Package: prodlim (via r-universe)

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Title Product-Limit Estimation for Censored Event History Analysis

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Description Fast and user friendly implementation of nonparametric estimators for censored event history (survival) analysis. Kaplan-Meier and Aalen-Johansen method.

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Suggests tibble, pammtools, ggthemes, riskRegression, testthat, etm, survey

LinkingTo Rcpp

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BugReports https://github.com/tagteam/prodlim/issues

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[.Hist *Subset an event history object*

Description

This method makes sure that the attributes are preserved

Usage

```
## S3 method for class 'Hist'
x[i, j, drop = FALSE]
```

Arguments

x	object obtained with Hist
i	passed on to next method
j	passed on to next method
drop	passed on to next method

as.data.frame.prodlim *Turn prodlim objects into a data.frame*

Description

Collect results of a fitted prodlim object in a data.frame

Usage

```
## S3 method for class 'prodlim'
as.data.frame(x, ...)
```

Arguments

x	object obtained with function prodlim
...	passed to summary.prodlim

Details

By default object contains results for all fitted time points and all strata. Use arguments times and newdata of summary.prodlim to subset.

Value

A data.table with the results of the prodlim object

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

prodlim

Examples

```
set.seed(8)
d <- SimCompRisk(17)
fit <- prodlim(Hist(time,event)~X1,data=d)
as.data.frame.prodlim(fit)
as.data.frame.prodlim(fit)
```

---

as.data.table.prodlim *Turn prodlim objects into a* data.table

---

Description

Collect results of a fitted prodlim object in a data.table

Usage

```
## S3 method for class 'prodlim'
as.data.table(x, keep.rownames = FALSE, ...)
```

Arguments

x	object obtained with function prodlim
keep.rownames	Not used
...	passed to summary.prodlim

Details

By default object contains results for all fitted time points and all strata. Use arguments times and newdata of summary.prodlim to subset.

Value

A data.table with the results of the prodlim object

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

prodlim, data.table

Examples

```
library(data.table)
set.seed(8)
d <- SimCompRisk(17)
fit <- prodlim(Hist(time,event)~X1,data=d)
as.data.table(fit)
```

---

as_tibble.prodlim *Turn prodlim objects into a* tibble

Description

Collect results of a fitted prodlim object in a tibble

Usage

```
as_tibble.prodlim(x, ...)
```

Arguments

x	object obtained with function prodlim
...	passed to summary.prodlim

Details

By default object contains results for all fitted time points and all strata. Use arguments times and newdata of summary.prodlim to subset.

Value

A data.table with the results of the prodlim object

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

prodlim, tibble

Examples

```
library(tibble)
set.seed(8)
d <- SimCompRisk(17)
fit <- prodlim(Hist(time,event)~X1,data=d)
tibble::as_tibble(fit)
```

---

atRisk *Drawing numbers of subjects at-risk of experiencing an event below Kaplan-Meier and Aalen-Johansen plots.*

Description

This function is invoked and controlled by `plot.prodlim`.

Usage

```
atRisk(
  x,
  newdata,
  times,
  line,
  col,
  labelcol = NULL,
  interspace,
  cex,
  labels,
  title = "",
  titlecol = NULL,
  pos,
  adj,
  dist,
  xdist,
  adjust.labels = TRUE,
  show.censored = FALSE,
  unit = "npc",
  ...
)
```

Arguments

x	an object of class 'prodlim' as returned by the `prodlim` function.
newdata	see `plot.prodlim`
times	Where to compute the atrisk numbers.
line	Distance of the atrisk numbers from the inner plot.

col	The color of the text.
labelcol	The color for the labels. Defaults to col.
interspace	Distance between rows of atrisk numbers.
cex	Passed on to mtext for both atrisk numbers and labels.
labels	Labels for the at-risk rows.
title	Title for the at-risk labels
titlecol	The color for the title. Defaults to 1 (black).
pos	The value is passed on to the mtext argument at for the labels (not the atrisk numbers).
adj	Passed on to mtext for the labels (not the atriks numbers).
dist	If line is missing, the distance of the upper most atrisk row from the inner plotting region: par()$mgp[2].
xdist	Distance in x-axis direction to define the distance between the labels and the numbers at-risk. Deftaults to strwidth("MM",cex=cex).
adjust.labels	If TRUE the labels are left adjusted.
show.censored	If TRUE the cumulative number of subjects lost to follow up is shown in parentheses.
unit	The graphical coordinate systems unit to convert from when line2user is calling grconvertX and grconvertY. Default is 'npc'
...	Further arguments that are passed to the function mtext.

Details

This function should not be called directly. The arguments can be specified as atRisk.arg in the call to plot.prodlim.

Value

Nil

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

plot.prodlim, confInt, markTime

backGround *Background and grid color control.*

Description

Some users like background colors, and it may be helpful to have grid lines to read off e.g. probabilities from a Kaplan-Meier graph. Both things can be controlled with this function. However, it mainly serves plot.prodlim.

Usage

```
backGround(
  xlim,
  ylim,
  bg = "white",
  fg = "gray77",
  horizontal = NULL,
  vertical = NULL,
  border = "black"
)
```

Arguments

xlim	Limits for the xaxis, defaults to par("usr")[1:2].
ylim	Limits for the yaxis, defaults to par("usr")[3:4].
bg	Background color. Can be multiple colors which are then switched at each horizontal line.
fg	Grid line color.
horizontal	Numerical values at which horizontal grid lines are plotted.
vertical	Numerical values at which vertical grid lines are plotted.
border	The color of the border around the background.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

Examples

```
plot(0,0)
backGround(bg="beige",fg="red",vertical=0,horizontal=0)

plot(0,0)
backGround(bg=c("yellow","green"),fg="red",xlim=c(-1,1),ylim=c(-1,1),horizontal=seq(0,1,.1))
backGround(bg=c("yellow","green"),fg="red",horizontal=seq(0,1,.1))
```

checkCauses *Check availability of a cause in competing risk settings*

Description

For competing risk settings, check if the requested cause is known to the object

Usage

```
checkCauses(cause, object)
```

Arguments

cause	cause of interest
object	object either obtained with Hist or prodlim

confInt *Add point-wise confidence limits to the graphs of Kaplan-Meier and Aalen-Johansen estimates.*

Description

This function is invoked and controlled by plot.prodlim.

Usage

```
confInt(ci, citype, col, lty, lwd, density = 55, ...)
```

Arguments

ci	A data.table with columns time, lower and upper.
citype	If "shadow" then confidence limits are drawn as colored shadows. Otherwise, dotted lines are used to show the upper and lower confidence limits.
col	the colour of the lines.
lty	the line type of the lines.
lwd	the line thickness of the lines.
density	For citype="shadow", the density of the shade. Default is 55 percent.
...	Further arguments that are passed to the function segments if type=="bars" and to lines else.

Details

This function should not be called directly. The arguments can be specified as Confint.arg in the call to plot.prodlim.

Value

Nil

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

plot.prodlim, atRisk, markTime

---

crModel *Competing risks model for simulation*

Description

Competing risks model for simulation

Usage

```
crModel()
```

Details

Create a competing risks model with to causes to simulate a right censored event time data without covariates

This function requires the lava package.

Value

A structural equation model initialized with four variables: the latent event times of two causes, the latent right censored time, and the observed right censored event time.

Author(s)

Thomas A. Gerds

Examples

```
library(lava)
m <- crModel()
d <- sim(m,6)
print(d)
```

dimColor *Dim a given color to a specified density*

Description

This function calls first col2rgb on a color name and then uses rgb to adjust the intensity of the result.

Usage

```
dimColor(col, density = 55)
```

Arguments

col	Color name or number passed to col2rgb.
density	Integer value passed as alpha coefficient to rgb between 0 and 255

Value

A character vector with the color code. See rgb for details.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

rgb col2rgb

Examples

```
dimColor(2,33)
dimColor("green",133)
```

EventHistory.frame *Event history frame*

Description

Extract event history data and design matrix including specials from call

Usage

```
EventHistory.frame(
  formula,
  data,
  unspecialsDesign = TRUE,
  specials,
  specialsFactor = TRUE,
  specialsDesign = FALSE,
  stripSpecials = NULL,
  stripArguments = NULL,
  stripAlias = NULL,
  stripUnspecials = NULL,
  dropIntercept = TRUE,
  check.formula = TRUE,
  response = TRUE,
  na.action = options()$na.action
)
```

Arguments

formula	Formula whose left hand side specifies the event history, i.e., either via Surv() or Hist().
data	Data frame in which the formula is interpreted
unspecialsDesign	Passed as is to model.design.
specials	Character vector of special function names. Usually the body of the special functions is function(x)x but e.g., strata from the survival package does treat the values
specialsFactor	Passed as is to model.design.
specialsDesign	Passed as is to model.design
stripSpecials	Passed as specials to strip.terms
stripArguments	Passed as arguments to strip.terms
stripAlias	Passed as alias.names to strip.terms
stripUnspecials	Passed as unspecials to strip.terms
dropIntercept	Passed as is to model.design
check.formula	If TRUE check if formula is a Surv or Hist thing.
response	If FALSE do not evaluate the left hand side of the formula and to not return the response (event.history).
na.action	Decide what to do with missing values.

Details

Obtain a list with the data used for event history regression analysis. This function cannot be used directly on the user level but inside a function to prepare data for survival analysis.

Value

A list which contains - the event.history (see Hist) - the design matrix (see model.design) - one entry for each special (see model.design)

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

model.frame model.design Hist

Examples

```
## Here are some data with an event time and no competing risks
## and two covariates X1 and X2.
## Suppose we want to declare that variable X1 is treated differently
## than variable X2. For example, X1 could be a cluster variable, or
## X1 should have a proportional effect on the outcome.
dsurv <- data.frame(time=1:7,
                    status=c(0,1,1,0,0,0,1),
                    X2=c(2.24,3.22,9.59,4.4,3.54,6.81,5.05),
                    X3=c(1,1,1,1,0,0,1),
                    X4=c(44.69,37.41,68.54,38.85,35.9,27.02,41.84),
                    X1=factor(c("a","b","a","c","c","a","b"),
                        levels=c("c","a","b")))
## We pass a formula and the data
e <- EventHistory.frame(Hist(time,status)~prop(X1)+X2+cluster(X3)+X4,
                        data=dsurv,
                        specials=c("prop","cluster"),
                        stripSpecials=c("prop","cluster"))
names(e)
## The first element is the event.history which is result of the left hand
## side of the formula:
e$event.history
## same as
with(dsurv,Hist(time,status))
## to see the structure do
colnames(e$event.history)
unclass(e$event.history)
## in case of competing risks there will be an additional column called event,
## see help(Hist) for more details

## The other elements are the design, i.e., model.matrix for the non-special covariates
e$design
## and a data.frame for the special covariates
e$prop
## The special covariates can be returned as a model.matrix
e2 <- EventHistory.frame(Hist(time,status)~prop(X1)+X2+cluster(X3)+X4,
                         data=dsurv,
                         specials=c("prop","cluster"),
                         stripSpecials=c("prop","cluster"),
```

```
                        specialsDesign=TRUE)
e2$prop
## and the non-special covariates can be returned as a data.frame
e3 <- EventHistory.frame(Hist(time,status)~prop(X1)+X2+cluster(X3)+X4,
                        data=dsurv,
                        specials=c("prop","cluster"),
                        stripSpecials=c("prop","cluster"),
                        specialsDesign=TRUE,
                        unspecialsDesign=FALSE)
e3$design

## the general idea is that the function is used to parse the combination of
## formula and data inside another function. Here is an example with
## competing risks
SampleRegression <- function(formula,data=parent.frame()){
    thecall <- match.call()
    ehf <- EventHistory.frame(formula=formula,
                              data=data,
                              stripSpecials=c("prop","cluster","timevar"),
                              specials=c("prop","timevar","cluster"))
    time <- ehf$event.history[,"time"]
    status <- ehf$event.history[,"status"]
    ## event as a factor
    if (attr(ehf$event.history,"model")=="competing.risks"){
        event <- ehf$event.history[,"event"]
        Event <- getEvent(ehf$event.history)
        list(response=data.frame(time,status,event,Event),X=ehf[-1])
    }
    else{ # no competing risks
        list(response=data.frame(time,status),X=ehf[-1])
    }
}
dsurv$outcome <- c("cause1","0","cause2","cause1","cause2","cause2","0")
SampleRegression(Hist(time,outcome)~prop(X1)+X2+cluster(X3)+X4,dsurv)
ehf <- EventHistory.frame(formula=Hist(time,outcome)~prop(X1)+X2+cluster(X3)+X4,
                          data=dsurv,
                          stripSpecials=c("prop","cluster","timevar"),
                          specials=c("prop","timevar","cluster"))

## let's test if the parsing works
form1 <- Hist(time,outcome!="0")~prop(X1)+X2+cluster(X3)+X4
form2 <- Hist(time,outcome)~prop(X1)+cluster(X3)+X4
ff <- list(form1,form2)
lapply(ff,function(f){SampleRegression(f,dsurv)})


## here is what the riskRegression package uses to
## distinguish between covariates with
## time-proportional effects and covariates with
## time-varying effects:
## Not run:
library(riskRegression)
data(Melanoma)
```

```
f <- Hist(time,status)~prop(thick)+strata(sex)+age+prop(ulcer,power=1)+timevar(invasion,test=1)
## here the unspecial terms, i.e., the term age is treated as prop
## also, strata is an alias for timvar

EHF <- prodlim::EventHistory.frame(formula,
                                   Melanoma[1:10],
                                   specials=c("timevar","strata","prop","const","tp"),
                                   stripSpecials=c("timevar","prop"),
                                   stripArguments=list("prop"=list("power"=0),
                                       "timevar"=list("test"=0)),
                                   stripAlias=list("timevar"=c("strata"),
                                       "prop"=c("tp","const")),
                                   stripUnspecials="prop",
                                   specialsDesign=TRUE,
                                   dropIntercept=TRUE)
EHF$prop
EHF$timevar

## End(Not run)
```

