Details

This function creates covariates based on the data in the sccsData object, according to the provided settings. It chops patient time into periods during which all covariates remain constant. The output details these periods, their durations, and a sparse representation of the covariate values.

## Value

An object of type sccsEraData.

## References

Farrington, C. P., Anaya-Izquierdo, A., Whitaker, H. J., Hocine, M.N., Douglas, I., and Smeeth, L. (2011). Self-Controlled case series analysis with event-dependent observation periods. Journal of the American Statistical Association 106 (494), 417-426

---

createSccsSimulationSettings

*Create SCCS simulation settings*

---

## Description

Create SCCS simulation settings

## Usage

```
createSccsSimulationSettings(meanPatientTime = 4 * 365, sdPatientTime = 2 *
  365, minAge = 18 * 365, maxAge = 65 * 365, minBaselineRate = 0.001,
  maxBaselineRate = 0.01, covariateIds = c(1, 2), patientUsages = c(0.2,
  0.1), usageRate = c(0.01, 0.01), meanPrescriptionDurations = c(14, 30),
  sdPrescriptionDurations = c(7, 14),
  simulationRiskWindows = list(createSimulationRiskWindow(relativeRisks = 1),
  createSimulationRiskWindow(relativeRisks = 1.5)), includeAgeEffect = TRUE,
  ageKnots = 5, includeSeasonality = TRUE, seasonKnots = 5,
  outcomeId = 10)
```

## Arguments

| meanPatientTime | |
| | Mean number of observation days per patient. |
| sdPatientTime | Standard deviation of the observation days per patient. |
| minAge | The minimum age in days. |

| maxAge | The maximum age in days. |
|---|---|

minBaselineRate

The minimum baseline rate (per day).

maxBaselineRate

The maximum baseline rate (per day).

| covariateIds | The IDs for the covariates to be generated. |
|---|---|
| patientUsages | The fraction of patients that use the drugs. |
| usageRate | The rate of prescriptions per person that uses the drug. |

meanPrescriptionDurations

The mean duration of a prescription, per drug.

sdPrescriptionDurations

The standard deviation of the duration of a prescription, per drug.

simulationRiskWindows

One or a list of objects of type simulationRiskWindow as created using the [createSimulationRiskWindow](createSimulationRiskWindow) function.

includeAgeEffect

Include an age effect for the outcome?

| ageKnots | Number of knots in the age spline. |
|---|---|

includeSeasonality

Include seasonality for the outcome?

| seasonKnots | Number of knots in the seasonality spline. |
|---|---|
| outcomeId | The ID to be used for the outcome. |

### Details

Create an object of settings for an SCCS simulation.

### Value

An object of type sccsSimulationSettings.

---

createSeasonalitySettings

*Create seasonality settings*

---

### Description

Create seasonality settings

### Usage

```
createSeasonalitySettings(includeSeasonality = FALSE, seasonKnots = 5,
  allowRegularization = FALSE)
```

## Arguments

includeSeasonality

> Should seasonlaity be included in the model?

seasonKnots       If a single number is provided this is assumed to indicate the number of knots to use for the spline, and the knots are automatically equaly spaced across the year. If more than one number is provided these are assumed to be the exact location of the knots in days relative to the start of the year.

allowRegularization

> When fitting the model, should the covariates defined here be allowed to be regularized?

## Details

Create an object specifing whether and how seasonality should be included in the model. Seasonality can be included by splitting patient time into calendar months. During a month, the relative risk attributed to season is assumed to be constant, and the risk from month to month is modeled using a cyclic cubic spline.

## Value

An object of type `seasonalitySettings`.

---

createSimulationRiskWindow

*Create a risk window definition for simulation*

---

## Description

Create a risk window definition for simulation

## Usage

```
createSimulationRiskWindow(start = 0, end = 0, addExposedDaysToEnd = TRUE,
  splitPoints = c(), relativeRisks = c(0))
```

## Arguments

start            Start of the risk window relative to exposure start.

end              End of risk window relative to exposure start, or if `addExposedDaysToEnd` is TRUE, relative to the end date.

addExposedDaysToEnd

> Should the length of exposure be added to the end date? In other words, should the exposure end date be used as reference point for the risk window end?

splitPoints      Subdivision of the risk window in to smaller sub-windows.

relativeRisks    Either a single number representing the relative risk in the risk window, or when splitPoints have been defined a vector of relative risks, one for each sub-window.

