

Package ‘CohortSurvival’

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Title Estimate Survival from Common Data Model Cohorts

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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)

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Author Edward Burn [aut, cre] (<<https://orcid.org/0000-0002-9286-1128>>), Kim López-Güell [aut] (<<https://orcid.org/0000-0002-8462-8668>>), Marti Catala [aut] (<<https://orcid.org/0000-0003-3308-9905>>), Xintong Li [aut] (<<https://orcid.org/0000-0002-6872-5804>>), Danielle Newby [aut] (<<https://orcid.org/0000-0002-3001-1478>>), Nuria Mercade-Besora [aut] (<<https://orcid.org/0009-0006-7948-3747>>)

Maintainer Edward Burn <edward.burn@ndorms.ox.ac.uk>

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

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)

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
  )

```

addCompetingRiskCohortSurvival
Add competing risk survival information to a cohort table

Description

Add competing risk survival information to a cohort table

Usage

```

addCompetingRiskCohortSurvival(
  x,
  cdm,
  outcomeCohortTable,
  outcomeCohortId = 1,
  outcomeDateVariable = "cohort_start_date",
  outcomeWashout = Inf,
  outcomeCensorOnCohortExit = FALSE,
  outcomeCensorOnDate = NULL,
  outcomeFollowUpDays = Inf,
  competingOutcomeCohortTable,
  competingOutcomeCohortId = 1,
  competingOutcomeDateVariable = "cohort_start_date",
  competingOutcomeWashout = Inf,

```

```

    competingOutcomeCensorOnCohortExit = FALSE,
    competingOutcomeCensorOnDate = NULL,
    competingOutcomeFollowUpDays = Inf
)

```

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

outcomeCensorOnCohortExit
If TRUE, an individual's follow up will be censored at their cohort exit

outcomeCensorOnDate
if not NULL, an individual's follow up will be censored at the given date

outcomeFollowUpDays
Number of days to follow up individuals (lower bound 1, upper bound Inf)

competingOutcomeCohortTable
The outcome cohort table of interest.

competingOutcomeCohortId
ID of event cohorts to include. Only one 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

competingOutcomeCensorOnCohortExit
If TRUE, an individual's follow up will be censored at their cohort exit

competingOutcomeCensorOnDate
if not NULL, an individual's follow up will be censored at the given date

competingOutcomeFollowUpDays
Number of days to follow up individuals (lower bound 1, upper bound Inf)

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 outcome event (value: 1), competing event (value:2) or did not have the event/is censored (value: 0)

Examples

```
cdm <- mockMGUS2cdm()
crsurvivaldata <- cdm$mgus_diagnosis %>%
  addCompetingRiskCohortSurvival(
    cdm = cdm,
    outcomeCohortTable = "progression",
    outcomeCohortId = 1,
    competingOutcomeCohortTable = "death_cohort",
    competingOutcomeCohortId = 1
  )
```

asSurvivalResult	<i>A tidy implementation of the summarised_characteristics object.</i>
------------------	--

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,  
  minCellCount = 5  
)
```

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
cancelOnCohortExit	If TRUE, an individual's follow up will be censored at their cohort exit
cancelOnDate	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
minCellCount	The minimum number of events to reported, below which results will be obscured. If 0, all results will be reported.

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,
  minCellCount = 5
)

```

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
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
minCellCount	The minimum number of events to reported, below which results will be obscured. If 0, all results will be reported.

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
)
```

```
generateDeathCohortSet
```

To create a death cohort

Description

[Deprecated]

Usage

```
generateDeathCohortSet(cdm, name, cohortTable = NULL, cohortId = NULL)
```

Arguments

cdm	CDM reference
name	name for the created death cohort table
cohortTable	name of the cohort table to create a death cohort for
cohortId	name of the cohort table to create a death cohort for

Value

A cohort table with a death cohort in cdm

Examples

```
library(CDMConnector)
library(CohortSurvival)
observation_period <- dplyr::tibble(
  observation_period_id = c(1, 2, 3, 4, 5,6),
  person_id = c(1, 2, 3, 4, 5,6),
  observation_period_start_date = c(
    rep(as.Date("1980-07-20"),6)
  ),
  observation_period_end_date = c(
    rep(as.Date("2023-05-20"),6)
  ),
  period_type_concept_id = c(rep(0,6))
)

deathTable <- dplyr::tibble(
  person_id = c(1,2,3),
  death_date = c(as.Date("2020-01-01"),
    as.Date("2020-01-02"),
    as.Date("2020-01-01"))
)

person <- dplyr::tibble(
  person_id = c(1, 2, 3, 4, 5),
  year_of_birth = c(rep("1990", 5)),
)
```

```

    month_of_birth = c(rep("02", 5)),
    day_of_birth = c(rep("11", 5)),
    gender_concept_id = c(rep(0,5)),
    ethnicity_concept_id = c(rep(0,5)),
    race_concept_id = c(rep(0,5))
  )

  cdm <- omopgenerics::cdmFromTables(
    tables = list(
      person = person,
      observation_period = observation_period,
      death = deathTable
    ),
    cdmName = "mock_es"
  )
  db <- DBI::dbConnect(duckdb::duckdb(), ":memory:")
  cdm2 = CDMConnector::copy_cdm_to(db,
                                   cdm,
                                   schema = "main")

  attr(cdm2, "cdm_schema") <- "main"
  attr(cdm2, "write_schema") <- "main"

  cdm2 <- generateDeathCohortSet(cdm=cdm2,
                                name = "death_cohort")

```

 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,
  x = "time",
  xscale = "days",
  ylim = c(0, NA),
  xlim = NULL,
  cumulativeFailure = FALSE,
  ribbon = TRUE,
  facet = NULL,
  colour = NULL,
  riskTable = FALSE,
  riskInterval = 30
)
```

Arguments

result	Survival results
x	Variable to plot on x axis
xscale	X axis scale. Can be "days" or "years".
ylim	Limits for the Y axis
xlim	Limits for the X axis
cumulativeFailure	whether to plot the cumulative failure probability instead of the survival probability
ribbon	If TRUE, the plot will join points using a ribbon
facet	Variables to use for facets
colour	Variables to use for colours
riskTable	Whether to print risk table below the plot
riskInterval	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)
```

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

Description

Table with survival summary

Usage

```
tableSurvival(
  x,
  times = NULL,
  timeScale = "days",
  splitStrata = TRUE,
  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
splitStrata	If TRUE strata will be split into columns, otherwise "strata_name" and "strata_level" columns will be kept.
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))

```

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