`followup` *Estimation of the median potential followup time.*

Description

The reverse Kaplan-Meier method estimates the median potential followup time.

Usage

```
followup(formula, cens.code = 0, data, ...)
```

Arguments

`formula`	A formula whose left hand side is a `Hist` or a `Surv` object specifying the event time and the event type where by default 0=censored, 1=event, 2=competing risk (if any). Use `cens.code` to change the value for censored.
`cens.code`	Value of the event
`data`	A data.frame in which all the variables of `formula` can be interpreted.
`...`	Arguments passed to `prodlim.quantile`.

Details

This is merely a wrapper for `prodlim` with argument reverse.

Value

The estimated median potential followup time with inter quartile ranges.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

References

Michael Schemper and Terry L. Smith. A note on quantifying follow-up in studies of failure time. Controlled Clinical Trials, 17(4):343–346, 1996.

See Also

prodlim

Examples

```
set.seed(8)
d <- SimCompRisk(117)

# overall
followup(Hist(time,event)~1,data=d)

# in strata defined by variable X1
followup(Hist(time,event)~X1,data=d)
```

---

geom_prodlim *Product-limit geoms for survival and competing risks curves*

Description

Draw Kaplan-Meier or Aalen-Johansen curves with optional confidence bands. For competing risks with multiple causes, the default display shows one curve per cause. When ‘cause = "stacked"‘, causes are drawn as stacked filled rectangles instead of step curves with confidence shadows.

Usage

```
geom_prodlim(
  mapping = NULL,
  data = NULL,
  position = "identity",
  na.rm = FALSE,
  show.legend = NA,
  inherit.aes = TRUE,
  type = "risk",
  cause = NULL,
  conf_int = TRUE,
  conf_int_alpha = 0.2,
  percent = TRUE,
  timeconverter = NULL,
  times = NULL,
```

```
  cens.code = "0",
  ...
)
```

Arguments

mapping	Set of aesthetic mappings created by [ggplot2::aes()].
data	Data frame.
position	Position adjustment.
na.rm	If ‘FALSE‘, missing values are removed with a warning.
show.legend	Logical. Should this layer be included in the legends?
inherit.aes	If ‘FALSE‘, overrides the default aesthetics.
type	Passed to [prodlim::prodlim()], usually ‘"risk"‘ or ‘"surv"‘.
cause	Cause(s) for competing risks. Can be a vector of causes or the string ‘"stacked"‘.
conf_int	Logical. Draw confidence intervals.
conf_int_alpha	Alpha level for confidence shadows.
percent	Logical. Passed to [prodlim::summary.prodlim()].
timeconverter	Optional time conversion string.
times	Optional evaluation times passed to [prodlim::summary.prodlim()].
cens.code	Censoring code passed to [prodlim::Hist()].
...	Further arguments passed to [ggplot2::layer()].

Details

When multiple causes are specified, ‘fill‘/‘colour‘ aesthetics are ignored and replaced by a cause-based mapping so that all causes are shown in a single legend. When ‘cause = "stacked"‘, causes are stacked on top of each other and confidence shadows are not drawn.

Examples

```
library(riskRegression)
library(data.table)
library(ggplot2)
data(Melanoma)
# Kaplan-Meier
ggplot(data = Melanoma,aes(x = time, event = 1*(status != 0)))+
       geom_prodlim(type = "surv")
# stratified Kaplan-Meier inherited aes
ggplot(data = Melanoma,aes(x = time, event = 1*(status != 0),fill = sex,color = sex))+
       geom_prodlim(type = "surv")
# stratified Kaplan-Meier geom aes
ggplot(data = Melanoma,aes(x = time, event = 1*(status != 0)))+
       geom_prodlim(aes(fill = sex,color = sex),type = "surv")
# facet
ggplot(data = Melanoma,aes(x = time, event = 1*(status != 0)))+
       geom_prodlim(type = "surv")+facet_grid(~sex)
```

```
# stratified and facet
ggplot(data = Melanoma,aes(x = time, event = 1*(status != 0),fill = epicel,color = epicel))+
       geom_prodlim(type = "surv")+facet_grid(~sex)

# Aalen-Johansen
ggplot(data = Melanoma,aes(x = time, event = status))+
       geom_prodlim(type = "surv",cause = 1:2)
# stratified Aalen-Johansen inherited aes
ggplot(data = Melanoma,aes(x = time, event = status,fill = sex,color = sex))+
       geom_prodlim(type = "surv")
# stratified Aalen-Johansen geom aes
ggplot(data = Melanoma,aes(x = time, event = status))+
       geom_prodlim(aes(fill = sex,color = sex),type = "surv")
# facet
ggplot(data = Melanoma,aes(x = time, event = status))+
       geom_prodlim(type = "surv")+facet_grid(~sex)
# stratified and facet
ggplot(data = Melanoma,aes(x = time, event = status,fill = epicel,color = epicel))+
       geom_prodlim(type = "surv")+facet_grid(~sex)
# stacked
ggplot(data = Melanoma,aes(x = time, event = status))+
       geom_prodlim(cause = "stacked")+facet_grid(~sex)
# stacked with cens.code option
ggplot(data = Melanoma,aes(x = time, event = event))+
       geom_prodlim(cens.code="censored",cause = "stacked")+facet_grid(~sex)
```

`getEvent` *Extract a column from an event history object.*

Description

Extract a column from an event history object, as obtained with the function `Hist`.

Usage

```
getEvent(object, mode = "factor", column = "event")
```

Arguments

`object`	Object of class `"Hist"`.
`mode`	Return mode. One of `"numeric"`, `"character"`, or `"factor"`.
`column`	Name of the column to extract from the object.

Details

Since objects of class `"Hist"` are also matrices, all columns are numeric or integer valued. To extract a correctly labeled version, the attribute `states` of the object is used to generate factor levels.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

Hist

Examples

```
dat= data.frame(time=1:5,event=letters[1:5])
x=with(dat,Hist(time,event))
## inside integer
unclass(x)
## extract event (the extra level "unknown" is for censored data)
getEvent(x)
```

---

getStates *States of a multi-state model*

Description

Extract the states of a multi-state model

Usage

```
getStates(object, ...)
```

Arguments

object	Object of class prodlim or Hist .
...	not used

Details

Applying this function to the fit of prodlim means to apply it to fit$model.response.

Value

A character vector with the states of the model.

Author(s)

Thomas A. Gerds

ggprodlim *ggplot2 support for prodlim objects*

Description

ggplot2 support for Kaplan-Meier and Aalen-Johansen estimators

Usage

```
ggprodlim(
  x,
  type = x$type,
  cause,
  xlim,
  ylim,
  y_breaks,
  x_breaks,
  position_atrisk,
  atrisk_title = "Number at risk",
  atrisk_labels = NULL,
  atrisk_title_line = 0.14,
  atrisk_title_step = 0.06,
  atrisk_line_step = 0.04,
  atrisk_bottom_margin = NULL,
  facet_panel_spacing_y = NULL,
  conf_int = TRUE,
  conf_int_alpha = 0.2,
  percent = TRUE,
  timeconverter,
  color_var,
  facet_formula,
  palette = NULL,
  return_data = FALSE,
  ...
)
```

Arguments

x	An object obtained with prodlim.
type	Either "surv" or "risk". Defaults to x$type.
cause	For competing risk models: a cause (passed to as.data.table.prodlim), "all" for all causes, or "stacked" for a stacked cumulative incidence plot.
xlim, ylim	Limits for the axes.
x_breaks, y_breaks	Breaks for axes.#

position_atrisk
: Numeric vector specifying x-positions where numbers at risk should be printed. If missing, a default grid is chosen.

atrisk_title
: Title shown left of the at-risk table.

atrisk_labels
: Optional replacement labels for strata/cause groups in the at-risk table (in plotting order).

atrisk_title_line
: Numeric. Position of the at-risk title below the plotting region, as an offset from `min(ylim)` in units of `diff(ylim)`.

atrisk_title_step
: Numeric. Vertical distance from the title to the first at-risk row, in units of `diff(ylim)`.

atrisk_line_step
: Numeric. Vertical spacing between at-risk rows, in units of `diff(ylim)`.

atrisk_bottom_margin
: Numeric. Bottom plot margin in lines when the at-risk table is shown.

facet_panel_spacing_y
: Optional numeric. Vertical spacing between facet rows in lines. If `NULL` and faceting is used together with an at-risk table, the default is `5 + n_colors`. The same value is used as the default bottom plot margin below the lowest facet row.

conf_int
: Logical. If TRUE and `lower`/`upper` are available, draw pointwise confidence intervals.

conf_int_alpha
: Alpha for CI shading.

percent
: Logical. If TRUE, y axis is shown in percent (0-100).

timeconverter
: Optional character, see `plot.prodlim` for supported values (e.g., "years2months").

color_var
: Covariate name must be included in `colnames(x$X)` and in competing risk models the word `"cause"`.

facet_formula
: Formula for facet_wrap. May include covariate names `colnames(x$X)` and in competing risk models also the word `"cause"`.

palette
: Optional vector of colors. If provided, applied via `scale_color_manual`/`scale_fill_manual`. Default NULL (do not impose a palette).

return_data
: Logical. If TRUE, return a list with plot and data.

...
: Passed to `as.data.table.prodlim`; commonly `newdata`, `times`, and for competing risks `cause`.

Details

A ggplot2-based alternative to `plot.prodlim` that returns a `ggplot` object, enabling ggplot theming, facetting, and composition.

Value

A ggplot object, or a list if `return_data=TRUE`.

