

# Package ‘SelfControlledCohort’

October 26, 2015

**Type** Package

**Title** Population-level estimation method that estimates  
incidence rate comparison of exposed/unexposed time within an exposed  
cohort

**Version** 1.1

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**Description** HOMEWORK- add more

**Depends** DatabaseConnector (>= 1.3.0)

**Imports** SqlRender (>= 1.1.1),  
OhdsiRTools

**License** Apache License 2.0

## R topics documented:

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selfControlledCohort    *selfControlledCohort*

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## Description

selfControlledCohort generates population-level estimation from OMOP CDMv4 instance by comparing exposed and unexposed time among exposed cohort.

## Usage

```
selfControlledCohort(connectionDetails, cdmDatabaseSchema, cdmVersion = 5,  
  oracleTempSchema, exposureIds, outcomeId,  
  exposureDatabaseSchema = cdmDatabaseSchema, exposureTable = "drug_era",  
  outcomeDatabaseSchema = cdmDatabaseSchema, outcomeTable = "condition_era",  
  firstOccurrenceDrugOnly = TRUE, firstOccurrenceConditionOnly = TRUE,  
  outcomeConditionTypeConceptIds = c(38000247), genderConceptids = c(8507,
```

```
8532), minAge = "", maxAge = "", studyStartDate = "",
studyEndDate = "", stratifyByGender = FALSE, stratifyByAge = FALSE,
stratifyByYear = FALSE, useLengthOfExposureExposed = TRUE,
timeAtRiskExposedStart = 1, surveillanceExposed = 30,
useLengthOfExposureUnexposed = TRUE, timeAtRiskUnexposedStart = -1,
surveillanceUnexposed = -30, hasFullTimeAtRisk = FALSE,
washoutWindow = 0, followupWindow = 0, shrinkage = 1e-04)
```

## Arguments

### connectionDetails

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

### cdmDatabaseSchema

Name of database schema that contains the OMOP CDM and vocabulary.

### cdmVersion

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

### oracleTempSchema

For Oracle only: the name of the database schema where you want all temporary tables to be managed. Requires create/insert permissions to this database.

### exposureIds

A vector containing the `drug_concept_ids` or `cohort_definition_ids` of the exposures of interest

### outcomeId

The `condition_concept_id` or `cohort_definition_id` of the outcome of interest

### 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`.

### outcomeTable

The tablename that contains the outcome cohorts. If `outcomeTable <> CONDITION_OCCURRENCE`, then expectation is `outcomeTable` has format of COHORT table: `COHORT_DEFINITION_ID`, `SUBJECT_ID`, `COHORT_START_DATE`, `COHORT_END_DATE`.

### outcomeConditionTypeConceptIds

A list of `TYPE_CONCEPT_ID` values that will restrict condition occurrences. Only applicable if `outcomeTable = CONDITION_OCCURRENCE`.

### firstOccurrenceDrugOnlyIf

TRUE, only use first occurrence of each drug concept id for each person

### firstOccurrenceConditionOnlyIf

TRUE, only use first occurrence of each condition concept id for each person.

### genderConceptidsList

of `gender_concept_id`, generally use MALE (8507) and FEMALE (8532).

### minAgeInteger

for minimum allowable age.

### maxAgeInteger

for maximum allowable age.

### studyStartDateDate

for minimum allowable data for index exposure.

### studyEndDateDate

for maximum allowable data for index exposure.

### stratifyByGenderIf

TRUE, analysis will be calculated overall, and stratified across all gender groups.

### stratifyByAgeIf

TRUE, analysis will be calculated overall, and stratified across all age groups (using `AGE_GROUP` table below).

**stratifyByYearIf**  
TRUE, analysis will be calculated overall, and stratified across all years of the index dates.

**useLengthOfExposureExposedIf**  
TRUE, use the duration from drugEraStart -> drugEraEnd as part of timeAtRisk.

**timeAtRiskExposedStartInteger**  
of days to add to drugEraStart for start of timeAtRisk (0 to include index date, 1 to start the day after).

**surveillanceExposedAdditional**  
window to add to end of exposure period (if useLengthOfExposureExposed = TRUE, then add to exposure end date, else add to exposure start date).

**useLengthOfExposureUnexposedIf**  
TRUE, use the duration from exposure start -> exposure end as part of timeAtRisk looking back before exposure start.

**timeAtRiskUnexposedStartinteger**  
of days to add to exposure start for start of timeAtRisk (0 to include index date, -1 to start the day before).

**surveillanceUnexposedadditional**  
window to add to end of exposure period (if useLengthOfExposureUnexposed = TRUE, then add to exposure end date, else add to exposure start date).

**hasFullTimeAtRiskif**  
TRUE, restrict to people who have full time-at-risk exposed and unexposed.

**washoutWindowinteger**  
to define required time observed before exposure start.

**followupWindowinteger**  
to define required time observed after exposure start.

**shrinkageshrinkage**  
used in IRR calculations, required >0 to deal with 0 case counts, but larger number means more shrinkage.

## Details

Population-level estimation method that estimates incidence rate comparison of exposed/unexposed time within an exposed cohort.

## Value

An object of type `sccResults` containing the results of the analysis.

## References

Ryan PB, Schuemie MJ, Madigan D. Empirical performance of a self-controlled cohort method: lessons for developing a risk identification and analysis system. *Drug Safety* 36 Suppl1:S95-106, 2013

## Examples

```
## Not run:
connectionDetails <- createConnectionDetails(dbms = "sql server",
                                             server = "RNDUSRDHIT07.jnj.com")
sccResult <- selfControlledCohort(connectionDetails,
                                 cdmDatabaseSchema = "cdm_truven_mdcr.dbo",
```

```
exposureIds = c(767410, 1314924, 907879),  
outcomeId = 444382,  
outcomeTable = "condition_era")
```

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

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