## Value

An object of type `simulationRiskWindow`.

---

cyclicSplineDesign      *Create a design matrix for a cyclic spline*

---

### Description

Create a design matrix for a cyclic spline

### Usage

```
cyclicSplineDesign(x, knots, ord = 4)
```

### Arguments

| | |
|---|---|
| x | Vector of coordinates of the points to be interpolated. |
| knots | Location of the knots. |
| ord | Order of the spline function. |

### Details

This function is used by other functions in this package.

---

fitSccsModel      *Fit the SCCS model*

---

### Description

Fit the SCCS model

### Usage

```
fitSccsModel(sccsEraData, prior = createPrior("laplace", useCrossValidation =
  TRUE), control = createControl(cvType = "auto", selectorType = "byPid",
  startingVariance = 0.1, noiseLevel = "quiet"))
```

### Arguments

| | |
|---|---|
| sccsEraData | An object of type sccsEraData as created using the createSccsEraData function. |
| prior | The prior used to fit the model. See createPrior for details. |
| control | The control object used to control the cross-validation used to determine the hyperparameters of the prior (if applicable). See createControl for details. |

### Details

Fits the SCCS model as a conditional Poisson regression. When allowed, coefficients for some or all covariates can be regularized.

### Value

An object of type sccsModel. Generic functions summary, coef, and confint are available.

**References**

Suchard, M.A., Simpson, S.E., Zorych, I., Ryan, P., and Madigan, D. (2013). Massive parallelization of serial inference algorithms for complex generalized linear models. ACM Transactions on Modeling and Computer Simulation 23, 10

---

| getDbSccsData | *Load data for SCCS from the database* |
| --- | --- |

---

**Description**

Load all data needed to perform an SCCS analysis from the database.

**Usage**

```
getDbSccsData(connectionDetails, cdmDatabaseSchema,
  oracleTempSchema = cdmDatabaseSchema,
  outcomeDatabaseSchema = cdmDatabaseSchema, outcomeTable = "condition_era",
  outcomeIds, exposureDatabaseSchema = cdmDatabaseSchema,
  exposureTable = "drug_era", exposureIds = c(),
  useCustomCovariates = FALSE,
  customCovariateDatabaseSchema = cdmDatabaseSchema,
  customCovariateTable = "cohort", customCovariateIds = c(),
  deleteCovariatesSmallCount = 100, studyStartDate = "",
  studyEndDate = "", cdmVersion = "4")
```

**Arguments**

connectionDetails

>              An R object of type `ConnectionDetails` created using the function `createConnectionDetails` in the `DatabaseConnector` package.

cdmDatabaseSchema

>              The name of the database schema that contains the OMOP CDM instance. Requires read permissions to this database. On SQL Server, this should specifiy both the database and the schema, so for example 'cdm_instance.dbo'.

oracleTempSchema

>              A schema where temp tables can be created in Oracle.

outcomeDatabaseSchema

>              The name of the database schema that is the location where the data used to define the outcome cohorts is available. If outcomeTable = CONDITION_ERA, outcomeDatabaseSchema is not used. Requires read permissions to this database.

outcomeTable

>              The tablename that contains the outcome cohorts. If outcomeTable is not CONDITION_OCCURRENCE or CONDITION_ERA, then expectation is outcomeTable has format of COHORT table: COHORT_DEFINITION_ID, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.

outcomeIds

>              A list of ids used to define outcomes. If outcomeTable = CONDITION_OCCURRENCE, the list is a set of ancestor CONCEPT_IDs, and all occurrences of all descendant concepts will be selected. If outcomeTable <> CONDITION_OCCURRENCE, the list contains records found in COHORT_DEFINITION_ID field.

exposureDatabaseSchema

> The name of the database schema that is the location where the exposure data
> used to define the exposure cohorts is available. If exposureTable = DRUG_ERA,
> exposureDatabaseSchema is not used but assumed to be cdmSchema. Requires
> read permissions to this database.

exposureTable    The tablename that contains the exposure cohorts. If exposureTable <> DRUG_ERA,
then expectation is exposureTable has format of COHORT table: cohort_concept_id,
SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.