See Also

plot.prodlim, as.data.table.prodlim

Examples

```
data(Melanoma,package = "riskRegression")
# marginal Kaplan-Maier
km <- prodlim(Hist(time,status != 0)~1,data = Melanoma)
ggprodlim(km)
# marginal Aalen-Johansen
aj <- prodlim(Hist(time,status)~1,data = Melanoma)
ggprodlim(aj)
ggprodlim(aj,facet_formula = ~cause)

ajsex <- prodlim(Hist(time,status)~sex,data = Melanoma)
ggprodlim(ajsex)
ggprodlim(ajsex,facet_formula = ~cause)
ggprodlim(ajsex,facet_formula = ~sex)
ggprodlim(ajsex,color_var = "sex")
ggprodlim(ajsex,color_var = "cause")

# stacking the causes
ggprodlim(ajsex,cause = "stacked")
# stacked with two covariates
   ajepisex <- prodlim(Hist(time,status)~sex+epicel,data = Melanoma)
   ggprodlim(ajepisex,
             cause = "stacked",
             facet_formula = sex~epicel,
             atrisk_title_line = 0.2)
```

---

head.Hist *Check the head of an event history object*

Description

The object is evaluated as a matrix

Usage

```
## S3 method for class 'Hist'
head(x)
```

Arguments

x	object obtained with Hist

`Hist` *Create an event history object*

Description

Functionality for managing censored event history response data. The function can be used as the left hand side of a formula: `Hist` serves `prodlim` in a similar way as `Surv` from the survival package serves 'survfit'. `Hist` provides the suitable extensions for dealing with right censored and interval censored data from competing risks and other multi state models. Objects generated with `Hist` have a print and a plot method.

Usage

```
Hist(
  time,
  event,
  entry = NULL,
  id = NULL,
  cens.code = "0",
  addInitialState = FALSE
)
```

Arguments

`time`	for right censored data a numeric vector of event times – for interval censored data a list or a data.frame providing two numeric vectors the left and right endpoints of the intervals. See `Details`.
`event`	A vector or a factor that specifies the events that occurred at the corresponding value of `time`. Numeric, character and logical values are recognized. It can also be a list or a data.frame for the longitudinal form of storing the data of a multi state model – see `Details`.
`entry`	Vector of delayed entry times (left-truncation) or list of two times when the entry time is interval censored.
`id`	Identifies the subjects to which multiple events belong for the longitudinal form of storing the data of a multi state model – see `Details`.
`cens.code`	A character or numeric vector to identify the right censored observations in the values of `event`. Defaults to "0" which is equivalent to 0.
`addInitialState`	If TRUE, an initial state is added to all ids for the longitudinal input form of a multi-state model.

Details

Specification of the event times

If `time` is a numeric vector then the values are interpreted as right censored event times, ie as the minimum of the event times and the censoring times.

If time is a list with two elements or data frame with two numeric columns The first element (column) is used as the left endpoints of interval censored observations and the second as the corresponding right endpoints. When the two endpoints are equal, then this observation is treated as an exact uncensored observation of the event time. If the value of the right interval endpoint is either NA or Inf, then this observation is treated as a right censored observation. Right censored observations can also be specified by setting the value of event to cens.code. This latter specification of right censored event times overwrites the former: if event equals cens.code the observation is treated as right censored no matter what the value of the right interval endpoint is.

Specification of the events

If event is a numeric, character or logical vector then the order of the attribute "state" given to the value of Hist is determined by the order in which the values appear. If it is a factor then the order from the levels of the factor is used instead.

Normal form of a multi state model

If event is a list or a data.frame with exactly two elements, then these describe the transitions in a multi state model that occurred at the corresponding time as follows: The values of the first element are interpreted as the from states of the transition and values of the second as the corresponding to states.

Longitudinal form of a multi state model

If id is given then event must be a vector. In this case two subsequent values of event belonging to the same value of id are treated as the from and to states of the transitions.

Value

An object of class Hist for which there are print and plot methods. The object's internal is a matrix with some of the following columns:

time	the right censored times
L	the left endpoints of internal censored event times
R	the right endpoints of internal censored event times
status	0 for right censored, 1 for exact, and 2 for interval censored event times.
event	an integer valued numeric vector that codes the events.
from	an integer valued numeric vector that codes the from states of a transition in a multi state model.
to	an integer valued numeric vector that codes the to states of a transition in a multi state model.

Further information is stored in attributes. The key to the official names given to the events and the from and to states is stored in an attribute "states".

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>, Arthur Allignol <arthur.allignol@fdm.uni-freiburg.de>

See Also

plot.Hist, summary.Hist, prodlim

Examples

```
## Right censored responses of a two state model
## ----------------------------------------------

Hist(time=1:10,event=c(0,1,0,0,0,1,0,1,0,0))

## change the code for events and censored observations

Hist(time=1:10,event=c(99,"event",99,99,99,"event",99,"event",99,99),cens.code=99)

TwoStateFrame <- SimSurv(10)
SurvHist <- with(TwoStateFrame,Hist(time,status))
summary(SurvHist)
plot(SurvHist)

## Right censored data from a competing risk model
## ------------------------------------------------

CompRiskFrame <- data.frame(time=1:10,event=c(1,2,0,3,0,1,2,1,2,1))
CRHist <- with(CompRiskFrame,Hist(time,event))
summary(CRHist)
plot(CRHist)

## Interval censored data from a survival model
icensFrame <- data.frame(L=c(1,1,3,4,6),R=c(2,NA,3,6,9),event=c(1,1,1,2,2))
with(icensFrame,Hist(time=list(L,R)))

## Interval censored data from a competing risk model
with(icensFrame,Hist(time=list(L,R),event))

## Multi state model
MultiStateFrame <- data.frame(time=1:10,
         from=c(1,1,3,1,2,4,1,1,2,1),
         to=c(2,3,1,2,4,2,3,2,4,4))
with(MultiStateFrame,Hist(time,event=list(from,to)))

##  MultiState with right censored observations

MultiStateFrame1 <- data.frame(time=1:10,
         from=c(1,1,3,2,1,4,1,1,3,1),
         to=c(2,3,1,0,2,2,3,2,0,4))
with(MultiStateFrame1,Hist(time,event=list(from,to)))

## Using the longitudinal input method
MultiStateFrame2 <- data.frame(time=c(0,1,2,3,4,0,1,2,0,1),
         event=c(1,2,3,0,1,2,4,2,1,2),
         id=c(1,1,1,1,2,2,2,2,3,3))
 with(MultiStateFrame2,Hist(time,event=event,id=id))
```

is.na.Hist *Check for missing values in event history object*

Description

The object has usually two or three columns and this function checks each column separately

Usage

```
## S3 method for class 'Hist'
is.na(x)
```

Arguments

x	object obtained with Hist

jackknife *Compute jackknife pseudo values.*

Description

Compute jackknife pseudo values.

Usage

```
jackknife(object, times, cause, keepResponse = FALSE, ...)
```

Arguments

object	Object of class "prodlim".
times	Time points at which to compute pseudo values.
cause	Character (other classes are converted with as.character). For competing risks the cause of failure.
keepResponse	If TRUE add the model response, i.e. event time, event status, etc. to the result.
...	not used

Details

Compute jackknife pseudo values based on marginal Kaplan-Meier estimate of survival, or based on marginal Aalen-Johansen estimate of the absolute risks, i.e., the cumulative incidence function.

Note

The R-package pseudo does a similar job, and appears to be a little faster in small samples, but much slower in large samples. See examples.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

References

Andersen PK & Perme MP (2010). Pseudo-observations in survival analysis Statistical Methods in Medical Research, 19(1), 71-99.

See Also

prodlim

Examples

```
## pseudo-values for survival models

d=SimSurv(20)
f=prodlim(Hist(time,status)~1,data=d)
jackknife(f,times=c(3,5))

## in some situations it may be useful to attach the
## the event time history to the result
jackknife(f,times=c(3,5),keepResponse=TRUE)

# pseudo-values for competing risk models
set.seed(15)
d=SimCompRisk(15)
f=prodlim(Hist(time,event)~1,data=d)
jackknife(f,times=c(3,5),cause=1)
jackknife(f,times=c(1,3,5),cause=2)
```

---

leaveOneOut *Compute jackknife pseudo values.*

Description

Compute leave-one-out estimates

Usage

```
leaveOneOut(object, times, cause, lag = FALSE, ...)
```

Arguments

object	Object of class "prodlim".
times	time points at which to compute leave-one-out event/survival probabilities.
cause	Character (other classes are converted with as.character). For competing risks the cause of interest.
lag	For survival models only. If TRUE lag the result, i.e. compute S(t-) instead of S(t).
...	not used

Details

This function is the work-horse for jackknife

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

jackknife

List2Matrix *Reduce list to a matrix or data.frame with names as new columns*

Description

This function is used by summary.prodlim to deal with results.

Usage

```
List2Matrix(list, depth, names)
```

Arguments

list	A named list which contains nested lists
depth	The depth in the list hierarchy until an rbindable object
names	Names for the list variables

Details

Reduction is done with rbind.

Value

Matrix or data.frame.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

Examples

```
x=list(a=data.frame(u=1,b=2,c=3),b=data.frame(u=3,b=4,c=6))
List2Matrix(x,depth=1,"X")
```

---

markTime *Marking product-limit plots at the censored times.*

Description

This function is invoked and controlled by `plot.prodlim`.

Usage

```
markTime(x, times, nlost, pch, col, ...)
```

Arguments

`x`	The values of the curves at `times`.
`times`	The times where there curves are plotted.
`nlost`	The number of subjects lost to follow-up (censored) at `times`.
`pch`	The symbol used to mark the curves.
`col`	The color of the symbols.
`...`	Arguments passed to `points`.

Details

This function should not be called directly. The arguments can be specified as `atRisk.arg` in the call to `plot.prodlim`.

Value

Nil

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

`plot.prodlim`, `confInt`, `atRisk`

meanNeighbors *Helper function to obtain running means for prodlim objects.*

Description

Compute average values of a variable according to neighborhoods.

Usage

```
meanNeighbors(x, y, ...)
```

Arguments

x	Object of class "neighborhood".
y	Vector of numeric values.
...	Not used.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

neighborhood

Examples

```
meanNeighbors(x=1:10,y=c(1,10,100,1000,1001,1001,1001,1002,1002,1002))
```

model.design *Extract a design matrix and specials from a model.frame*

Description

Extract design matrix and data specials from a model.frame

Usage

```
model.design(
  terms,
  data,
  xlev = NULL,
  dropIntercept = FALSE,
  maxOrder = 1,
  unspecialsDesign = TRUE,
  specialsFactor = FALSE,
  specialsDesign = FALSE
)
```

Arguments

terms	terms object as obtained either with function terms or strip.terms.
data	A data set in which terms are defined.
xlev	a named list of character vectors giving the full set of levels to be assumed for the factors. Can have less elements, in which case the other levels are learned from the data.
dropIntercept	If TRUE drop intercept term from the design matrix
maxOrder	An error is produced if special variables are involved in interaction terms of order higher than max.order.
unspecialsDesign	A logical value: if TRUE apply model.matrix to unspecial covariates. If FALSE extract unspecial covariates from data.
specialsFactor	A character vector containing special variables which should be coerced into a single factor. If TRUE all specials are treated in this way, if FALSE none of the specials is treated in this way.
specialsDesign	A character vector containing special variables which should be transformed into a design matrix via model.matrix. If TRUE all specials are treated in this way.

Details

The function separates special terms from the unspecial terms and returns a list of design matrices, one for unspecial terms and one for each special. Some special specials cannot or should not be evaluated in data. E.g., y~a+dummy(x)+strata(v) the function strata can and should be evaluated, but in order to have model.frame also evaluate dummy(x) one would be to define and export the function dummy. Still the term dummy(x) can be used to identify a special treatment of the variable x. To deal with this case, one can specify stripSpecials="dummy". In addition, the data should include variables strata(z) and x, not dummy(x). See examples. The function untangle.specials of the survival function does a similar job.

