

# Package ‘CohortSurvival’

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**Title** Estimate Survival from Common Data Model Cohorts

**Version** 1.0.0

**Description** Estimate survival using data mapped to the Observational Medical Outcomes Partnership common data model. Survival can be estimated based on user-defined study cohorts.

**License** Apache License (>= 2)

**Encoding** UTF-8

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**Suggests** testthat (>= 3.0.0), CodelistGenerator, roxygen2, knitr, tictoc, rmarkdown, ggplot2, patchwork, cmprsk, duckdb, gt, flextable, scales, visOmopResults (>= 1.0.0)

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**URL** <https://darwin-eu-dev.github.io/CohortSurvival/>

**NeedsCompilation** no

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## Contents

addCohortSurvival . . . . .	2
asSurvivalResult . . . . .	3
estimateCompetingRiskSurvival . . . . .	4
estimateSingleEventSurvival . . . . .	6
mockMGUS2cdm . . . . .	8
optionsTableSurvival . . . . .	8
plotSurvival . . . . .	9
riskTable . . . . .	10
tableSurvival . . . . .	11
<b>Index</b>	<b>12</b>

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addCohortSurvival	<i>Add survival information to a cohort table</i>
-------------------	---

---

### Description

Add survival information to a cohort table

### Usage

```
addCohortSurvival(
  x,
  cdm,
  outcomeCohortTable,
  outcomeCohortId = 1,
  outcomeDateVariable = "cohort_start_date",
  outcomeWashout = Inf,
  censorOnCohortExit = FALSE,
  censorOnDate = NULL,
  followUpDays = Inf,
  name = NULL
)
```

### Arguments

x	cohort table to add survival information
cdm	CDM reference
outcomeCohortTable	The outcome cohort table of interest.
outcomeCohortId	ID of event cohorts to include. Only one outcome (and so one ID) can be considered.
outcomeDateVariable	Variable containing date of outcome event
outcomeWashout	Washout time in days for the outcome

censorOnCohortExit	If TRUE, an individual's follow up will be censored at their cohort exit
censorOnDate	if not NULL, an individual's follow up will be censored at the given date
followUpDays	Number of days to follow up individuals (lower bound 1, upper bound Inf)
name	Name of the new table, if NULL a temporary table is returned.

### Value

Two additional columns will be added to x. The "time" column will contain number of days to censoring. The "status" column will indicate whether the patient had the event (value: 1), or did not have the event (value: 0)

### Examples

```
cdm <- mockMGUS2cdm()
cdm$mgus_diagnosis <- cdm$mgus_diagnosis %>%
  addCohortSurvival(
    cdm = cdm,
    outcomeCohortTable = "death_cohort",
    outcomeCohortId = 1
  )
```

---

asSurvivalResult *A tidy implementation of the summarised\_characteristics object.*

---

### Description

A tidy implementation of the summarised\_characteristics object.

### Usage

```
asSurvivalResult(result)
```

### Arguments

result *A summarised\_characteristics object.*

### Value

A tibble with a tidy version of the summarised\_characteristics object.

**Examples**

```

cdm <- mockMGUS2cdm()
surv <- estimateSingleEventSurvival(
  cdm = cdm,
  targetCohortTable = "mgus_diagnosis",
  targetCohortId = 1,
  outcomeCohortTable = "death_cohort",
  outcomeCohortId = 1,
  eventGap = 7
) %>%
  asSurvivalResult()

```

---

```
estimateCompetingRiskSurvival
```

*Estimate survival for a given event and competing risk of interest using cohorts in the OMOP Common Data Model*

---

**Description**

Estimate survival for a given event and competing risk of interest using cohorts in the OMOP Common Data Model

**Usage**

```

estimateCompetingRiskSurvival(
  cdm,
  targetCohortTable,
  outcomeCohortTable,
  competingOutcomeCohortTable,
  targetCohortId = NULL,
  outcomeCohortId = NULL,
  outcomeDateVariable = "cohort_start_date",
  outcomeWashout = Inf,
  competingOutcomeCohortId = NULL,
  competingOutcomeDateVariable = "cohort_start_date",
  competingOutcomeWashout = Inf,
  censorOnCohortExit = FALSE,
  censorOnDate = NULL,
  followUpDays = Inf,
  strata = NULL,
  eventGap = 30,
  estimateGap = 1,
  restrictedMeanFollowUp = NULL,
  minimumSurvivalDays = 1
)