exposureIds      A list of identifiers to define the exposures of interest. If exposureTable =
DRUG_ERA, exposureIds should be CONCEPT_ID. If exposureTable <> DRUG_ERA,
exposureIds is used to select the cohort_concept_id in the cohort-like table. If no
exposureIds are provided, all drugs or cohorts in the exposureTable are included
as exposures.

useCustomCovariates

> Create covariates from a custom table?

customCovariateDatabaseSchema

> The name of the database schema that is the location where the custom covariate
> data is available.

customCovariateTable

> Name of the table holding the custom covariates. This table should have the
> same structure as the cohort table.

customCovariateIds

> A list of cohort definition IDS identifying the records in the customCovari-
> ateTable to use for building custom covariates.

deleteCovariatesSmallCount

> The minimum count for a covariate to appear in the data to be kept.

studyStartDate   A calendar date specifying the minimum date where data is used. Date format
is 'yyyymmdd'.

studyEndDate     A calendar date specifying the maximum date where data is used. Date format
is 'yyyymmdd'.

cdmVersion       Define the OMOP CDM version used: currently support "4" and "5".

**Details**

This function downloads several types of information:

- Information on the occurrences of the outcome(s) of interest. Note that information for mul-
  tiple outcomes can be fetched in one go, and later the specific outcome can be specified for
  which we want to build a model.

- Information on the observation time and age for the people with the outcomes.

- Information on exposures of interest which we want to include in the model.

Four different database schemas can be specified, for four different types of information: The
cdmDatabaseSchema is used to extract patient age and observation period. The outcomeDatabaseSchema
is used to extract information about the outcomes, the exposureDatabaseSchema is used to retrieve
information on exposures, and the customCovariateDatabaseSchema is optionally used to find ad-
ditional, user-defined covariates. All four locations could point to the same database schema.

**Value**

Returns an object of type sccsData, containing information on the cases, their outcomes, exposures, and potentially other covariates. Information about multiple outcomes can be captured at once for efficiency reasons. This object is a list with the following components:

**cases** An ffdf object listing the persons that have the outcome(s), their age, and observation time.

**eras** An ffdf object listing the exposures, outcomes and other covariates.

**covariateRef** An ffdf object describing the covariates that have been extracted.

**metaData** A list of objects with information on how the sccsData object was constructed.

The generic summary() function has been implemented for this object.

---

getModel                    *Output the full model*

---

**Description**

Output the full model

**Usage**

```
getModel(sccsModel)
```

**Arguments**

sccsModel        An object of type sccsModel as created using the [fitSccsModel](#) function.

**Value**

A data frame with the coefficients and confidence intervals (when not-regularized) for all covariates in the model.

---

loadExposureOutcomeList
                    *Load a list of exposureOutcome from file*

---

**Description**

Load a list of objects of type exposureOutcome from file. The file is in JSON format.

**Usage**

```
loadExposureOutcomeList(file)
```

**Arguments**

file             The name of the file

**Value**

A list of objects of type exposureOutcome.

loadSccsAnalysisList     *Load a list of sccsAnalysis from file*

### Description

Load a list of objects of type `sccsAnalysis` from file. The file is in JSON format.

### Usage

```
loadSccsAnalysisList(file)
```

### Arguments

| | |
|---|---|
| file | The name of the file |

### Value

A list of objects of type `sccsAnalysis`.

loadSccsData     *Load the SCCS data from a folder*

### Description

`loadSccsData` loads an object of type sccsData from a folder in the file system.

### Usage

```
loadSccsData(folder, readOnly = TRUE)
```

### Arguments

| | |
|---|---|
| folder | The name of the folder containing the data. |
| readOnly | 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 cohortData.

---

loadSccsEraData *Load the SCCS era data from a folder*

---

### Description

loadSccsEraData loads an object of type sccsEraData from a folder in the file system.

### Usage

```
loadSccsEraData(folder, readOnly = FALSE)
```

### Arguments

folder          The name of the folder containing the data.

readOnly        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 sccsEraData

---

plotAgeEffect *Plot the age effect*

---

### Description

Plot the age effect

### Usage

```
plotAgeEffect(sccsModel, rrLim = c(0.1, 10), fileName = NULL)
```

### Arguments

sccsModel       An object of type sccsModel as created using the [fitSccsModel](#) function.

rrLim           The limits on the incidence rate ratio scale in the plot.

fileName        Name of the file where the plot should be saved, for example 'plot.png'. See the
                function ggsave in the ggplot2 package for supported file formats.