Value

A list which contains - the design matrix with the levels of the variables stored in attribute 'levels' - separate data.frames which contain the values of the special variables.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

EventHistory.frame model.frame terms model.matrix .getXlevels

Examples

```
# specials that are evaluated. here ID needs to be defined
set.seed(8)
d <- data.frame(y=rnorm(5),x=factor(c("a","b","b","a","c")),z=c(2,2,7,7,7),v=sample(letters)[1:5])
d$z <- factor(d$z,levels=c(1:8))
ID <- function(x)x
f <- formula(y~x+ID(z))
t <- terms(f,special="ID",data=d)
mda <- model.design(terms(t),data=d,specialsFactor=TRUE)
mda$ID
mda$design
##
mdb <- model.design(terms(t),data=d,specialsFactor=TRUE,unspecialsDesign=FALSE)
mdb$ID
mdb$design

# set x-levels
attr(mdb$ID,"levels")
attr(model.design(terms(t),data=d,xlev=list("ID(z)"=1:10),
     specialsFactor=TRUE)$ID,"levels")

# special specials (avoid define function SP)
f <- formula(y~x+SP(z)+factor(v))
t <- terms(f,specials="SP",data=d)
st <- strip.terms(t,specials="SP",arguments=NULL)
md2a <- model.design(st,data=d,specialsFactor=TRUE,specialsDesign="SP")
md2a$SP
md2b <- model.design(st,data=d,specialsFactor=TRUE,specialsDesign=FALSE)
md2b$SP

# special function with argument
f2 <- formula(y~x+treat(z,power=2)+treat(v,power=-1))
t2 <- terms(f2,special="treat")
st2 <- strip.terms(t2,specials="treat",arguments=list("treat"=list("power")))
model.design(st2,data=d,specialsFactor=FALSE)
model.design(st2,data=d,specialsFactor=TRUE)
model.design(st2,data=d,specialsDesign=TRUE)

library(survival)
data(pbc)
t3 <- terms(Surv(time,status!=0)~factor(edema)*age+strata(I(log(bili)>1))+strata(sex),
            specials=c("strata","cluster"))
st3 <- strip.terms(t3,specials=c("strata"),arguments=NULL)
md3 <- model.design(terms=st3,data=pbc[1:4,])
```

```
md3$strata
md3$cluster

f4 <- Surv(time,status)~const(age)+prop(factor(edema),power=2)+
                        strata(sex,test=0)+prop(bili,power=1)+tp(albumin)
t4 <- terms(f4,specials=c("prop","timevar","strata","tp","const"))
st4 <- strip.terms(t4,
                   specials=c("prop","timevar"),
                   unspecials="prop",
                   alias.names=list("timevar"="strata","prop"=c("const","tp")),
                   arguments=list("prop"=list("power"=0),"timevar"=list("test"=0)))
formula(st4)
md4 <- model.design(st4,data=pbc[1:4,],specialsDesign=TRUE)
md4$prop
md4$timevar
```

---

neighborhood *Nearest neighborhoods for kernel smoothing*

Description

Nearest neighborhoods for the values of a continuous predictor. The result is used for the conditional Kaplan-Meier estimator and other conditional product limit estimators.

Usage

```
neighborhood(x, bandwidth = NULL, kernel = "box")
```

Arguments

x	Numeric vector – typically the observations of a continuous random variate.
bandwidth	Controls the distance between neighbors in a neighborhood. It can be a decimal, i.e.\ the bandwidth, or the string '"smooth"', in which case `N^{-1/4}` is used, `N` being the sample size, or `NULL` in which case the `dpik` function of the package KernSmooth is used to find the optimal bandwidth.
kernel	Only the rectangular kernel ("box") is implemented.

Value

An object of class 'neighborhood'. The value is a list that includes the unique values of 'x' (`values`) for which a neighborhood, consisting of the nearest neighbors, is defined by the first neighbor (`first.nbh`) of the usually very long vector `neighbors` and the size of the neighborhood (`size.nbh`).

Further values are the arguments `bandwidth`, `kernel`, the total sample size `n` and the number of unique values `nu`.

Author(s)

Thomas Gerds

References

Stute, W. "Asymptotic Normality of Nearest Neighbor Regression Function Estimates", *The Annals of Statistics*, 1984,12,917–926.

See Also

dpik, prodlim

Examples

```
d <- SimSurv(20)
neighborhood(d$X2)
```

---

parseFormula *Parse Formula*

Description

Parse a formula to extract terms and handle special functions

Usage

```
parseFormula(
  formula,
  data = NULL,
  specials,
  special.default.values = NULL,
  alias.names = NULL
)
```

Arguments

formula	A model formula (e.g., Y ~ X + Z or Y ~ fun(X, param = value)).
data	An optional data frame containing the variables referenced in the formula.
specials	A character vector of special function names that should be specifically handled.
special.default.values	A named list of named lists specifying default argument values for each special.
alias.names	A named list mapping special names to their alias(es) (e.g., ‘list("special" = "alias")‘).

Details

This function parses a model formula, extracts terms, and processes specified 'special' functions and their arguments. It allows defining default values for special functions and specifying aliases for those names.

Value

A list where each element corresponds to a special function in the formula and contains the parsed terms and their arguments.

A named list with an element for each special that contains a named list where each element corresponds to a formula term that is affected by the special that contains the value(s) of the additional argument(s) for this term.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

[stats::terms()], [strip.terms()]

model.design strip.terms

Examples

```
# Basic usage with specials
parseFormula(Y ~ fun(X, a = 1), specials = "fun")

# With defaults and aliases
parseFormula(Y ~ gfun(X, a = 7),
             specials = "fun",
             alias.names = list("fun" = "gfun"),
             special.default.values = list("fun" = list("a" = 0)))

# Complex use case with multiple specials
parseFormula(Surv(time, status) ~ age + strata(sex, test = 1) + prop(albumin),
             specials = c("prop", "strata"),
         special.default.values = list("prop" = list(power = 0), "strata" = list(test = 1)))
parseFormula(Y~fun(X,a=1),specials="fun",special.default.values=list("fun"=list("a"=0)))
parseFormula(Y~fun(X),specials="fun",special.default.values=list("fun"=list("a"=0)))
parseFormula(Y~gfun(X,a=7),specials="fun",
             alias.names=list("fun"="gfun"),
             special.default.values=list("fun"=list("a"=0)))
parseFormula(formula = Surv(time,status)~age
                            +const(factor(edema))
                            +strata(sex,test=0)
                            +prop(alb)+prop(bili,power=1)
                            +tp(albumin),
                 specials = c("prop","timevar","strata","tp","const"),
                 special.default.values =list("prop" = list(power = 0),
                                              "strata" = list(test = 1)))
```

```
parseFormula(formula = Surv(time,status)~age
                            +const(factor(edema))
                            +strata(sex,test=0)
                            +prop(alb)+prop(bili,power=1)
                            +tp(albumin),
                  specials = c("prop","timevar","strata","tp"),
                  special.default.values =list("prop" = list(power = 0),
                                               "strata" = list(test = 1)),
                  alias.names=list("prop"="const"))
```

`parseSpecialNames` *Parse special terms*

Description

Extract from a vector of character strings the names of special functions and auxiliary arguments

Usage

```
parseSpecialNames(x, special, arguments)
```

Arguments

`x`	Vector of character strings.
`special`	A character string: the name of the special argument.
`arguments`	A vector which contains the arguments of the special function

Details

Signals an error if an element has more arguments than specified by argument arguments.

Value

A named list of parsed arguments. The names of the list are the special variable names, the elements are lists of arguments.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

model.design

Examples

```
## ignore arguments
parseSpecialNames("treat(Z)",special="treat")
## set default to 0
parseSpecialNames(c("log(Z)","a","log(B)"),special="log",arguments=list("base"=0))
## set default to 0
parseSpecialNames(c("log(Z,3)","a","log(B,base=1)"),special="log",arguments=list("base"=0))
## different combinations of order and names
parseSpecialNames(c("log(Z,3)","a","log(B,1)"),
                  special="log",
                  arguments=list("base"=0))
parseSpecialNames(c("log(Z,1,3)","a","log(B,u=3)"),
                  special="log",
                  arguments=list("base"=0,"u"=1))
parseSpecialNames(c("log(Z,u=1,base=3)","a","log(B,u=3)"),
                  special="log",
                  arguments=list("base"=0,"u"=1))
parseSpecialNames(c("log(Z,u=1,base=3)","a","log(B,base=8,u=3)"),
                  special="log",
                  arguments=list("base"=0,"u"=1))
parseSpecialNames("treat(Z,u=2)",
                  special="treat",
                  arguments=list("u"=1,"k"=1))
parseSpecialNames(c("treat(Z,1,u=2)","treat(B,u=2,k=3)"),
                  special="treat",
                  arguments=list("u"=NA,"k"=NULL))
## does not work to set default to NULL:
parseSpecialNames(c("treat(Z,1,u=2)","treat(B,u=2)"),
                  special="treat",
                  arguments=list("u"=NA,"k"=NULL))
```

`PercentAxis` *Percentage-labeled axis.*

Description

Use percentages instead of decimals to label the an axis with a probability scale .

Usage

```
PercentAxis(x, at, ...)
```

Arguments

`x`	Side of the axis
`at`	Positions (decimals) at which to label the axis.
`...`	Given to `axis`.

Author(s)

Thomas Alexander Gerds

See Also

plot.prodlim

Examples

```
plot(0,0,xlim=c(0,1),ylim=c(0,1),axes=FALSE)
PercentAxis(1,at=seq(0,1,.25))
PercentAxis(2,at=seq(0,1,.25))
```

---

plot.Hist *Box-arrow diagrams for multi-state models.*

Description

Automated plotting of the states and transitions that characterize a multi states model.

Usage

```
## S3 method for class 'Hist'
plot(
  x,
  nrow,
  ncol,
  box.width,
  box.height,
  box.padding,
  xbox.position,
  ybox.position,
  stateLabels,
  arrowLabels,
  arrowLabelStyle = "symbolic",
  arrowLabelSymbol = "lambda",
  changeArrowLabelSide,
  curved,
  tagBoxes = FALSE,
  startCountZero = TRUE,
  oneFitsAll,
  margin,
  cex,
  rasta = FALSE,
  verbose = FALSE,
  ...
)
```

Arguments

x	An object of class Hist.
nrow	the number of graphic rows
ncol	the number of graphic columns
box.width	the widths of the boxes on the scale from 0 to 100
box.height	the heights of the boxes on the scale from 0 to 100
box.padding	how much room there should be between the label and the border of a box. Two values on the scale from 0 to 100: the first for the horizontal x-direction and the second for the vertical y-direction padding.
xbox.position	the x box positions (left lower corner) on the scale from 0 to 100.
ybox.position	the y box positions (left lower corner) on the scale from 0 to 100.
stateLabels	Vector of names to appear in the boxes (states). Defaults to attr(x,"state.names"). The boxes can also be individually labeled by smart arguments of the form box3.label="diseased", see examples.
arrowLabels	Vector of labels to appear in the boxes (states). One for each arrow. The arrows can also be individually labeled by smart arguments of the form arrow1.label=paste(expression(eta(see examples.
arrowLabelStyle	Either "symbolic" for automated symbolic arrow labels, or "count" for arrow labels that reflect the number of transitions in the data.
arrowLabelSymbol	Symbol for automated symbolic arrow labels. Defaults to "lambda".
changeArrowLabelSide	A vector of mode logical (TRUE,FALSE) one for each arrow to change the side of the arrow on which the label is placed.
curved	The curvature of curved arrows via diagram::curvedarrow. Experimental. Values between 0 (no curvature) and 1 are meaningful.
tagBoxes	Logical. If TRUE the boxes are numbered in the upper left corner. The size can be controlled with smart argument boxtags.cex. The default is boxtags.cex=1.28.
startCountZero	Control states numbers for symbolic arrow labels and box tags.
oneFitsAll	If FALSE then boxes have individual size, depending on the size of the label, otherwise all boxes have the same size dependent on the largest label.
margin	Set the figure margin via par(mar=margin). Less than 4 values are repeated.
cex	Initial cex value for the state and the arrow labels.
rasta	For construction purposes.
verbose	If TRUE echo various things.
...	Smart control of arguments for the subroutines text (box label), rect (box), arrows, text (arrow label). Thus the three dots can be used to draw individual boxes with individual labels, arrows and arrow labels. E.g. arrow2.label="any label" changes the label of the second arrow. See examples.

Note

Use the functionality of the unix program 'dot' http://www.graphviz.org/About.php via R package Rgraphviz to obtain more complex graphs.

