

# Package ‘SelfControlledCaseSeries’

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**Type** Package

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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 (>= 2.0.0)

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

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

**License** Apache License 2.0

**LinkingTo** Rcpp

**NeedsCompilation** yes

**RoxygenNote** 6.0.1

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computeMdr	<i>Compute the minimum detectable relative risk</i>
------------	---

---

## Description

Compute the minimum detectable relative risk

## Usage

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

## Arguments

sccsEraData	An object containing study population observation time, outcomes and covariates as created using the <a href="#">createSccsEraData</a> 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 observed 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	<i>Create age settings</i>
-------------------	----------------------------

---

### 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 specifying 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	<i>Create covariate settings</i>
-------------------------	----------------------------------

---

### 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 exposures 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 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**

Create an object defining the parameter values.

---

`createExposureOutcome` *Create a exposure-outcome combination.*

---

**Description**

Create a exposure-outcome combination.

**Usage**

```
createExposureOutcome(exposureId, outcomeId, ...)
```

**Arguments**

<code>exposureId</code>	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 number to be used can be specified using the <code>#'</code> <code>exposureType</code> parameter in the <a href="#">createSccsAnalysis</a> function.
<code>outcomeId</code>	A concept ID indentifying the outcome in the outcome table.
<code>...</code>	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**

<code>prior</code>	The prior used to fit the model. See <code>createPrior</code> for details.
<code>control</code>	The control object used to control the cross-validation used to determine the hyperparameters of the prior (if applicable). See <code>createControl</code> 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 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'.

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.

customCovariateIds

A list of cohort definition IDS identifying the records in the 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 <a href="#">getDbSccsData</a> function.
createSccsEraDataArgs	An object representing the arguments to be used when calling the <a href="#">createSccsEraData</a> function.
fitSccsModelArgs	An object representing the arguments to be used when calling the <a href="#">fitSccsModel</a> function.

**Details**

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

---

createSccsEraData	<i>Create SCCS era data</i>
-------------------	-----------------------------

---

**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 <a href="#">getDbSccsData</a> 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 <a href="#">createCovariateSettings</a> function, or a list of such objects.



ageSettings	An object of type ageSettings as created using the <a href="#">createAgeSettings</a> function.
seasonalitySettings	An object of type seasonalitySettings as created using the <a href="#">createSeasonalitySettings</a> 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 <code>simulationRiskWindow</code> as created using the <code>createSimulationRiskWindow</code> 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 seasonality 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 equally 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 specifying 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 <code>addExposedDaysToEnd</code> 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 <code>splitPoints</code> 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 <a href="#">createSccsEraData</a> function.
prior	The prior used to fit the model. See <a href="#">createPrior</a> for details.
control	The control object used to control the cross-validation used to determine the hyperparameters of the prior (if applicable). See <a href="#">createControl</a> 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	<i>Load data for SCCS from the database</i>
---------------	---

---

## 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 <code>ConnectionDetails</code> created using the function <code>createConnectionDetails</code> in the <code>DatabaseConnector</code> 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 specify both the database and the schema, so for example <code>'cdm_instance.dbo'</code> .
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 <code>outcomeTable = CONDITION_ERA</code> , <code>outcomeDatabaseSchema</code> is not used. Requires read permissions to this database.
outcomeTable	The tablename that contains the outcome cohorts. If <code>outcomeTable</code> is not <code>CONDITION_OCCURRENCE</code> or <code>CONDITION_ERA</code> , then expectation is <code>outcomeTable</code> has format of COHORT table: <code>COHORT_DEFINITION_ID</code> , <code>SUBJECT_ID</code> , <code>COHORT_START_DATE</code> , <code>COHORT_END_DATE</code> .
outcomeIds	A list of ids used to define outcomes. If <code>outcomeTable = CONDITION_OCCURRENCE</code> , the list is a set of ancestor <code>CONCEPT_ID</code> s, and all occurrences of all descendant concepts will be selected. If <code>outcomeTable &lt;&gt; CONDITION_OCCURRENCE</code> , the list contains records found in <code>COHORT_DEFINITION_ID</code> 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 customCovariateTable 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 multiple 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 additional, 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	<i>Output the full model</i>
----------	------------------------------

---

**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	<i>Load a list of exposureOutcome from file</i>
-------------------------	---

---

**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	<i>Load a list of sccsAnalysis from file</i>
----------------------	--

---

**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	<i>Load the SCCS data from a folder</i>
--------------	---

---

**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	<i>Load the SCCS era data from a folder</i>
-----------------	---

---

**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	<i>Plot the age effect</i>
---------------	----------------------------

---

**Description**

Plot the age effect

**Usage**

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

**Arguments**

sccsModel	An object of type <code>sccsModel</code> as created using the <a href="#">fitSccsModel</a> 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 <code>ggsave</code> in the <code>ggplot2</code> package for supported file formats.

**Details**

Plot the spline curve of the age effect.

---

plotSeasonality	<i>Plot the seasonality effect</i>
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---

### 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 <a href="#">fitSccsModel</a> 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	<i>Run a list of analyses</i>
-----------------	-------------------------------

---

### 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. Requires read permissions to this database. On SQL Server, this should specify 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 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.
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 <a href="#">createSccsAnalysis</a> function.
exposureOutcomeList	A list of objects of type exposureOutcome as created using the <a href="#">createExposureOutcome</a> 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	<i>Save the SCCS data to folder</i>
--------------	-------------------------------------

---

**Description**

saveSccsData saves an object of type `sccsData` to folder.

**Usage**

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

**Arguments**

<code>sccsData</code>	An object of type <code>sccsData</code> as generated using <a href="#">getDbSccsData</a> .
<code>folder</code>	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	<i>Save the SCCS era data to folder</i>
-----------------	---

---

**Description**

saveSccsEraData saves an object of type `sccsEraData` to folder.

**Usage**

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

**Arguments**

<code>sccsEraData</code>	An object of type <code>sccsEraData</code> as generated using <a href="#">createSccsEraData</a> .
<code>folder</code>	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	<i>SelfControlledCaseSeries</i>
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---

**Description**

SelfControlledCaseSeries

---

simulateSccsData	<i>Simulate SCCS data</i>
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---

**Description**

Simulate SCCS data

**Usage**

```
simulateSccsData(nCases, settings)
```

**Arguments**

nCases	The number of cases to simulate.
settings	An object of type <code>sccsSimulationSettings</code> as created using the <a href="#">createSccsSimulationSettings</a> function.

**Value**

An object of type `sccsData`.

---

summarizeSccsAnalyses	<i>Create a summary report of the analyses</i>
-----------------------	--

---

**Description**

Create a summary report of the analyses

**Usage**

```
summarizeSccsAnalyses(outcomeReference)
```

**Arguments**

outcomeReference	A data.frame as created by the <a href="#">runSccsAnalyses</a> 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.

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