Package 'CohortSurvival'

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Title Estimate Survival from Common Data Model Cohorts

Version 1.0.2

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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Contents

`addCohortSurvival` *Add survival information to a cohort table*

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

`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 <- 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,
  logLog = FALSE,
  timeScale = "days"
)
```

Arguments

`result`	Survival results
`ribbon`	If TRUE, the plot will join points using a ribbon
`facet`	Variables to use for facets
`colour`	Variables to use for colours
`cumulativeFailure`	whether to plot the cumulative failure probability instead of the survival probability
`riskTable`	Whether to print risk table below the plot
`riskInterval`	Interval of time to print risk table below the plot
`logLog`	If TRUE, the survival probabilities are transformed using the log-log formula
`timeScale`	The scale of time in the x-axis. Can be "days", "months", or "years"

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` *Table with survival summary*

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))
```

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