

Package ‘cr17’

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Type Package

Title Testing Differences Between Competing Risks Models and Their Visualisations

Version 0.1.0

Description Tool for analyzing competing risks models. The main point of interest is testing differences between groups (as described in R.J Gray (1988) <doi:10.1214/aos/1176350951> and J.P. Fine, R.J Gray (1999) <doi:10.2307/2670170>) and visualizations of survival and cumulative incidence curves.

License GPL

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LazyData true

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Suggests knitr, rmarkdown

URL <https://github.com/geneticsMiNIing/cr17>

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Author Magda Młynarczyk [aut, cre],
Przemysław Biecek [aut, ths]

Maintainer Magda Młynarczyk <magmlynarczyk@gmail.com>

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eventTab	<i>Number of events tables</i>
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Description

Creates a table for each risk, containing number of events up to given time in groups.

Usage

```
eventTab(time, risk, group, cens = NULL, title = "Number of Events")
```

Arguments

time	vector with times of the first event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (if NULL, the first value of 'risk' vector will be taken).
title	title of a table.

Value

A grob with n tables, where n is number of risks. Each table contains number of events that have happened in each group up to given time point (the time points correspond to breaks at x-axis of plots with cumulative incidence curves).

See Also

[plotCuminc](#)

Examples

```
eventTab(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive",
title = "Number of events")
```

fitCuminc	<i>Cumulative Incidences Curves</i>
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Description

Fits cumulative incidence function across different groups and risks.

Usage

```
fitCuminc(time, risk, group, cens = NULL)
```

Arguments

time	vector with times of the first event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (if NULL, the first value of 'risk' vector will be taken).

Value

list of length [(number of risks)*(number of groups) + 1], containing estimation of cumulative incidences curves for each risk and group. The last element of a list is a data.frame with results of a K-sample test, containing test statistic, p-value and degrees of freedom for each risk.

See Also

[cuminc](#)

Examples

```
fitCuminc(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive")
```

fitReg	<i>Regression Models for Competing Risks</i>
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Description

fits Cox model for every type of an event including occurring of competing risks.

Usage

```
fitReg(time, risk, group, cens = NULL)
```

Arguments

time	vector with times of the first event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (if NULL, the first value of 'risk' vector will be taken).

Value

a list of length n, where n is number of different types of events. Each element of a list is a result of crr function from cmprsk package for given type of event.

See Also

[crr](#)

Examples

```
fitReg(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive")
```

fitSurvival

Estimation of survival curves for each risk separately

Description

Fits survival curves for each risk and group, treating other types of events as censoring.

Usage

```
fitSurvival(time, risk, group, cens = NULL, type = "kaplan-meier",
  conf.int = 0.95, conf.type = "log")
```

Arguments

time	vector with times of the first event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (if NULL, the first value of 'risk' vector will be taken).
type	type of survival curve to be fitted. Possible values are "kaplan-meier" (default), "fleming-harrington" or "fh2".
conf.int	level of two-sided confidence interval (default = 0.95).
conf.type	type of confidence interval. Possible values: "none", "plain", "log" (default), "log-log".

Value

List, which elements are `survfit.summary` objects from the package `Survival` for each risk separately.

See Also

[survfit.summary.survfit](#)

Examples

```
fitSurvival(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive",
  type = "kaplan-meier", conf.int = 0.95, conf.type = "log")
```

 LUAD

LUAD dataset from The Cancer Genome Atlas Project

Description

Contains following information about patients with lung cancer:

- "time" is a time from beginning of an observation to an event or follow-up,
- "event" is a type of event that have happened ("death", "new_tumor" or "alive" when the observation was censored),
- "gender" is a gender of a patient (grouping variable).

The dataset is published in 'RTCGA.clinical' package: <https://bioconductor.org/packages/release/data/experiment/manuals/R>

 plotCuminc

Cumulative incidences curves

Description

Plots cumulative incidences curves for each risk and group.

