Package ‘Greg’

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Title Regression Helper Functions
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Description Methods for manipulating regression models and for describing these in a style adapted for medical journals. Contains functions for generating an HTML table with crude and adjusted estimates, plotting hazard ratio, plotting model estimates and confidence intervals using forest plots, extending this to comparing multiple models in a single forest plots. In addition to the descriptive methods, there are add-ons for the robust covariance matrix provided by the 'sandwich' package, a function for adding non-linearities to a model, and a wrapper around the 'Epi' package's Lexis() functions for time-splitting a dataset when modeling non-proportional hazards in Cox regressions.
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Description

This R-package provides functions that primarily aimed at helping you work with regression models. While much of the data presented by the standard regression output is useful and important - there is often a need for further simplification prior to publication. The methods implemented in this package are inspired by some of the top journals such as NEJM, BMJ, and other medical journals as this is my research field.

Output functions

The package has function that automatically prints the crude unadjusted estimates of a function next to the adjusted estimates, a common practice for medical publications.

The forestplot wrappers allows for easily displaying regression estimates, often convenient for models with a large number of variables. There is also functionality that can help you comparing different models, e.g. subsets of patients or compare different regression types.

Time-splitter

When working with Cox regressions the proportional hazards can sometimes be violated. As the \texttt{tt()} approach doesn’t lend itself that well to big datasets I often rely on time-splitting the dataset and then using the start time as an interaction term. See the function \texttt{timeSplitter()} and the associated vignette("timeSplitter").

Other regression functions

In addition to these function the package has some extensions to linear regression where it extends the functionality by allowing for robust covariance matrices. by integrating the \texttt{sandwich}-package for \texttt{rms::ols()}. 

R topics documented: 

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- addNonlinearity
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Important notice

This package has an extensive test-set for ensuring that everything behaves as expected. Despite this I strongly urge you to check that the values make sense. I commonly use the regression methods available in the 'rms'-package and in the 'stats'-package. In addition I use the `coxph()` in many of my analyses and should also be safe. Please send me a notice if you are using the package with some other regression models, especially if you have some tests verifying the functionality.

Author(s)

Max Gordon

---

addNonlinearity  Add a nonlinear function to the model

Description

This function takes a model and adds a non-linear function if the likelihood-ratio supports this (via the `anova(...,test="chisq")` test for `stats` while for `rms` you need to use the `rcs()` spline that is automatically evaluated for non-linearity).

Usage

```r
addNonlinearity(
  model, 
  variable, 
  spline_fn, 
  flex_param = 2:7, 
  min_fn = AIC, 
  sig_level = 0.05, 
  verbal = FALSE, 
  workers, 
  ... 
)
```

```r
## S3 method for class 'negbin'
addNonlinearity(model, ...)
```

Arguments

- **model**: The model that is to be evaluated and adapted for non-linearity.
- **variable**: The name of the parameter that is to be tested for non-linearity. Note that the variable should be included plain (i.e. as a linear variable) form in the model.
- **spline_fn**: Either a string or a function that is to be used for testing alternative non-linearity models.
- **flex_param**: A vector with values that are to be tested as the default second parameter for the non-linearity function that you want to evaluate. This defaults to 2:7, for the `ns()` it tests the degrees of freedom ranging between 2 and 7.
min_fn
This is the function that we want to minimize if the variable supports the non-linearity assumption. E.g. BIC() or AIC, note that the BIC() will in the majority of cases support a lower complexity than the AIC().

sig_level
The significance level for which the non-linearity is deemed as significant, defaults to 0.05.

verbal
Set this to TRUE if you want print statements with the anova test and the chosen knots.

workers
The function tries to run everything in parallel. Under some circumstances you may want to restrict the number of parallel threads to less than the default detectCores() -1, e.g. you may run out of memory then you can provide this parameter. If you do not want to use parallel then simply set workers to FALSE. The cluster created using makeCluster() function.

... Passed onto internal prNlChooseDf() function.

Examples

library(Greg)
library(magrittr)
data("melanoma", package = "boot", envir = environment())

library(dplyr)
library(magrittr)
melanoma %<>%
  mutate(status = factor(status,
    levels = 1:3,
    labels = c("Died from melanoma",
      "Alive",
      "Died from other causes")),
  ulcer = factor(ulcer,
    levels = 0:1,
    labels = c("Absent", "Present")),
  time = time/365.25, # All variables should be in the same time unit
  sex = factor(sex,
    levels = 0:1,
    labels = c("Female", "Male")))

library(survival)
model <- coxph(Surv(time, status == "Died from melanoma") ~ sex + age,
  data = melanoma)

nl_model <- addNonlinearity(model, "age",
  spline_fn = "pspline",
  verbal = TRUE,
  workers = FALSE)

# Note that there is no support for nonlinearity in this case
caDescribeOpts

A function for gathering all the description options

Description

Since there are so many different description options for the `printCrudeAndAdjustedModel()` function they have been gathered into a list. This function is simply a helper in order to generate a valid list.