Author(s)

Thomas A Gerds <tag@biostat.ku.dk>

See Also

HistSmartControl

Examples

```
## A simple survival model

SurvFrame <- data.frame(time=1:10,status=c(0,1,1,0,0,1,0,0,1,0))
SurvHist <- with(SurvFrame,Hist(time,status))
plot(SurvHist)
plot(SurvHist,box2.col=2,box2.label="experienced\nR user")
plot(SurvHist,
     box2.col=2,
     box1.label="newby",
     box2.label="experienced\nR user",
     oneFitsAll=FALSE,
     arrow1.length=.5,
     arrow1.label="",
     arrow1.lwd=4)

## change the cex of all box labels:
plot(SurvHist,
     box2.col=2,
     box1.label="newby",
     box2.label="experienced\nR user",
     oneFitsAll=FALSE,
     arrow1.length=.5,
     arrow1.label="",
     arrow1.lwd=4,
     label.cex=1)

## change the cex of single box labels:
plot(SurvHist,
     box2.col=2,
     box1.label="newby",
     box2.label="experienced\nR user",
     oneFitsAll=FALSE,
     arrow1.length=.5,
     arrow1.label="",
     arrow1.lwd=4,
     label1.cex=1,
     label2.cex=2)
```

```
## The pbc data set from the survival package
library(survival)
data(pbc)
plot(with(pbc,Hist(time,status)),
     stateLabels=c("randomized","transplant","dead"),
     arrowLabelStyle="count")

## two competing risks
comprisk.model <- data.frame(time=1:3,status=1:3)
CRHist <- with(comprisk.model,Hist(time,status,cens.code=2))
plot(CRHist)
plot(CRHist,arrow1.label=paste(expression(eta(s,u))))

plot(CRHist,box2.label="This\nis\nstate 2",arrow1.label=paste(expression(gamma[1](t))))
plot(CRHist,box3.label="Any\nLabel",arrow2.label="any\nlabel")

## change the layout
plot(CRHist,
     box1.label="Alive",
     box2.label="Dead\n cause 1",
     box3.label="Dead\n cause 2",
     arrow1.label=paste(expression(gamma[1](t))),
     arrow2.label=paste(expression(eta[2](t))),
     box1.col=2,
     box2.col=3,
     box3.col=4,
     nrow=2,
     ncol=3,
     box1.row=1,
     box1.column=2,
     box2.row=2,
     box2.column=1,
     box3.row=2,
     box3.column=3)

## more competing risks
comprisk.model2 <- data.frame(time=1:4,status=1:4)
CRHist2 <- with(comprisk.model2,Hist(time,status,cens.code=2))
plot(CRHist2,box1.row=2)

## illness-death models
illness.death.frame <- data.frame(time=1:4,
      from=c("Disease\nfree",
                                      "Disease\nfree",
                                      "Diseased",
                                      "Disease\nfree"),
      to=c("0","Diseased","Dead","Dead"))
IDHist <- with(illness.death.frame,Hist(time,event=list(from,to)))
plot(IDHist)

## illness-death with recovery
```

```
illness.death.frame2 <- data.frame(time=1:5,
from=c("Disease\nfree","Disease\nfree","Diseased","Diseased","Disease\nfree"),
to=c("0","Diseased","Disease\nfree","Dead","Dead"))
IDHist2 <- with(illness.death.frame2,Hist(time,event=list(from,to)))
plot(IDHist2)

## 4 state models
x=data.frame(from=c(1,2,1,3,4),to=c(2,1,3,4,1),time=1:5)
y=with(x,Hist(time=time,event=list(from=from,to=to)))
plot(y)

## moving the label of some arrows

d <- data.frame(time=1:5,from=c(1,1,1,2,2),to=c(2,3,4,3,4))
h <- with(d,Hist(time,event=list(from,to)))
plot(h,box.padding=c(5,2),
tagBoxes=TRUE,
stateLabels=c("Remission\nwithout\nGvHD",
    "Remission\nwith\nGvHD",
    "Relapse",
    "Death\nwithout\nrelapse"),
arrowLabelSymbol='alpha',
arrowlabel3.x=35,
arrowlabel3.y=53,
arrowlabel4.y=54,
arrowlabel4.x=68)

##'
```

`plot.prodlim` *Plotting event probabilities over time*

Description

Function to plot survival probabilities or absolute risks (cumulative incidence function) against time.

Usage

```
## S3 method for class 'prodlim'
plot(
  x,
  type,
  cause,
  select,
  newdata,
  add = FALSE,
  col,
  lty,
  lwd,
```

```
  ylim,
  xlim,
  ylab,
  xlab = "Time",
  num.digits = 2,
  timeconverter,
  legend = TRUE,
  short.labels = TRUE,
  logrank = FALSE,
  marktime = FALSE,
  confint = TRUE,
  automar,
  atrisk = ifelse(add, FALSE, TRUE),
  timeOrigin = 0,
  axes = TRUE,
  background = TRUE,
  percent = TRUE,
  minAtrisk = 0,
  limit = 10,
  ...
)
```

Arguments

x	an object of class 'prodlim' as returned by the prodlim function.
type	Either "surv" or "risk" AKA "cuminc". Controls what part of the object is plotted. Defaults to object$type.
cause	For competing risk models. Character (other classes are converted with as.character). The argument cause determines the event of interest. Currently one cause is allowed at a time, but you can call the function again with add=TRUE to add the lines of the other causes. Also, if cause="stacked" is specified the absolute risks of all causes are stacked.
select	Select which lines to plot. This can be used when there are many strata or many competing risks to select a subset of the lines. However, a more clean way to select covariate strata is to use the argument newdata. Another application is when there are several competing risks and the stacked plot (cause="stacked") should only show a selected subset of the available causes.
newdata	a data frame containing covariate strata for which to show curves. When omitted element X of object x is used.
add	if TRUE curves are added to an existing plot.
col	color for curves. Default is 1:number(curves)
lty	line type for curves. Default is 1.
lwd	line width for all curves. Default is 3.
ylim	limits of the y-axis
xlim	limits of the x-axis
ylab	label for the y-axis

xlab	label for the x-axis
num.digits	Number of digits when rounding off numerical values for legend and at-risk tables.
timeconverter	The following options are supported: "days2years" (conversion factor: 1/365.25) "months2years" (conversion factor: 1/12) "days2months" (conversion factor 1/30.4368499) "years2days" (conversion factor 365.25) "years2months" (conversion factor 12) "months2days" (conversion factor 30.4368499)
legend	if TRUE a legend is plotted by calling the function legend. Optional arguments of the function legend can be given in the form legend.x=val where x is the name of the argument and val the desired value. See also Details.
short.labels	Logical. When FALSE construct labels as cause=1, var1=v1, var2=v2 else as 1, v1, v2.
logrank	If TRUE, the logrank p-value will be extracted from a call to survdiff and added to the legend. This works only for survival models, i.e. Kaplan-Meier with discrete predictors.
marktime	if TRUE the curves are tick-marked at right censoring times by invoking the function markTime. Optional arguments of the function markTime can be given in the form confint.x=val as with legend. See also Details.
confint	Logical. If TRUE pointwise confidence intervals are plotted by invoking the function confInt. Optional arguments of the function confInt can be given in the form confint.x=val as with legend. See also Details.
automar	If TRUE the function trys to find suitable values for the figure margins around the main plotting region.
atrisk	if TRUE display numbers of subjects at risk by invoking the function atRisk. Optional arguments of the function atRisk can be given in the form atrisk.x=val as with legend. See also Details.
timeOrigin	Start of the time axis
axes	If true axes are drawn. See details.
background	If TRUE the background color and grid color can be controlled using smart arguments SmartControl, such as background.bg="yellow" or background.bg=c("gray66","gray88"). The following defaults are passed to background by plot.prodlim: horizontal=seq(0,1,.25), vertical=NULL, bg="gray77", fg="white". See background for all arguments, and the examples below.
percent	If true the y-axis is labeled in percent.
minAtrisk	Integer. Show the curve only until the number at-risk is at least minAtrisk
limit	When newdata is not specified and the number of lines in element X of object x exceeds limits, only the results for covariate constellations of the first, the middle and the last row in X are shown. Otherwise all lines of X are shown.
...	Parameters that are filtered by SmartControl and then passed to the functions plot, legend, axis, atRisk, confInt, markTime, backGround

Details

From version 1.1.3 on the arguments legend.args, atrisk.args, confint.args are obsolete and only available for backward compatibility. Instead arguments for the invoked functions `atRisk`, `legend`, `confInt`, `markTime`, `axis` are simply specified as `atrisk.cex=2`. The specification is not case sensitive, thus `atRisk.cex=2` or `atRISK.cex=2` will have the same effect. The function `axis` is called twice, and arguments of the form `axis1.labels`, `axis1.at` are used for the time axis whereas `axis2.pos`, `axis1.labels`, etc. are used for the y-axis.

These arguments are processed via `...{}` of `plot.prodlim` and inside by using the function `SmartControl`. Documentation of these arguments can be found in the help pages of the corresponding functions.

Value

The (invisible) object.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

`plot`, `legend`, `axis`, `prodlim`,`plot.Hist`,`summary.prodlim`, `neighborhood`, `atRisk`, `confInt`, `markTime`, `backGround`

Examples

```
## simulate right censored data from a two state model
set.seed(100)
dat <- SimSurv(100)
# with(dat,plot(Hist(time,status)))

### marginal Kaplan-Meier estimator
kmfit <- prodlim(Hist(time, status) ~ 1, data = dat)
plot(kmfit)
plot(kmfit,atrisk.show.censored=1L,atrisk.at=seq(0,12,3))
plot(kmfit,timeconverter="years2months")

# change time range
plot(kmfit,xlim=c(0,4))

# change scale of y-axis
plot(kmfit,percent=FALSE)

# mortality instead of survival
plot(kmfit,type="risk")

# change axis label and position of ticks
plot(kmfit,
     xlim=c(0,10),
     axis1.at=seq(0,10,1),
     axis1.labels=0:10,
     xlab="Years",
```

```
     axis2.las=2,
     atrisk.at=seq(0,10,2.5),
     atrisk.title="")

# change background color
plot(kmfit,
     xlim=c(0,10),
     confint.citype="shadow",
     col=1,
     axis1.at=0:10,
     axis1.labels=0:10,
     xlab="Years",
     axis2.las=2,
     atrisk.at=seq(0,10,2.5),
     atrisk.title="",
     background=TRUE,
     background.fg="white",
     background.horizontal=seq(0,1,.25/2),
     background.vertical=seq(0,10,2.5),
     background.bg=c("gray88"))

# change type of confidence limits
plot(kmfit,
     xlim=c(0,10),
     confint.citype="dots",
     col=4,
     background=TRUE,
     background.bg=c("white","gray88"),
     background.fg="gray77",
     background.horizontal=seq(0,1,.25/2),
     background.vertical=seq(0,10,2))


### Kaplan-Meier in discrete strata
kmfitX <- prodlim(Hist(time, status) ~ X1, data = dat)
plot(kmfitX,atrisk.show.censored=1L)
# move legend
plot(kmfitX,legend.x="bottomleft",atRisk.cex=1.3,
     atrisk.title="No. subjects")

## Control the order of strata
## since version 1.5.1 prodlim does  obey the order of
## factor levels
dat$group <- factor(cut(dat$X2,c(-Inf,0,0.5,Inf)),
                    labels=c("High","Intermediate","Low"))
kmfitG <- prodlim(Hist(time, status) ~ group, data = dat)
plot(kmfitG)

## relevel
dat$group2 <- factor(cut(dat$X2,c(-Inf,0,0.5,Inf)),
                     levels=c("(0.5, Inf]","(0,0.5]","(-Inf,0]"),
                     labels=c("Low","Intermediate","High"))
kmfitG2 <- prodlim(Hist(time, status) ~ group2, data = dat)
```

```
plot(kmfitG2)

# add log-rank test to legend
plot(kmfitX,
     atRisk.cex=1.3,
     logrank=TRUE,
     legend.x="topright",
     atrisk.title="at-risk")

# change atrisk labels
plot(kmfitX,
     legend.x="bottomleft",
     atrisk.title="Patients",
     atrisk.cex=0.9,
     atrisk.labels=c("X1=0","X1=1"))

# multiple categorical factors

kmfitXG <- prodlim(Hist(time,status)~X1+group2,data=dat)
plot(kmfitXG,select=1:2)

### Kaplan-Meier in continuous strata
kmfitX2 <- prodlim(Hist(time, status) ~ X2, data = dat)
plot(kmfitX2,xlim=c(0,10))

# specify values of X2 for which to show the curves
plot(kmfitX2,xlim=c(0,10),newdata=data.frame(X2=c(-1.8,0,1.2)))

### Cluster-correlated data
library(survival)
cdat <- cbind(SimSurv(20),patnr=sample(1:5,size=20,replace=TRUE))
kmfitC <- prodlim(Hist(time, status) ~ cluster(patnr), data = cdat)
plot(kmfitC)
plot(kmfitC,atrisk.labels=c("Units","Patients"))

kmfitC2 <- prodlim(Hist(time, status) ~ X1+cluster(patnr), data = cdat)
plot(kmfitC2)
plot(kmfitC2,atrisk.labels=c("Teeth","Patients","Teeth","Patients"),
     atrisk.col=c(1,1,2,2))


### Cluster-correlated data with strata
n = 50
foo = runif(n)
bar = rexp(n)
baz = rexp(n,1/2)
d = stack(data.frame(foo,bar,baz))
d$cl = sample(10, 3*n, replace=TRUE)
fit = prodlim(Surv(values) ~ ind + cluster(cl), data=d)
plot(fit)


## simulate right censored data from a competing risk model
```

```
datCR <- SimCompRisk(100)
with(datCR,plot(Hist(time,event)))

### marginal Aalen-Johansen estimator
ajfit <- prodlim(Hist(time, event) ~ 1, data = datCR)
plot(ajfit) # same as plot(ajfit,cause=1)
plot(ajfit,atrisk.show.censored=1L)

# cause 2
plot(ajfit,cause=2)

# both in one
plot(ajfit,cause=1)
plot(ajfit,cause=2,add=TRUE,col=2)

### stacked plot

plot(ajfit,cause="stacked",select=2)

### stratified Aalen-Johansen estimator
ajfitX1 <- prodlim(Hist(time, event) ~ X1, data = datCR)
plot(ajfitX1)

## add total number at-risk to a stratified curve
ttt = 1:10
plot(ajfitX1,atrisk.at=ttt,col=2:3)
plot(ajfit,add=TRUE,col=1)
atRisk(ajfit,newdata=datCR,col=1,times=ttt,line=3,labels="Total")


## stratified Aalen-Johansen estimator in nearest neighborhoods
## of a continuous variable
ajfitX <- prodlim(Hist(time, event) ~ X1+X2, data = datCR)
plot(ajfitX,newdata=data.frame(X1=c(1,1,0),X2=c(4,10,10)))
plot(ajfitX,newdata=data.frame(X1=c(1,1,0),X2=c(4,10,10)),cause=2)

## stacked plot

plot(ajfitX,
     newdata=data.frame(X1=0,X2=0.1),
     cause="stacked",
     legend.title="X1=0,X2=0.1",
     legend.legend=paste("cause:",getStates(ajfitX$model.response)),
     plot.main="Subject specific stacked plot")
```