Usage

```
plotCuminc(ci, cens = NULL, target = NULL, ggtheme = theme_minimal(),
  titleCuminc = "Cumulative incidence functions", xtitle = "Time",
  ytitleCuminc = "Cumulative incidences", legendtitle = "Group")
```

Arguments

ci	a result of function fitCuminc.
cens	value of 'risk' indicating censored observation (default 0).
target	point in time, in which the confidence bounds should be plotted (default NULL, no confidence bounds plotted).
ggtheme	ggtheme to be used (default: theme_minimal()).
titleCuminc	a title of a plot (default: "Cumulative incidence functions").
xtitle	a title of x axis (default: "Time").
ytitleCuminc	a title of y axis (default: "Cumulative incidences")
legendtitle	a title of a legend (default: "Group").

Value

a ggplot containing n graphs, where n is number of risks. Each graph represents cumulative incidence curves for given risk. One curve corresponds to one group.

See Also

[ggplot ggtheme](#)

Examples

```
fitC <- fitCuminc(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive")
plotCuminc(ci = fitC, cens = "alive", target = 1200)
```

plotSurvival

Survival curves

Description

Plots survival curves for each risk and group.

Usage

```
plotSurvival(fit, target = NULL, ggtheme = theme_minimal(),
  titleSurv = "Survival curves", xtitle = "Time",
  ytitleSurv = "Probability of surviving up to time t",
  legendtitle = "Group")
```

Arguments

fit	a result of fitSurvival function.
target	point in time, in which the confidence bounds should be plotted (if NULL, no confidence bounds will be plotted).
ggtheme	ggtheme to be used (default: theme_minimal()).
titleSurv	a title of a plot (default: "Survival curves").
xtitle	a title of x axis (default: "Time").
ytileSurv	a title of y axis (default: "Probability of surviving up to time t")
legendtitle	a title of a legend (default: "Group").

Value

a ggplot containing n graphs, where n is number of risks. Each graph represents survival curves for given risk. One curve corresponds to one group.

See Also

[ggplot ggtheme](#)

Examples

```
fits <- fitSurvival(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive")
plotSurvival(fit = fits, target = 1200)
```

riskTab	<i>Number at risk table</i>
---------	-----------------------------

Description

Creates a table for each risk, containing number of observation at risk in given time points in groups.

Usage

```
riskTab(time, risk, group, cens = NULL, title = "Number at risk")
```

Arguments

time	vector with times of the first event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (if NULL, the first value of 'risk' vector will be taken).
title	title of a table

Value

A grob with n tables, where n is number of risks. Each table contains number of observations at risk in each group in given time points (the time points correspond to breaks at x-axis of plots with survival curves).

See Also

[plotSurvival](#)

Examples

```
riskTab(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive",
title = "Number at risk")
```

simpleCox

Cox model for each type of event separately

Description

fits Cox models for each risk and group, treating other type of events as censoring.

Usage

```
fitCox(time, risk, group, cens = NULL, conf.int = 0.95)
```

Arguments

time	vector with times of the first event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (if NULL, the first value of 'risk' vector will be taken).
conf.int	conf.int level of two-sided confidence interval (default = 0.95).

Value

a list of length n , where n is number of risks. Each element of a list is a result of `summary.coxph` function from package `survival`, where there is only one type of event possible (other are treating as censored).

See Also

[coxph summary.coxph](#)

Examples

```
fitCox(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive", conf.int = 0.95)
```


Description

Generates summarized report, including visualisation of survival and cumulative incidences curves, diagnostic tables and p-values of tests comparing models between groups.