Usage

```r
caDescribeOpts(
  show_tot_perc = FALSE,
  numb_first = TRUE,
  continuous_fn = describeMean,
  prop_fn = describeFactors,
  factor_fn = describeFactors,
  digits = 1,
  colnames = c("Total", "Event")
)
```

Arguments

- `show_tot_perc` Show percentages for the total column
- `numb_first` Whether to show the number before the percentages
- `continuous_fn` Stat function used for the descriptive statistics, defaults to `describeMean()`
- `prop_fn` Stat function used for the descriptive statistics, defaults to `describeFactors()` since there has to be a reference in the current setup.
- `factor_fn` Stat function used for the descriptive statistics, defaults to `describeFactors()`
- `digits` Number of digits to use in the descriptive columns. Defaults to the general digits if not specified.
- `colnames` The names of the two descriptive columns. By default Total and Event.

Value

- `list` Returns a list with all the options
A confint function for the ols

Description

This function checks that there is a df.residual before running the qt(). If not found it then defaults to the qnorm() function. Otherwise it is a copy of the confint() function.

Usage

## S3 method for class 'ols'
confint(object, parm, level = 0.95, ...)

Arguments

- **object**: a fitted ols-model object.
- **parm**: a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
- **level**: the confidence level required.
- **...**: additional argument(s) for methods.

Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as (1-level)/2 and 1 - (1-level)/2 in

Examples

# Generate some data
n <- 500
x1 <- runif(n)*2
x2 <- runif(n)
y <- x1^3 + x2 + rnorm(n)

library(rms)
library(sandwich)
dd <- datadist(x1, x2, y)
org.op <- options(datadist = "dd")

# Main function
f <- ols(y ~ rcs(x1, 3) + x2)

# Check the bread
bread(f)
# Check the HC-matrix
vcovHC(f, type="HC4m")
# Adjust the model so that it uses the HC4m variance
f_rob <- robcov_alt(f, type="HC4m")
# Get the new HC4m-matrix
# - this function just returns the f_rob$var matrix
vcov(f_rob)
# Now check the confidence interval for the function
confint(f_rob)

options(org.op)

---

**confint_robust** *The confint function adapted for vcovHC*

### Description

The `confint.lm` uses the t-distribution as the default confidence interval estimator. When there is reason to believe that the normal distribution is violated an alternative approach using the `vcovHC()` may be more suitable.

### Usage

```r
confint_robust(
  object,  # The regression model object, either an ols or lm object
  parm,    # a specification of which parameters are to be given confidence intervals, either
            # a vector of numbers or a vector of names. If missing, all parameters are considered.
  level = 0.95,  # the confidence level required.
  HC_type = "HC3",  # See options for vcovHC()
  t_distribution = FALSE,  # A boolean for if the t-distribution should be used or not. Defaults to FALSE. According to Cribari-Nieto and Lima’s study from 2009 this should not be the case.
  ...  # Additional parameters that are passed on to vcovHC()
)
```

### Arguments

- **object**: The regression model object, either an ols or lm object.
- **parm**: A specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
- **level**: The confidence level required.
- **HC_type**: See options for `vcovHC()`.
- **t_distribution**: A boolean for if the t-distribution should be used or not. Defaults to FALSE. According to Cribari-Nieto and Lima’s study from 2009 this should not be the case.

### Value

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as $(1\text{-level})/2$ and $1 - (1\text{-level})/2$ in
References


Examples

```r
n <- 50
x <- runif(n)
y <- x + rnorm(n)

fit <- lm(y~x)
library("sandwich")
confint_robust(fit, HC_type = "HC4m")
```

forestplotCombineRegrObj

*Compared different scores in different regression objects.*

Description

Creates a composite from different regression objects into one forestplot where you can choose the variables of interest to get an overview and easier comparison.

Usage

```r
forestplotCombineRegrObj(
  regr.obj,
  variablesOfInterest.regexp,
  reference.names,
  rowname.fn,
  estimate.txt,
  exp = xlog,
  add_first_as_ref = FALSE,
  ref_txt = "ref.",
  ref_labels = c(),
  digits = 1,
  is.summary,
  xlab,
  zero,
  xlog,
  ...
)
```

Arguments

- **regr.obj** A list with all the fits that have variables that are to be identified through the regular expression
variablesOfInterest.regexp

A regular expression identifying the variables that are of interest of comparing. For instance it can be ":score|index|measure:" that finds scores in different models that should be compared.

reference.names

Additional reference names to be added to each model

digits

Number of digits to use for the estimate output

is.summary

A vector indicating by TRUE/FALSE if the value is a summary value which means that it will have a different font-style

xlab

x-axis label

zero

Indicates what is zero effect. For survival/logistic fits the zero is 1 while in most other cases it’s 0.

xlog

If TRUE, x-axis tick marks are to follow a logarithmic scale, e.g. for logistic regression (OR), survival estimates (HR), poisson regression etc. Note: This is an intentional break with the original forestplot function as I’ve found that exponentiated ticks/clips/zero effect are more difficult to for non-statisticians and there are sometimes issues with rounding the tick marks properly.