---

plotCompetingRiskModel

Plotting a competing-risk-model.

Description

Plotting a competing-risk-model.

Usage

```
plotCompetingRiskModel(stateLabels, horizontal = TRUE, ...)
```

Arguments

stateLabels	Labels for the boxes.
horizontal	The orientation of the plot.
...	Arguments passed to plot.Hist.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

plotIllnessDeathModel, plot.Hist

Examples

```
plotCompetingRiskModel()
plotCompetingRiskModel(labels=c("a","b"))
plotCompetingRiskModel(labels=c("a","b","c"))
```

---

plotIllnessDeathModel *Plotting an illness-death-model.*

Description

Plotting an illness-death-model using plot.Hist.

Usage

```
plotIllnessDeathModel(stateLabels, style = 1, recovery = FALSE, ...)
```

Arguments

stateLabels	Labels for the three boxes.
style	Either 1 or anything else, switches the orientation of the graph. Hard to explain in words, see examples.
recovery	Logical. If TRUE there will be an arrow from the illness state to the initial state.
...	Arguments passed to plot.Hist.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

plotCompetingRiskModel, plot.Hist

Examples

```
plotIllnessDeathModel()
plotIllnessDeathModel(style=2)
plotIllnessDeathModel(style=2,
                      stateLabels=c("a","b\nc","d"),
                      box1.col="yellow",
                      box2.col="green",
                      box3.col="red")
```

---

predict.prodlim *Predicting event probabilities from product limit estimates*

Description

Evaluation of estimated survival or event probabilities at given times and covariate constellations.

Usage

```
## S3 method for class 'prodlim'
predict(
  object,
  times,
  newdata,
  level.chaos = 1,
  type = c("surv", "risk", "cuminc", "list"),
  mode = "list",
  bytime = FALSE,
  cause,
  ...
)
```

Arguments

object	A fitted object of class "prodlim".
times	Vector of times at which to return the estimated probabilities (survival or absolute event risks).
newdata	A data frame with the same variable names as those that appear on the right hand side of the 'prodlim' formula. If there are covariates this argument is required.

level.chaos	Integer specifying the sorting of the output: '0' sort by time and newdata; '1' only by time; '2' no sorting at all
type	Choice between "surv","risk","cuminc","list": "surv": predict survival probabilities only survival models "risk"/"cuminc": predict absolute risk, i.e., cumulative incidence function. "list": find the indices corresponding to times and newdata. See value. Defaults to "surv" for two-state models and to "risk" for competing risk models.
mode	Only for type=="surv" and type=="risk". Can either be "list" or "matrix". For "matrix" the predicted probabilities will be returned in matrix form.
bytime	Logical. If TRUE and mode=="matrix" the matrix with predicted probabilities will have a column for each time and a row for each newdata. Only when object$covariate.type>1 and more than one time is given.
cause	Character (other classes are converted with as.character). The cause for predicting the absolute risk of an event, i.e., the cause-specific cumulative incidence function, in competing risk models. At any time after time zero this is the absolute risk of an event of type cause to occur between time zero and times .
...	Only for compatibility reasons.

Details

Predicted (survival) probabilities are returned that can be plotted, summarized and used for inverse of probability of censoring weighting.

Value

type=="surv" A list or a matrix with survival probabilities for all times and all newdata.

type=="risk" or type=="cuminc" A list or a matrix with cumulative incidences for all times and all newdata.

type=="list" A list with the following components:

times	The argument times carried forward
predictors	The relevant part of the argument newdata.
indices	A list with the following components time: Where to find values corresponding to the requested times strata: Where to find values corresponding to the values of the variables in newdata. Together time and strata show where to find the predicted probabilities.
dimensions	a list with the following components: time : The length of times strata : The number of rows in newdata names.strata : Labels for the covariate values.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

predictSurvIndividual

Examples

```
dat <- SimSurv(400)
fit <- prodlim(Hist(time,status)~1,data=dat)

## predict the survival probs at selected times
predict(fit,times=c(3,5,10))

## NA is returned when the time point is beyond the
## range of definition of the Kaplan-Meier estimator:
predict(fit,times=c(-1,0,10,100,1000,10000))

## when there are strata, newdata is required
## or neighborhoods (i.e. overlapping strata)
mfit <- prodlim(Hist(time,status)~X1+X2,data=dat)
predict(mfit,times=c(-1,0,10,100,1000,10000),newdata=dat[18:21,])

## this can be requested in matrix form
predict(mfit,times=c(-1,0,10,100,1000,10000),newdata=dat[18:21,],mode="matrix")

## and even transposed
predict(mfit,times=c(-1,0,10,100,1000,10000),newdata=dat[18:21,],mode="matrix",bytime=TRUE)
```

---

predictSurvIndividual *Predict individual survival probabilities*

Description

Function to extract the predicted probabilities at the individual event times that have been used for fitting a prodlim object.

Usage

```
predictSurvIndividual(object, lag = 1)
```

Arguments

object	A fitted object of class "prodlim".
lag	Integer. '0' means predictions at the individual times, 1 means just before the individual times, etc.

Value

A vector of survival probabilities.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

predict.prodlim,predictSurv,

Examples

```
SurvFrame <- data.frame(time=1:10,status=rbinom(10,1,.5))
x <- prodlim(formula=Hist(time=time,status!=0)~1,data=SurvFrame)
predictSurvIndividual(x,lag=1)
```

---

print.prodlim *Print objects in the prodlim library*

Description

Pretty printing of objects created with the functionality of the 'prodlim' library.

Usage

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

Arguments

x	Object of class prodlim, Hist and neighborhood.
...	Not used.

Author(s)

Thomas Gerds <tag@biostat.ku.dk>

See Also

summary.prodlim, predict.prodlim

prodlim *product limit method*

Description

Nonparametric estimation in event history analysis. Featuring fast algorithms and user friendly syntax adapted from the survival package. The product limit algorithm is used for right censored data; the self-consistency algorithm for interval censored data.

Usage

```
prodlim(
  formula,
  data = parent.frame(),
  subset,
  na.action = NULL,
  reverse = FALSE,
  conf.int = 0.95,
  bandwidth = NULL,
  caseweights,
  discrete.level = 3,
  x = TRUE,
  maxiter = 1000,
  grid,
  tol = 7,
  method = c("npmle", "one.step", "impute.midpoint", "impute.right"),
  exact = TRUE,
  type
)
```

Arguments

formula	A formula whose left hand side is a Hist object. In some special cases it can also be a Surv response object, see the details section. The right hand side is as usual a linear combination of covariates which may contain at most one continuous factor. Whether or not a covariate is recognized as continuous or discrete depends on its class and on the argument discrete.level. The right hand side may also be used to specify clusters, see the details section.
data	A data.frame in which all the variables of formula can be interpreted.
subset	Passed as argument subset to function subset which applied to data before the formula is processed.
na.action	All lines in data with any missing values in the variables of formula are removed.
reverse	For right censored data, if reverse=TRUE then the censoring distribution is estimated.
conf.int	The level (between 0 and 1) for two-sided pointwise confidence intervals. Defaults to 0.95. Remark: only plain Wald-type confidence limits are available.

bandwidth	Smoothing parameter for nearest neighborhoods based on the values of a continuous covariate. See function neighborhood for details.
caseweights	Weights applied to the contribution of each subject to change the number of events and the number at risk. This can be used for bootstrap and survey analysis. Should be a vector of the same length and the same order as data.
discrete.level	Numeric covariates are treated as factors when their number of unique values exceeds not discrete.level. Otherwise the product limit method is applied, in overlapping neighborhoods according to the bandwidth.
x	logical value: if TRUE, the full covariate matrix with is returned in component model.matrix. The reduced matrix contains unique rows of the full covariate matrix and is always returned in component X.
maxiter	For interval censored data only. Maximal number of iterations to obtain the nonparametric maximum likelihood estimate. Defaults to 1000.
grid	For interval censored data only. When method=one.step grid for one-step product limit estimate. Defaults to sorted list of unique left and right endpoints of the observed intervals.
tol	For interval censored data only. Numeric value whose negative exponential is used as convergence criterion for finding the nonparametric maximum likelihood estimate. Defaults to 7 meaning exp(-7).
method	For interval censored data only. If equal to "npmle" (the default) use the usual Turnbull algorithm, else the product limit version of the self-consistent estimate.
exact	If TRUE the grid of time points used for estimation includes all the L and R endpoints of the observed intervals.
type	In two state models either "surv" for the Kaplan-Meier estimate of the survival function or "risk" for 1-Kaplan-Meier. Default is "surv" when reverse==FALSE and "risk" when reverse==TRUE. In competing risks models it has to be "risk" Aalen-Johansen estimate of the cumulative incidence function.

Details

The response of formula (ie the left hand side of the '~' operator) specifies the model.

In two-state models – the classical survival case – the standard Kaplan-Meier method is applied. For this the response can be specified as a Surv or as a Hist object. The Hist function allows you to change the code for censored observations, e.g. Hist(time,status,cens.code="4").

Besides a slight gain of computing efficiency, there are some extensions that are not included in the current version of the survival package:

(0) The Kaplan-Meier estimator for the censoring times reverse=TRUE is correctly estimated when there are ties between event and censoring times.

(1) A conditional version of the kernel smoothed Kaplan-Meier estimator for at most one continuous predictors using nearest neighborhoods (Beran 1981, Stute 1984, Akritas 1994).