### Details

Plot the spline curve of the age effect.

---

plotSeasonality            *Plot the seasonality effect*

---

### Description

Plot the seasonality effect

### Usage

```
plotSeasonality(sccsModel, rrLim = c(0.1, 10), fileName = NULL)
```

### Arguments

| | |
|---|---|
| sccsModel | An object of type sccsModel as created using the [fitSccsModel](#) function. |
| rrLim | The limits on the incidence rate ratio scale in the plot. |
| fileName | Name of the file where the plot should be saved, for example 'plot.png'. See the function ggsave in the ggplot2 package for supported file formats. |

### Details

Plot the spline curve of the seasonality effect.

---

runSccsAnalyses            *Run a list of analyses*

---

### Description

Run a list of analyses

### Usage

```
runSccsAnalyses(connectionDetails, cdmDatabaseSchema,
  oracleTempSchema = cdmDatabaseSchema,
  exposureDatabaseSchema = cdmDatabaseSchema, exposureTable = "drug_era",
  outcomeDatabaseSchema = cdmDatabaseSchema, outcomeTable = "condition_era",
  customCovariateDatabaseSchema = cdmDatabaseSchema,
  customCovariateTable = "cohort", cdmVersion = 5,
  outputFolder = "./SccsOutput", sccsAnalysisList, exposureOutcomeList,
  combineDataFetchAcrossOutcomes = TRUE, getDbSccsDataThreads = 1,
  createSccsEraDataThreads = 1, fitSccsModelThreads = 1, cvThreads = 1)
```

### Arguments

connectionDetails

> An R object of type ConnectionDetails created using the function createConnectionDetails
> in the DatabaseConnector package.

cdmDatabaseSchema

> The name of the database schema that contains the OMOP CDM instance. Re-
> quires read permissions to this database. On SQL Server, this should specifiy
> both the database and the schema, so for example 'cdm_instance.dbo'.

oracleTempSchema

> A schema where temp tables can be created in Oracle.

exposureDatabaseSchema

> The name of the database schema that is the location where the exposure data used to define the exposure cohorts is available. If exposureTable = DRUG_ERA, exposureDatabaseSchema is not used but assumed to be cdmSchema. Requires read permissions to this database.

exposureTable     The tablename that contains the exposure cohorts. If exposureTable <> DRUG_ERA, then expectation is exposureTable has format of COHORT table: cohort_concept_id, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.

outcomeDatabaseSchema

> The name of the database schema that is the location where the data used to define the outcome cohorts is available. If outcomeTable = CONDITION_ERA, outcomeDatabaseSchema is not used. Requires read permissions to this database.

outcomeTable     The tablename that contains the outcome cohorts. If outcomeTable is not CON-DITION_OCCURRENCE or CONDITION_ERA, then expectation is outcomeTable has format of COHORT table: COHORT_DEFINITION_ID, SUBJECT_ID, COHORT_START_DATE, COHORT_END_DATE.

customCovariateDatabaseSchema

> The name of the database schema that is the location where the custom covariate data is available.

customCovariateTable

> Name of the table holding the custom covariates. This table should have the same structure as the cohort table.

cdmVersion     Define the OMOP CDM version used: currently support "4" and "5".

outputFolder     Name of the folder where all the outputs will written to.

sccsAnalysisList

> A list of objects of type sccsAnalysis as created using the [createSccsAnalysis](createSccsAnalysis) function.

exposureOutcomeList

> A list of objects of type exposureOutcome as created using the [createExposureOutcome](createExposureOutcome) function.

combineDataFetchAcrossOutcomes

> Should fetching data from the database be done one outcome at a time, or for all outcomes in one fetch? Combining fetches will be more efficient if there is large overlap in the subjects that have the different outcomes.

getDbSccsDataThreads

> The number of parallel threads to use for building the sccsData objects.

createSccsEraDataThreads

> The number of parallel threads to use for building the sccsEraData objects.

fitSccsModelThreads

> The number of parallel threads to use for fitting the models.

cvThreads     The number of parallel threads to use for the cross- validation when estimating the hyperparameter for the outcome model. Note that the total number of CV threads at one time could be 'fitSccsModelThreads * cvThreads'.

