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Title Restricted Mean Time in Favor of Treatment

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URL https://sites.google.com/view/lmaowisc/, https://lmaowisc.github.io/rmt/

Description Contains inferential and graphical routines for comparing two treatment arms in terms of the restricted mean time in favor of treatment.

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LazyData true

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`bouquet` *Bouquet plot*

Description

Construct the bouquet plot based on the estimated stage-wise restricted mean win/loss times.

Usage

```
bouquet(
  x,
  Kmax = NULL,
  xlim = NULL,
  ylim = NULL,
  xlab = "Restricted mean win/loss time",
  ylab = "Follow-up time",
  group.label = TRUE,
  cex.group = 1,
  ...
)
```

Arguments

`x`	An object returned by `rmtfit`.
`Kmax`	A positive integer; If specified, the stage-wise estimates over `Kmax`, . . . , K will be aggregated.
`xlim`	The x limits of the plot.
`ylim`	The y limits of the plot.
`xlab`	A label for the x axis, defaults to a description of x.
`ylab`	A label for the y axis, defaults to a description of x.
`group.label`	If `TRUE`, group labels will appear on the two sides of the plot.
`cex.group`	Font size of the group labels if `group.label=TRUE`.
`...`	Other arguments that can be passed to the underlying `plot` method.

Value

No return value, called for side effects.

See Also

rmtfit, summary.rmtfit, plot.rmtfit.

Examples

```
# load the colon cancer trial data
library(rmt)
head(colon_lev)
# fit the data
obj=rmtfit(ms(id,time,status)~rx,data=colon_lev)
# bouquet plot
bouquet(obj)
```

---

colon_lev *A dataset from a landmark colon cancer trial*

Description

A landmark colon cancer trial on the efficacy of levamisole and fluorouracil was reported by Moertel et al. (1990). The trial recruited 929 patients with stage C disease and randomly assigned them to levamisole treatment alone, levamisole combined with fluorouracil, and the control. The dataset here is restricted to the comparison between the combined treatment and control groups, consisting of 304 and 314 patients, respectively.

Usage

```
colon_lev
```

Format

A data frame with 915 rows and 6 variables:

id Unique patient ID.

time Event time (years).

status Event type; 1 = cancer relapse, 2 = death.

rx "Lev+5FU" = combined treatment, "Control" = control.

age Patient age (years) at randomization.

sex 0 = female, 1 = male.

References

MOERTEL, C. G., FLEMING, T. R., MACDONALD, J. S., HALLER, D. G., LAURIE, J. A., GOODMAN, P. J., UNGERLEIDER, J. S., EMERSON, W. A., TORMEY, D. C., GLICK, J. H. et al. (1990). Levamisole and fluorouracil for adjuvant therapy of resected colon carcinoma. New Engl. J. Med. 322, 352–358.

`hfaction` *A dataset from the HF-ACTION trial*

Description

Over two thousand heart failure patients across the USA, Canada, and France participated in the Heart Failure: A Controlled Trial Investigating Outcomes of Exercise Training (HF-ACTION) between 2003–2007 (O'Connor et al., 2009). The primary objective of the trial was to evaluate the effect of adding exercise training to the usual patient care on the composite endpoint of all-cause hospitalization and death. The dataset here contains a subgroup of 426 non-ischemic patients with baseline cardio-pulmonary exercise test less than or equal to nine minutes.

Usage

```
hfaction
```

Format

A data frame with 1,448 rows and 5 variables:

patid Unique patient ID.

time Event time (years).

status Event type; 1 = hospitalization, 2 = death.

trt_ab 1 = exercise training, 0 = usual care.

age60 1 = 60 years or older, 0 = otherwise.

References

O'CONNOR, C. M., WHELLAN, D. J., LEE, K. L., KETEYIAN, S. J., COOPER, L. S., ELLIS, S. J., LEIFER, E. S., KRAUS, W. E., KITZMAN, D. W., BLUMENTHAL, J. A. et al. (2009). Efficacy and safety of exercise training in patients with chronic heart failure: Hf-action randomized controlled trial. J. Am. Med. Assoc. 301, 1439–1450.

ms *Create a multistate event object*

Description

Create a multistate event object

Usage

```
ms(id, time, status)
```

Arguments

id	A vector of id variable.
time	A vector of follow-up times.
status	A vector of event type, k if transitioning to state k, 0 if censored and $K+1$ represents death.

Value

An object of class ms used as an argument for rmtfit.

plot.rmtfit *Plot the estimated treatment effect curve*

Description

Plot the estimated overall or stage-wise restricted mean times in favor of treatment as a function of follow-up time.

Usage

```
## S3 method for class 'rmtfit'
plot(
  x,
  k = NULL,
  conf = FALSE,
  main = NULL,
  xlim = NULL,
  ylim = NULL,
  xlab = "Follow-up time",
  ylab = "Restricted mean time in favor",
  conf.col = "black",
  conf.lty = 3,
  ...
)
```

Arguments

x	An object returned by rmtfit.
k	If specified, $\mu_k(\tau)$ is plotted; otherwise, $\mu(\tau)$ is plotted.
conf	If TRUE, 95% confidence limits for the target curve are overlaid.
main	A main title for the plot
xlim	The x limits of the plot.
ylim	The y limits of the plot.
xlab	A label for the x axis, defaults to a description of x.
ylab	A label for the y axis, defaults to a description of y.
conf.col	Color for the confidence limits if conf=TRUE.
conf.lty	Line type for the confidence limits if conf=TRUE.
...	Other arguments that can be passed to the underlying plot method.

Value

No return value, called for side effects.

See Also

rmtfit, summary.rmtfit, bouquet.