(2) For cluster-correlated data the right hand side of formula may identify a cluster variable. In that case Greenwood's variance formula is replaced by the formula of Ying and Wei (1994).

(3) Competing risk models can be specified via Hist response objects in formula.

The Aalen-Johansen estimator is applied for estimating the absolute risk of the competing causes, i.e., the cumulative incidence functions.

Under construction:

(U0) Interval censored event times specified via Hist are used to find the nonparametric maximum likelihood estimate. Currently this works only for two-state models and the results should match with those from the package 'Icens'.

(U1) Extensions to more complex multi-states models

(U2) The nonparametric maximum likelihood estimate for interval censored observations of competing risks models.

Value

Object of class "prodlim". See print.prodlim, predict.prodlim, predict, summary.prodlim, plot.prodlim.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

References

Andersen, Borgan, Gill, Keiding (1993) Springer 'Statistical Models Based on Counting Processes'

Akritas (1994) The Annals of Statistics 22, 1299-1327 Nearest neighbor estimation of a bivariate distribution under random censoring.

R Beran (1981) http://anson.ucdavis.edu/~beran/paper.html 'Nonparametric regression with randomly censored survival data'

Stute (1984) The Annals of Statistics 12, 917–926 'Asymptotic Normality of Nearest Neighbor Regression Function Estimates'

Ying, Wei (1994) Journal of Multivariate Analysis 50, 17-29 The Kaplan-Meier estimate for dependent failure time observations

See Also

predictSurv, predictSurvIndividual, predictAbsrisk, Hist, neighborhood, Surv, survfit, strata,

Examples

```
##----------------------two-state survival model------------
dat <- SimSurv(30)
with(dat,plot(Hist(time,status)))
fit <- prodlim(Hist(time,status)~1,data=dat)
print(fit)
plot(fit)
summary(fit)
quantile(fit)

## Subset
```

```
fit1a <- prodlim(Hist(time,status)~1,data=dat,subset=dat$X1==1)
fit1b <- prodlim(Hist(time,status)~1,data=dat,subset=dat$X1==1 & dat$X2>0)

## --------------------clustered data---------------------
library(survival)
cdat <- cbind(SimSurv(30),patnr=sample(1:5,size=30,replace=TRUE))
fit <- prodlim(Hist(time,status)~cluster(patnr),data=cdat)
print(fit)
plot(fit)
summary(fit)


##-----------compare Kaplan-Meier to survival package---------

dat <- SimSurv(30)
pfit <- prodlim(Surv(time,status)~1,data=dat)
pfit <- prodlim(Hist(time,status)~1,data=dat) ## same thing
sfit <- survfit(Surv(time,status)~1,data=dat,conf.type="plain")
##  same result for the survival distribution function
all(round(pfit$surv,12)==round(sfit$surv,12))
summary(pfit,digits=3)
summary(sfit,times=quantile(unique(dat$time)))

##-----------estimating the censoring survival function----------------

rdat <- data.frame(time=c(1,2,3,3,3,4,5,5,6,7),status=c(1,0,0,1,0,1,0,1,1,0))
rpfit <- prodlim(Hist(time,status)~1,data=rdat,reverse=TRUE)
rsfit <- survfit(Surv(time,1-status)~1,data=rdat,conf.type="plain")
## When there are ties between times at which events are observed
## times at which subjects are right censored, then the convention
## is that events come first. This is not obeyed by the above call to survfit,
## and hence only prodlim delivers the correct reverse Kaplan-Meier:
cbind("Wrong:"=rsfit$surv,"Correct:"=rpfit$surv)
##----------------  quantiles of the potential followup time-----

G=prodlim(Hist(time,status)~X1,data=dat,reverse=TRUE)
quantile(G)

##-------------------stratified Kaplan-Meier---------------------

stratfit <- prodlim(Surv(time,status)~X1,data=dat)
summary(stratfit)
summary(stratfit,intervals=TRUE)
plot(stratfit)

##----------continuous covariate: Stone-Beran estimate------------

SB=prodlim(Surv(time,status)~X2,data=dat)
summary(SB,newdata=data.frame(X2=c(-0.3,0,.5)))

##-------------both discrete and continuous covariates------------

prodlim(Surv(time,status)~X2+X1,data=dat)
```

```
##----------------------interval censored data----------------------

dat <- data.frame(L=1:10,R=c(2,3,12,8,9,10,7,12,12,12),status=c(1,1,0,1,1,1,1,0,0,0))
with(dat,Hist(time=list(L,R),event=status))

dat$event=1
npmle.fitml <- prodlim(Hist(time=list(L,R),event)~1,data=dat)

##-------------competing risks-------------------

CompRiskFrame <- data.frame(time=1:100,event=rbinom(100,2,.5),X=rbinom(100,1,.5))
crFit <- prodlim(Hist(time,event)~X,data=CompRiskFrame)
summary(crFit)
plot(crFit)
summary(crFit,cause=2)
plot(crFit,cause=2)


# Changing the cens.code:
dat <- data.frame(time=1:10,status=c(1,2,1,2,5,5,1,1,2,2))
fit <- prodlim(Hist(time,status)~1,data=dat)
print(fit$model.response)
fit <- prodlim(Hist(time,status,cens.code="2")~1,data=dat)
print(fit$model.response)
plot(fit)
plot(fit,cause="5")


##------------delayed entry----------------------

## left-truncated event times with competing risk endpoint

dat <- data.frame(entry=c(7,3,11,12,11,2,1,7,15,17,3),time=10:20,status=c(1,0,2,2,0,0,1,2,0,2,0))
fitd <- prodlim(Hist(time=time,event=status,entry=entry)~1,data=dat)
summary(fitd)
plot(fitd)
```

`quantile.prodlim` *Quantiles for Kaplan-Meier and Aalen-Johansen estimates.*

Description

Quantiles for Kaplan-Meier and Aalen-Johansen estimates.

Usage

```
## S3 method for class 'prodlim'
quantile(x, q, cause = 1, ...)
```

Arguments

x	Object of class "prodlim".
q	Quantiles. Vector of values between 0 and 1.
cause	For competing risks the cause of interest.
...	not used

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

Examples

```
library(lava)
set.seed(1)
d=SimSurv(30)

# Quantiles of the potential followup time
g=prodlim(Hist(time,status)~1,data=d,reverse=TRUE)
quantile(g)

# survival time
f=prodlim(Hist(time,status)~1,data=d)
f1=prodlim(Hist(time,status)~X1,data=d)
# default: median and IQR
quantile(f)
quantile(f1)
# median alone
quantile(f,.5)
quantile(f1,.5)

# competing risks
set.seed(3)
dd = SimCompRisk(30)
ff=prodlim(Hist(time,event)~1,data=dd)
ff1=prodlim(Hist(time,event)~X1,data=dd)
## default: median and IQR
quantile(ff)
quantile(ff1)

print(quantile(ff1),na.val="NA")
print(quantile(ff1),na.val="Not reached")
```

---

redist *Calculation of Efron's re-distribution to the right algorithm to obtain the Kaplan-Meier estimate.*

Description

Calculation of Efron's re-distribution to the right algorithm to obtain the Kaplan-Meier estimate.

Usage

```
redist(time, status)
```

Arguments

time	A numeric vector of event times.
status	The event status vector takes the value 1 for observed events and the value 0 for right censored times.

Value

Calculations needed to

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

prodlim

Examples

```
redist(time=c(.35,0.4,.51,.51,.7,.73),status=c(0,1,1,0,0,1))
```

---

row.match *Identifying rows in a matrix or data.frame*

Description

Function for finding matching rows between two matrices or data.frames. First the matrices or data.frames are vectorized by row wise pasting together the elements. Then it uses the function match. Thus the function returns a vector with the row numbers of (first) matches of its first argument in its second.

Usage

```
row.match(x, table, nomatch = NA)
```

Arguments

x	Vector or matrix whose rows are to be matched
table	Matrix or data.frame that contain the rows to be matched against.
nomatch	the value to be returned in the case when no match is found. Note that it is coerced to 'integer'.

Value

A vector of the same length as 'x'.

Author(s)

Thomas A. Gerds

See Also

`match`

Examples

```
tab <- data.frame(num=1:26,abc=letters)
x <- c(3,"c")
row.match(x,tab)
x <- data.frame(n=c(3,8),z=c("c","h"))
row.match(x,tab)
```

`SimCompRisk` *Simulate competing risks data*

Description

Simulate right censored competing risks data with two covariates X1 and X2. Both covariates have effect exp(1) on the hazards of event 1 and zero effect on the hazard of event 2.

Usage

```
SimCompRisk(N, ...)
```

Arguments

`N`	sample size
`...`	do nothing.

Details

This function calls `crModel`, then adds covariates and finally calls `sim.lvm`.

Value

data.frame with simulated data

Author(s)

Thomas Alexander Gerds

Examples

```
SimCompRisk(10)
```

`SimSurv` *Simulate survival data*

Description

Simulate right censored survival data with two covariates X1 and X2, both have effect exp(1) on the hazard of the unobserved event time.

Usage

```
SimSurv(N, ...)
```

Arguments

`N`	sample size
`...`	do nothing

Details

This function calls `survModel`, then adds covariates and finally calls `sim.lvm`.

Value

data.frame with simulated data

Author(s)

Thomas Alexander Gerds

References

Bender, Augustin & Blettner. Generating survival times to simulate Cox proportional hazards models. Statistics in Medicine, 24: 1713-1723, 2005.

Examples

```
SimSurv(10)
```

sindex *Index for evaluation of step functions.*

Description

Returns an index of positions. Intended for evaluating a step function at selected times. The function counts how many elements of a vector, e.g. the jump times of the step function, are smaller or equal to the elements in a second vector, e.g. the times where the step function should be evaluated.

Usage

```
sindex(jump.times, eval.times, comp = "smaller", strict = FALSE)
```

Arguments

jump.times	Numeric vector: e.g. the unique jump times of a step function.
eval.times	Numeric vector: e.g. the times where the step function should be evaluated
comp	If "greater" count the number of jump times that are greater (greater or equal when strict==FALSE) than the eval times
strict	If TRUE make the comparison of jump times and eval times strict

Details

If all jump.times are greater than a particular eval.time the sindex returns 0. This must be considered when sindex is used for subsetting, see the Examples below.

Value

Index of the same length as eval.times containing the numbers of the jump.times that are smaller than or equal to eval.times.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

Examples

```
test <- list(time = c(1, 1,5,5,2,7,9),
  status = c(1,0,1,0,1,1,0))
fit <- prodlim(Hist(time,status)~1,data=test)
jtimes <- fit$time
etimes <- c(0,.5,2,8,10)
fit$surv
c(1,fit$surv)[1+sindex(jtimes,etimes)]
```

`SmartControl` *Function to facilitate the control of arguments passed to subroutines.*

Description

Many R functions need to pass several arguments to several different subroutines. Such arguments can are given as part of the three magic dots "...". The function SmartControl reads the dots together with a list of default values and returns for each subroutine a list of arguments.

Usage

```
SmartControl(
  call,
  keys,
  ignore,
  defaults,
  forced,
  split,
  ignore.case = TRUE,
  replaceDefaults,
  verbose = TRUE
)
```

Arguments

`call`	A list of named arguments, as for example can be obtained via `list(...)`.
`keys`	A vector of names of subroutines.
`ignore`	A list of names which are removed from the argument `call` before processing.
`defaults`	A named list of default argument lists for the subroutines.
`forced`	A named list of forced arguments for the subroutines.
`split`	Regular expression used for splitting keys from arguments. Default is `"\."`.
`ignore.case`	If `TRUE` then all matching and splitting is not case sensitive.
`replaceDefaults`	If `TRUE` default arguments are replaced by given arguments. Can also be a named list with entries for each subroutine.
`verbose`	If `TRUE` warning messages are given for arguments in `call` that are not ignored via argument `ignore` and that do not match any `key`.