## Details

Run a list of analyses for the drug-comparator-outcomes of interest. This function will run all specified analyses against all hypotheses of interest, meaning that the total number of outcome

models is 'length(cmAnalysisList) * length(drugComparatorOutcomesList)' (if all analyses specify an outcome model should be fitted). When you provide several analyses it will determine whether any of the analyses have anything in common, and will take advantage of this fact. For example, if we specify several analyses that only differ in the way the outcome model is fitted, then this function will extract the data and fit the propensity model only once, and re-use this in all the analysis.

## Value

A data frame with the following columns:

| | |
|---|---|
| analysisId | The unique identifier for a set of analysis choices. |
| exposureId | The ID of the target drug. |
| outcomeId | The ID of the outcome. |
| sccsDataFolder | The folder where the sccsData object is stored. |
| sccsEraDataFolder | The folder where the sccsEraData object is stored. |
| sccsModelFile | The file where the fitted SCCS model is stored. |

---

saveExposureOutcomeList

*Save a list of exposureOutcome to file*

---

## Description

Write a list of objects of type exposureOutcome to file. The file is in JSON format.

## Usage

```
saveExposureOutcomeList(exposureOutcomeList, file)
```

## Arguments

| | |
|---|---|
| exposureOutcomeList | |
| | The exposureOutcome list to be written to file |
| file | The name of the file where the results will be written |

---

saveSccsAnalysisList     *Save a list of sccsAnalysis to file*

---

## Description

Write a list of objects of type sccsAnalysis to file. The file is in JSON format.

## Usage

```
saveSccsAnalysisList(sccsAnalysisList, file)
```

## Arguments

| | |
|---|---|
| sccsAnalysisList | |
| | The sccsAnalysis list to be written to file |
| file | The name of the file where the results will be written |

---

saveSccsData *Save the SCCS data to folder*

---

### Description

sccsData saves an object of type sccsData to folder.

### Usage

```
saveSccsData(sccsData, folder)
```

### Arguments

sccsData      An object of type sccsData as generated using [getDbSccsData](#).

folder          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 specified folder.

### Examples

```
# todo
```

---

saveSccsEraData *Save the SCCS era data to folder*

---

### Description

saveSccsEraData saves an object of type sccsEraData to folder.

### Usage

```
saveSccsEraData(sccsEraData, folder)
```

### Arguments

sccsEraData    An object of type sccsEraData as generated using [createSccsEraData](#).

folder          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 specified folder.

SelfControlledCaseSeries

*SelfControlledCaseSeries*

### Description

SelfControlledCaseSeries

simulateSccsData            *Simulate SCCS data*

### Description

Simulate SCCS data

### Usage

    simulateSccsData(nCases, settings)

### Arguments

| | |
|---|---|
| nCases | The number of cases to simulate. |
| settings | An object of type sccsSimulationSettings as created using the [createSccsSimulationSettings](#) |

### Value

An object of type sccsData.

summarizeSccsAnalyses  *Create a summary report of the analyses*

### Description

Create a summary report of the analyses

### Usage

    summarizeSccsAnalyses(outcomeReference)

### Arguments

outcomeReference

A data.frame as created by the [runSccsAnalyses](#) function.

### Value

A data frame with the following columns:

| | |
|---|---|
| analysisId | The unique identifier for a set of analysis choices. |
| targetId | The ID of the target drug. |
| comparatorId | The ID of the comparator group. |
| indicationConceptIds | The ID(s) of indications in which to nest to study. |
| outcomeId | The ID of the outcome. |
| rr | The estimated effect size. |
| ci95lb | The lower bound of the 95 percent confidence interval. |
| ci95ub | The upper bound of the 95 percent confidence interval. |
| treated | The number of subjects in the treated group (after any trimming and matching). |
| comparator | The number of subjects in the comparator group (after any trimming and matching). |
| eventsTreated | The number of outcomes in the treated group (after any trimming and matching). |
| eventsComparator | The number of outcomes in the comparator group (after any trimming and matching). |
| logRr | The log of the estimated relative risk. |
| seLogRr | The standard error of the log of the estimated relative risk. |

# Index