Examples

```
# load the colon cancer trial data
library(rmt)
head(colon_lev)
# fit the data
obj=rmtfit(ms(id,time,status)~rx,data=colon_lev)
# plot overal effect mu(tau)
plot(obj)
# set-up plot parameters
oldpar <- par(mfrow = par("mfrow"))
par(mfrow=c(1,2))
# Plot of component-wise RMT in favor of treatment over time
plot(obj,k=2,conf=TRUE,col='red',conf.col='blue', xlab="Follow-up time (years)",
    ylab="RMT in favor of treatment (years)",main="Survival")
plot(obj,k=1,conf=TRUE,col='red',conf.col='blue', xlab="Follow-up time (years)",
    ylab="RMT in favor of treatment (years)",main="Pre-relapse")
par(oldpar)
```

print.rmtfit *Print a short summary of rmtfit objects*

Description

Print the results for the restricted mean times in favor of treatment.

Usage

```
## S3 method for class 'rmtfit'
print(x, ...)
```

Arguments

x	An object returned by rmtfit.
...	Further arguments passed to or from other methods

Value

No return value, called for side effects.

print.summary.rmtfit *Print method for summary.rmtfit objects*

Description

Produces a printed summary of the results for the restricted mean times in favor of treatment

Usage

```
## S3 method for class 'summary.rmtfit'
print(x, ...)
```

Arguments

x	An object returned by summary.rmtfit.
...	Further arguments passed to or from other methods

Value

No return value, called for side effects.

rec *Create a recurrent event object*

Description

Create a recurrent event object

Usage

```
rec(id, time, status)
```

Arguments

id	A vector of id variable.
time	A vector of follow-up times.
status	A vector of event type, 1 = recurrent event, 2 = death, and 0 = censoring;

Value

An object of class rec used as an argument for rmtfit.

rmtfit *Estimate restricted mean times in favor of treatment*

Description

Estimate and make inference on the overall and component-wise restricted mean times in favor of treatment.

Usage

```
rmtfit(...)

## Default S3 method:
rmtfit(id, time, status, trt, type = "multistate", ...)

## S3 method for class 'formula'
rmtfit(formula, data, ...)
```

Arguments

...	Further arguments.
id	A vector of id variable.
time	A vector of follow-up times.
status	For type="multistate", k = entering into state k ($K+1$ represents death) and 0 = censoring; For type="recurrent", 1 = recurrent event, 2 = death, and 0 = censoring;
trt	A vector of binary variable for treatment group.
type	"multistate" = multistate data; "recurrent" = recurrent event data.
formula	A formula object. For multistate data, use ms(id,time,status)~trt; for recurrent event data, use rec(id,time,status)~trt.
data	A data frame, which contains the variables names in the formula.

Value

An object of class rmtfit. See rmtfit.object for details.

Methods (by class)

- rmtfit(default): Default
- rmtfit(formula): Formula

See Also

rmtfit.object, summary.rmtfit, plot.rmtfit, bouquet.

Examples

```
######################
# Multistate outcome  #
######################
# load the colon cancer trial data
library(rmt)
head(colon_lev)
# fit the data
obj=rmtfit(ms(id,time,status)~rx,data=colon_lev)
# print the event numbers by group
obj
# summarize the inference results for tau=7.5 years
summary(obj,tau=7.5)

############################
# Recurrent event outcome  #
############################
# load the HF-ACTION trial data
library(rmt)
head(hfaction)
# fit the data
```

```
obj=rmtfit(rec(patid,time,status)~trt_ab,data=hfaction)
# print the event numbers by group
obj
# summarize the inference results for tau=3.5 years
summary(obj,tau=3.5,Kmax=4) # aggregating results for recurrent-event
# frequency >=4.
```

`rmtfit.object` *Estimated restricted mean times in favor of treatment*

Description

This class of objects is returned by the `rmtfit` class of functions. Objects of this class have methods for the functions `print`, `summary`, `plot`, and `bouquet`.

Value

`t`	A vector of follow-up times τ.
`mu`	A matrix with $K+2$ rows; The kth row $(k=1,\ldots,K)$ is $\mu_k(\tau)$, the restricted mean time in favor of treatment on the kth state (or recurrent event); The $(K+1)$th row is the net restricted mean survival time; The last row is the overal effect $\mu(\tau)$.
`var`	A matrix with $K+2$ rows containing the variance estimates for `mu`.
`mu10`, `mu01`	Matrices with $K+1$ rows; The kth row $(k=1,\ldots,K)$ is the restricted mean win (`mu10`) and loss (`mu01`) times by the treatment on the kth state (or recurrent event); The $(K+1)$th row is that on the survival time.
`...`	

See Also

`rmtfit`, `summary.rmtfit`, `plot.rmtfit`, `bouquet`.

`summary.rmtfit` *Summary of the analysis results*

Description

Summarize the overall and stage-wise inferential results for the restricted mean times in favor of treatment at a user-specified length of follow-up.

Usage

```
## S3 method for class 'rmtfit'
summary(object, tau = NULL, Kmax = NULL, ...)
```

Arguments

object	An object returned by rmtfit.
tau	A positive real number for the follow-up time; Default is the maximum event time in the data.
Kmax	A positive integer; If specified, the stage-wise estimates over Kmax, . . . , K will be aggregated.
. . .	Additional arguments affecting the summary produced.

Value

An object of class summary.rmtfit with components

WL	A $2 \times (K+2)$-dimensional matrix; Each row contains the estimates for the stage-wise and overall restricted mean win times for each group.
tab	A $(K+2) \times 4$-dimensional matrix summarizing the inferential results for the stage-wise and overall restricted mean times in favor of treatment; Columns include Estimate, Std.Err, Z value, and Pr(>|z|).
. . .	

See Also

rmtfit, plot.rmtfit, bouquet.

Examples

```
#See examples for rmtfit().
```

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