Author(s)

Thomas Alexander Gerds <tag@biostat.ku.dk>

See Also

`plot.prodlim`

Examples

```
myPlot = function(...){
 ## set defaults
 plot.DefaultArgs=list(x=0,y=0,type="n")
 lines.DefaultArgs=list(x=1:10,lwd=3)
 ## apply smartcontrol
 x=SmartControl(call=list(...),
           defaults=list("plot"=plot.DefaultArgs, "lines"=lines.DefaultArgs),
        ignore.case=TRUE,keys=c("plot","axis2","lines"),
            forced=list("plot"=list(axes=FALSE),"axis2"=list(side=2)))
 ## call subroutines
 do.call("plot",x$plot)
 do.call("lines",x$lines)
 do.call("axis",x$axis2)
}
myPlot(plot.ylim=c(0,5),plot.xlim=c(0,20),lines.lty=3,axis2.At=c(0,3,4))
```

`stopTime` *Stop the time of an event history object*

Description

All event times are stopped at a given time point and corresponding events are censored

Usage

```
stopTime(object, stop.time)
```

Arguments

`object`	Event history object as obtained with `Hist`
`stop.time`	Time point at which to stop the event history object

Value

Stopped event history object where all times are censored at `stop.time`. All observations with times greater than `stop.time` are set to `stop.time` and the event status is set to `attr(object,"cens.code")`. A new column `"stop.time"` is equal to `1` for stopped observations and equal to `0` for the other observations.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

Hist

Examples

```
set.seed(29)
d <- SimSurv(10)
h <- with(d,Hist(time,status))
h
stopTime(h,8)
stopTime(h,5)

## works also with Surv objects
library(survival)
s <- with(d,Surv(time,status))
stopTime(s,5)

## competing risks
set.seed(29)
dr <- SimCompRisk(10)
hr <- with(dr,Hist(time,event))
hr
stopTime(hr,8)
stopTime(hr,5)
```

---

str.Hist *Check the structure of an event history object*

Description

The object is evaluated as a matrix

Usage

```
## S3 method for class 'Hist'
str(x)
```

Arguments

x	object obtained with Hist

---

strip.terms *Strip special functions from terms*

Description

Reformulate a terms object such that some specials are stripped off

Usage

```
strip.terms(
  terms,
  specials,
  alias.names = NULL,
  unspecials = NULL,
  arguments,
  keep.response = TRUE
)
```

Arguments

terms	Terms object
specials	Character vector of specials which should be stripped off
alias.names	Optional. A named list with alias names for the specials.
unspecials	Optional. A special name for treating all the unspecial terms.
arguments	A named list of arguments, one for each element of specials. Elements are passed to parseSpecialNames.
keep.response	Keep the response in the resulting object?

Details

This function is used to remove special specials, i.e., those which cannot or should not be evaluated. IMPORTANT: the unstripped terms need to know about all specials including the aliases. See examples.

Value

Reformulated terms object with an additional attribute which contains the stripped.specials.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

parseSpecialNames reformulate drop.terms

Examples

```
## parse a survival formula and identify terms which
## should be treated as proportional or timevarying:
f <- Surv(time,status)~age+prop(factor(edema))+timevar(sex,test=0)+prop(bili,power=1)
tt <- terms(f,specials=c("prop","timevar"))
attr(tt,"specials")
st <- strip.terms(tt,specials=c("prop","timevar"),arguments=NULL)
formula(st)
attr(st,"specials")
```

```
attr(st,"stripped.specials")

## provide a default value for argument power of proportional treatment
## and argument test of timevarying treatment:
st2 <- strip.terms(tt,
                   specials=c("prop","timevar"),
                   arguments=list("prop"=list("power"=0),"timevar"=list("test"=0)))
formula(st2)
attr(st2,"stripped.specials")
attr(st2,"stripped.arguments")

## treat all unspecial terms as proportional
st3 <- strip.terms(tt,
                   unspecials="prop",
                   specials=c("prop","timevar"),
                   arguments=list("prop"=list("power"=0),"timevar"=list("test"=0)))
formula(st3)
attr(st3,"stripped.specials")
attr(st3,"stripped.arguments")

## allow alias names: strata for timevar and tp, const for prop.
## IMPORTANT: the unstripped terms need to know about
## all specials including the aliases
f <- Surv(time,status)~age+const(factor(edema))+strata(sex,test=0)+prop(bili,power=1)+tp(albumin)
tt2 <- terms(f,specials=c("prop","timevar","strata","tp","const"))
st4 <- strip.terms(tt2,
                   specials=c("prop","timevar"),
                   unspecials="prop",
                   alias.names=list("timevar"="strata","prop"=c("const","tp")),
                   arguments=list("prop"=list("power"=0),"timevar"=list("test"=0)))
formula(st4)
attr(st4,"stripped.specials")
attr(st4,"stripped.arguments")

## test if alias works also without unspecial argument
st5 <- strip.terms(tt2,
                   specials=c("prop","timevar"),
                   alias.names=list("timevar"="strata","prop"=c("const","tp")),
                   arguments=list("prop"=list("power"=0),"timevar"=list("test"=0)))
formula(st5)
attr(st5,"stripped.specials")
attr(st5,"stripped.arguments")

library(survival)
data(pbc)
model.design(st4,data=pbc[1:3,],specialsDesign=TRUE)
model.design(st5,data=pbc[1:3,],specialsDesign=TRUE)
```

---

subset.Hist *Subset an event history object*

Description

This method makes sure that the attributes are preserved

Usage

```
## S3 method for class 'Hist'
subset(x, subset, select, drop, ...)
```

Arguments

x	object obtained with Hist
subset	passed on to next method
select	passed on to next method
drop	passed on to next method
...	passed on to the next method

---

summary.Hist *Summary of event histories*

Description

Describe events and censoring patterns of an event history.

Usage

```
## S3 method for class 'Hist'
summary(object, verbose = TRUE, ...)
```

Arguments

object	An object with class 'Hist' derived with Hist
verbose	Logical. If FALSE any printing is supressed.
...	Not used

Value

NULL for survival and competing risk models. For other multi-state models, it is a list with the following entries:

states	the states of the model
transitions	the transitions between the states
trans.frame	a data.frame with the from and to states of the transitions

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

Hist, plot.Hist

Examples

```
icensFrame <- data.frame(L=c(1,1,3,4,6),R=c(2,NA,3,6,9),event=c(1,1,1,2,2))
with(icensFrame,summary(Hist(time=list(L,R))))
```

---

summary.prodlim *Summary method for prodlim objects.*

Description

Summarizing the result of the product limit method in life-table format. Calculates the number of subjects at risk and counts events and censored observations at specified times or in specified time intervals.

Usage

```
## S3 method for class 'prodlim'
summary(
  object,
  times,
  newdata,
  max.tables = 20,
  surv = TRUE,
  cause,
  intervals = FALSE,
  percent = FALSE,
  format = "df",
  ...
)
```

Arguments

object	An object with class 'prodlim' derived with prodlim
times	Vector of times at which to return the estimated probabilities.
newdata	A data frame with the same variable names as those that appear on the right hand side of the 'prodlim' formula. Defaults to object$X.
max.tables	Integer. If newdata is not given the value of max.tables decides about the maximal number of tables to be shown. Defaults to 20.
surv	Logical. If FALSE report event probabilities instead of survival probabilities. Only available for object$model=="survival".

cause	For competing risk models. The event of interest for which predictions of the absolute risks are obtained by evaluating the cause-specific cumulative incidence functions at times.
intervals	Logical. If TRUE count events and censored in intervals between the values of times.
percent	Logical. If TRUE all estimated values are multiplied by 100 and thus interpretable on a percent scale.
format	Control format of output. Since May 2021, the result is a data.table and data.frame with attributes. When there are multiple covariate strata or competing risks, these are indicated by columns. Set format to "list" to get the old behaviour.
...	Further arguments that are passed to the print function.

Details

For cluster-correlated data the number of clusters at-risk are are also given. Confidence intervals are displayed when they are part of the fitted object.

Value

A data.frame with the relevant information.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

See Also

prodlim, summary.Hist

Examples

```
library(lava)
set.seed(17)
m <- survModel()
distribution(m,~age) <- uniform.lvm(30,80)
distribution(m,~sex) <- binomial.lvm()
m <- categorical(m,~z,K=3)
regression(m,eventtime~age) <- 0.01
regression(m,eventtime~sex) <- -0.4
d <- sim(m,50)
d$sex <- factor(d$sex,levels=c(0,1),labels=c("female","male"))
d$Z <- factor(d$z,levels=c(1,0,2),labels=c("B","A","C"))

# Univariate Kaplan-Meier
# ------------------------------------------------------------------------------------------
fit0 <- prodlim(Hist(time,event)~1,data=d)
summary(fit0)

## show survival probabilities as percentage and
## count number of events within intervals of a
```

```
## given time-grid:
summary(fit0,times=c(1,5,10,12),percent=TRUE,intervals=TRUE)

## the result of summary has a print function
## which passes ... to print and print.listof
sx <- summary(fit0,times=c(1,5,10,12),percent=TRUE,intervals=TRUE)
print(sx,digits=3)

## show absolute risks, i.e., cumulative incidences (1-survival)
summary(fit0,times=c(1,5,10,12),surv=FALSE,percent=TRUE,intervals=TRUE)

# Stratified Kaplan-Meier
# ------------------------------------------------------------------------------------------

fit1 <- prodlim(Hist(time,event)~sex,data=d)
print(summary(fit1,times=c(1,5,10),intervals=TRUE,percent=TRUE),digits=3)
# old behaviour
print(summary(fit1,times=c(1,5,10),intervals=TRUE,percent=TRUE,format="list"),digits=3)

summary(fit1,times=c(1,5,10),intervals=TRUE,percent=TRUE)

fit2 <- prodlim(Hist(time,event)~Z,data=d)
print(summary(fit2,times=c(1,5,10),intervals=TRUE,percent=TRUE),digits=3)

## Continuous strata (Beran estimator)
# ------------------------------------------------------------------------------------------
fit3 <- prodlim(Hist(time,event)~age,data=d)
print(summary(fit3,
              times=c(1,5,10),
              newdata=data.frame(age=c(20,50,70)),
              intervals=TRUE,
              percent=TRUE),digits=3)

## stratified Beran estimator
# ------------------------------------------------------------------------------------------
fit4 <- prodlim(Hist(time,event)~age+sex,data=d)
print(summary(fit4,
              times=c(1,5,10),
              newdata=data.frame(age=c(20,50,70),sex=c("female","male","male")),
              intervals=TRUE,
              percent=TRUE),digits=3)

print(summary(fit4,
              times=c(1,5,10),
              newdata=data.frame(age=c(20,50,70),sex=c("female","male","male")),
              intervals=TRUE,
              percent=TRUE),digits=3)

## assess results from summary
x <- summary(fit4,times=10,newdata=expand.grid(age=c(60,40,50),sex=c("male","female")))
cbind(names(x$table),do.call("rbind",lapply(x$table,round,2)))

x <- summary(fit4,times=10,newdata=expand.grid(age=c(60,40,50),sex=c("male","female")))
```

```
## Competing risks: Aalen-Johansen
# ------------------------------------------------------------------------------------------
d <- SimCompRisk(30)
crfit <- prodlim(Hist(time,event)~X1,data=d)
summary(crfit,times=c(1,2,5))
summary(crfit,times=c(1,2,5),cause=1,intervals=TRUE)
summary(crfit,times=c(1,2,5),cause=1)
summary(crfit,times=c(1,2,5),cause=1:2)


# extract the actual tables from the summary
sumfit <- summary(crfit,times=c(1,2,5),print=FALSE)
sumfit$table[[1]] # cause 1
sumfit$table[[2]] # cause 2


# '
```

`survModel` *Survival model for simulation*

Description

Create a survival model to simulate a right censored event time data without covariates

Usage

```
survModel()
```

Details

This function requires the `lava` package.

Value

A structural equation model initialized with three variables: the latent event time, the latent right censored time, and the observed right censored event time.

Author(s)

Thomas A. Gerds <tag@biostat.ku.dk>

`tail.Hist` *Check the tail of an event history object*

Description

The object is evaluated as a matrix

Usage

```
## S3 method for class 'Hist'
tail(x)
```

Arguments

`x`	object obtained with `Hist`

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