```

**Arguments**

cdm	CDM reference
targetCohortTable	targetCohortTable
outcomeCohortTable	The outcome cohort table of interest.
competingOutcomeCohortTable	The competing outcome cohort table of interest.
targetCohortId	targetCohortId
outcomeCohortId	ID of event cohorts to include. Only one outcome (and so one ID) can be considered.
outcomeDateVariable	Variable containing date of outcome event
outcomeWashout	Washout time in days for the outcome
competingOutcomeCohortId	ID of event cohorts to include. Only one competing outcome (and so one ID) can be considered.
competingOutcomeDateVariable	Variable containing date of competing outcome event
competingOutcomeWashout	Washout time in days for the competing outcome
censorOnCohortExit	If TRUE, an individual's follow up will be censored at their cohort exit
censorOnDate	if not NULL, an individual's follow up will be censored at the given date
followUpDays	Number of days to follow up individuals (lower bound 1, upper bound Inf)
strata	strata
eventGap	Days between time points for which to report survival events, which are grouped into the specified intervals.
estimateGap	Days between time points for which to report survival estimates. First day will be day zero with risk estimates provided for times up to the end of follow-up, with a gap in days equivalent to eventGap.
restrictedMeanFollowUp	number of days of follow-up to take into account when calculating restricted mean for all cohorts
minimumSurvivalDays	Minimum number of days required for the main cohort to have survived

**Value**

tibble with survival information for desired cohort, including: time, people at risk, survival probability, cumulative incidence, 95 CIs, strata and outcome. A tibble with the number of events is outputted as an attribute of the output

## Examples

```
cdm <- mockMGUS2cdm()
surv <- estimateCompetingRiskSurvival(
  cdm = cdm,
  targetCohortTable = "mgus_diagnosis",
  targetCohortId = 1,
  outcomeCohortTable = "progression",
  outcomeCohortId = 1,
  competingOutcomeCohortTable = "death_cohort",
  competingOutcomeCohortId = 1,
  eventGap = 7
)
```

---

estimateSingleEventSurvival

*Estimate survival for a given event of interest using cohorts in the OMOP Common Data Model*

---

## Description

Estimate survival for a given event of interest using cohorts in the OMOP Common Data Model

## Usage

```
estimateSingleEventSurvival(
  cdm,
  targetCohortTable,
  outcomeCohortTable,
  targetCohortId = NULL,
  outcomeCohortId = NULL,
  outcomeDateVariable = "cohort_start_date",
  outcomeWashout = Inf,
  censorOnCohortExit = FALSE,
  censorOnDate = NULL,
  followUpDays = Inf,
  strata = NULL,
  eventGap = 30,
  estimateGap = 1,
  restrictedMeanFollowUp = NULL,
  minimumSurvivalDays = 1
)
```

## Arguments

cdm                    CDM reference

targetCohortTable	targetCohortTable
outcomeCohortTable	The outcome cohort table of interest.
targetCohortId	targetCohortId
outcomeCohortId	ID of event cohorts to include. Only one outcome (and so one ID) can be considered.
outcomeDateVariable	Variable containing date of outcome event
outcomeWashout	Washout time in days for the outcome
sensorOnCohortExit	If TRUE, an individual's follow up will be censored at their cohort exit
sensorOnDate	if not NULL, an individual's follow up will be censored at the given date
followUpDays	Number of days to follow up individuals (lower bound 1, upper bound Inf)
strata	strata
eventGap	Days between time points for which to report survival events, which are grouped into the specified intervals.
estimateGap	Days between time points for which to report survival estimates. First day will be day zero with risk estimates provided for times up to the end of follow-up, with a gap in days equivalent to eventGap.
restrictedMeanFollowUp	number of days of follow-up to take into account when calculating restricted mean for all cohorts
minimumSurvivalDays	Minimum number of days required for the main cohort to have survived

**Value**

tibble with survival information for desired cohort, including: time, people at risk, survival probability, cumulative incidence, 95 CIs, strata and outcome. A tibble with the number of events is outputted as an attribute of the output

**Examples**

```

cdm <- mockMGUS2cdm()
surv <- estimateSingleEventSurvival(
  cdm = cdm,
  targetCohortTable = "mgus_diagnosis",
  targetCohortId = 1,
  outcomeCohortTable = "death_cohort",
  outcomeCohortId = 1,
  eventGap = 7
)

```

---

`mockMGUS2cdm`*Create mock CDM reference with survival::mgus2 dataset*

---

**Description**

Create mock CDM reference with survival::mgus2 dataset

**Usage**

```
mockMGUS2cdm()
```

**Value**

CDM reference containing data from the survival::mgus2 dataset

**Examples**

```
cdm <- mockMGUS2cdm()
cdm$person
```

---

`optionsTableSurvival`*Additional arguments for the function tableSurvival()*

---

**Description**

It provides a list of allowed inputs for .option argument in tableSurvival and their given default value.