Usage

```
summarizeCR(time, risk, group, cens = NULL, rho = 0, target = NULL,
  type = "kaplan-meier", conf.int = 0.95, conf.type = "log",
  ggtheme = theme_minimal(), titleSurv = "Survival curves",
  titleCuminc = "Cumulative incidence functions", xtitle = "Time",
  ytitleSurv = "Probability of surviving up to time t",
  ytitleCuminc = "Cumulative incidences", legendtitle = "Group",
  riskTabTitle = "Number at risk", eventTabTitle = "Number of events")
```

Arguments

time	vector with times of an event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (if NULL, the first value of 'risk' vector will be taken).
rho	rho parameter from Fleming-Harrington Test.
target	point in time, in which the confidence bounds should be plotted (default NULL, no confidence bounds plotted).
type	type of survival curve to be fitted. Possible values are "kaplan-meier" (default), "fleming-harrington" or "fh2".
conf.int	conf.int level of two-sided confidence interval (default = 0.95).
conf.type	type of confidence interval. Possilble values: "none", "plain", "log" (default), "log-log".
ggtheme	ggtheme to be used in plots (default: theme_minimal()).
titleSurv	a title of a survival curves plot (default: "Survival curves").
titleCuminc	a title of a cumulative incidences plot (default: "Cumulative incidence functions").
xtitle	a title of x axis of survival curves and cumulative incidences plots(default: "Time").
ytitleSurv	a title of y axis of survial curves plot (default: "Probability of surviving up to time t").
ytitleCuminc	a title of y axis (default: "Cumulative incidences").
legendtitle	a title of a legend (default: "Group").
riskTabTitle	a title of table with number at risk.
eventTabTitle	a title of table with number of events.

Value

Results of all functions implemented in the package summarised in an one-page report.

Examples

```
summarizeCR(time = LUAD$time/365, risk = LUAD$event, group = LUAD$gender, cens = "alive")
```

```
summarizeCR(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive",  
target = 1200, type = "fleming-harrington", conf.int = 0.99, conf.type = "log-log",  
ggtheme = theme_bw())
```

```
summarizeCR(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive", rho = 1,  
target = 800, type = "kaplan-meier", ggtheme = theme_gray(), titleSurv = "Survival analysis",  
titleCuminc = "Competing risks models", xtitle = "Days", ytitleSurv = "Survival curves",  
ytitleCuminc = "Cumulative incidence functions", legendtitle = "Gender")
```

testCox

Testing differences between groups in Cox models.

Description

The function provides 3 tests for comparing models estimated from fitCox function. The tests are: Likelihood Ratio Test, Wald Test and Logrank Test.

Usage

```
testCox(fitCox)
```

Arguments

fitCox a result of function fitCox.

Value

a data.frame with p-values of 3 tests for each risk.

See Also

[fitCox](#)

Examples

```
fitC <- fitCox(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive")  
testCox(fitC)
```

testCuminc	<i>K-sample Test for Competing Risks</i>
------------	--

Description

tests differences in cumulative incidences function between groups using K-sample test.

Usage

```
testCuminc(ci)
```

Arguments

ci a result of fitCumin function.

Value

data.frame containing p-values of K-sample test for each risk.

See Also

[fitCuminc](#)

Examples

```
fitC <- fitCuminc(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive")
testCuminc(fitC)
```

testReg	<i>Regression models difference testing</i>
---------	---

Description

Testing differences in Competing Risks Regression Models between groups.

Usage

```
testReg(reg, conf.int = 0.95)
```

Arguments

reg a result of fitReg function.
conf.int level of two-sided confidence interval (default 0.95).

Value

a data.frame containing p-values of Modified Log-Rank Test for each type of event. The test compares differences between groups in Competing Risks Cox Models.

See Also

[fitReg](#)

Examples

```
fitR <- fitReg(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive")
testReg(fitR)
```

testSurvival

Fleming-Harrington test for differences between groups

Description

Tests, if there are differences between groups for survival curves estimating for all risks separately (treating other events as censoring).

Usage

```
testSurvival(time, risk, group, cens = 0, rho = 0)
```

Arguments

time	vector with times of the first event or follow-up, must be numeric.
risk	vector with type of event, can be numeric or factor/character.
group	vector with group variable, can be numeric or factor/character.
cens	value of 'risk' indicating censored observation (default 0).
rho	rho parameter from Fleming-Harrington Test.

Value

a data.frame containing p-values of Fleming-Harrington Test for each risk.

See Also

[survdiff](#)

Examples

```
testSurvival(time = LUAD$time, risk = LUAD$event, group = LUAD$gender, cens = "alive", rho = 0)
```

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