**Usage**

```
optionsTableSurvival()
```

**Value**

The default .options named list.

**Examples**

```
{
optionsTableSurvival()
}
```



---

`plotSurvival`*Plot survival results*

---

**Description**

Plot survival results

**Usage**

```
plotSurvival(  
  result,  
  ribbon = TRUE,  
  facet = NULL,  
  colour = NULL,  
  cumulativeFailure = FALSE,  
  riskTable = FALSE,  
  riskInterval = 30  
)
```

**Arguments**

<code>result</code>	Survival results
<code>ribbon</code>	If TRUE, the plot will join points using a ribbon
<code>facet</code>	Variables to use for facets
<code>colour</code>	Variables to use for colours
<code>cumulativeFailure</code>	whether to plot the cumulative failure probability instead of the survival probability
<code>riskTable</code>	Whether to print risk table below the plot
<code>riskInterval</code>	Interval of time to print risk table below the plot

**Value**

A plot of survival probabilities over time

**Examples**

```
cdm <- mockMGUS2cdm()  
surv <- estimateSingleEventSurvival(cdm,  
                                     targetCohortTable = "mgus_diagnosis",  
                                     outcomeCohortTable = "death_cohort")  
  
plotSurvival(surv)
```

---

 riskTable
 

---



---

*Table with survival events*


---

**Description**

Table with survival events

**Usage**

```

riskTable(
  x,
  eventGap = NULL,
  header = c("estimate"),
  type = "gt",
  groupColumn = NULL,
  .options = list()
)

```

**Arguments**

x	Result from estimateSingleEventSurvival or estimateCompetingRiskSurvival.
eventGap	Event gap defining the times at which to report the risk table information. Must be one of the eventGap inputs used for the estimation function. If NULL, all available are reported.
header	A vector containing which elements should go into the header. Allowed are: cdm_name, group, strata, additional, variable, estimate, and settings.
type	Type of desired formatted table, possibilities: "gt", "flextable", and "tibble".
groupColumn	Columns to use as group labels.
.options	Named list with additional formatting options. CohortSurvival::optionsTableSurvival() shows allowed arguments and their default values.

**Value**

A tibble containing the risk table information (n\_risk, n\_events, n\_censor) for all times within the event gap specified.

**Examples**

```

cdm <- mockMGUS2cdm()
surv <- estimateSingleEventSurvival(cdm,
                                   targetCohortTable = "mgus_diagnosis",
                                   outcomeCohortTable = "death_cohort")

riskTable(surv)

```

---

tableSurvival	<i>Table with survival summary</i>
---------------	------------------------------------

---

**Description**

Table with survival summary

**Usage**

```
tableSurvival(
  x,
  times = NULL,
  timeScale = "days",
  header = c("estimate"),
  type = "gt",
  groupColumn = NULL,
  .options = list()
)
```

**Arguments**

x	Result from estimateSingleEventSurvival or estimateCompetingRiskSurvival
times	Times at which to report survival in the summary table
timeScale	Time unit to report survival in: days, months or years
header	A vector containing which elements should go into the header. Allowed are: cdm_name, group, strata, additional, variable, estimate, and settings.
type	Type of desired formatted table, possibilities: "gt", "flextable", and "tibble".
groupColumn	Columns to use as group labels.
.options	Named list with additional formatting options. CohortSurvival::optionsTableSurvival() shows allowed arguments and their default values.

**Value**

A tibble containing a summary of observed survival in the required units

**Examples**

```
cdm <- mockMGUS2cdm()
surv <- estimateSingleEventSurvival(cdm,
                                   targetCohortTable = "mgus_diagnosis",
                                   outcomeCohortTable = "death_cohort")
tableSurvival(surv, times = c(50,100,365))
```

# Index

`addCohortSurvival`, [2](#)  
`asSurvivalResult`, [3](#)  
  
`estimateCompetingRiskSurvival`, [4](#)  
`estimateSingleEventSurvival`, [6](#)  
  
`mockMGUS2cdm`, [8](#)  
  
`optionsTableSurvival`, [8](#)  
  
`plotSurvival`, [9](#)  
  
`riskTable`, [10](#)  
  
`tableSurvival`, [11](#)