... Passed to forestplot()

See Also

Other forestplot wrappers: forestplotRegrObj

Examples

org.par <- par("ask" = TRUE)

# simulated data to test
set.seed(10)
ftime <- rexp(200)
fstatus <- sample(0:1,200,replace=TRUE)
cov <- data.frame(
  x1 = runif(200),
  x2 = runif(200),
...
```
x3 = runif(200))

library(rms)
ddist <- datadist(cov)
options(datadist = "ddist")

fit1 <- cph(Surv(ftime, fstatus) ~ x1 + x2, data=cov)
fit2 <- cph(Surv(ftime, fstatus) ~ x1 + x3, data=cov)

forestplotCombineRegrObj (  
  regr.obj = list(fit1, fit2),  
  variablesOfInterest.regexp = "(x2|x3)",  
  reference.names = c("First model", "Second model"),  
  new_page = TRUE)

modifyNameFunction <- function(x){
  if (x == "x1")
    return ("Covariate A")
  if (x == "x2")
    return (expression(paste("My \(\beta_2\)")))
  return (x)
}

forestplotCombineRegrObj (  
  regr.obj = list(fit1, fit2),  
  variablesOfInterest.regexp = "(x2|x3)",  
  reference.names = c("First model", "Second model"),  
  rowname.fn = modifyNameFunction,  
  new_page = TRUE)

par(org.par)
```

---

**forestplotRegrObj**

*Forest plot for multiple models*

---

**Description**

Plot different model fits with similar variables in order to compare the model’s estimates and confidence intervals. Each model is represented by a separate line on top of each other and are therefore ideal for comparing different models. This extra appealing when you have lots of variables included in the models.

**Usage**

```
forestplotRegrObj(  
  regr.obj,  
  skip.variables,  
  add.empty_row,
```
```r
order.regexps,
order.addrows,
box.default.size,
rowname.fn,
xlab,
xlog,
exp,
estimate.txt = xlab,
zero,
get_box_size = fpBoxSize,
...)

fpBoxSize(p_values, variable_count, box.default.size, significant = 0.05)
```

### Arguments

- **regr.obj**: A regression model object. It should be of coxph, crr or glm class. Warning: The glm is not fully tested.
- **skip.variables**: Which variables to use. The variables should be the names of the fit output and not the true output names if you’re using the rowname_translate_function.
- **add.empty_row**: Add empty rows. This can either be a vector or a list. When you have a vector the number indicates the row number where the empty row should be added, the format is: c(3, 5). If you give a list you have the option of specifying the name of the row, the format is: list(list(3,"my rowname"),list(5,"my other rowname")). The rows will be added at the 3rd row and 5th row from the original position. Ie you don’t have take into account that the 5:th row will be at the 6:th position after adding the 3rd row.
- **order.regexps**: A regexp vector that searches for matches along the original rownames and reorders according to those.
- **order.addrows**: If there are ordered groups then often you want empty rows that separate the different groups. Set this to true if you want to add these empty rows between groups.
- **box.default.size**: The default box size.
- **rowname.fn**: A function that takes a rowname and sees if it needs beautifying. The function has only one parameter the coefficients name and should return a string or expression.
- **xlab**: x-axis label.
- **xlog**: If TRUE, x-axis tick marks are to follow a logarithmic scale, e.g. for logistic regression (OR), survival estimates (HR), poisson regression etc. Note: This is an intentional break with the original forestplot function as I’ve found that exponentiated ticks/clips/zero effect are more difficult to for non-statisticians and there are sometimes issues with rounding the tick marks properly.
- **exp**: Report in exponential form. Default true since the function was built for use with survival models.
estimate.txt  The text of the estimate, usually HR for hazard ratio, OR for odds ratio
zero  Indicates what is zero effect. For survival/logistic fits the zero is 1 while in most other cases it’s 0.
get_box_size  A function for extracting the box sizes
p_values  The p-values that will work as the foundation for the box size
variable_count  The number of variables
significant  Level of significance .05

See Also
Other forestplot wrappers: forestplotCombineRegrObj

Examples

```r
org.par <- par("ask" = TRUE)

# simulated data to test
set.seed(10)
ftime <- rexp(200)
fstatus <- sample(0:2, 200, replace=TRUE)
cov <- data.frame(
x1 = runif(200),
x2 = runif(200),
x3 = runif(200))

library(rms)
dd <- datadist(cov)
options(datadist="dd")

fit1 <- cph(Surv(ftime, fstatus == 1) ~ x1 + x2 + x3, data=cov)
fit2 <- cph(Surv(ftime, fstatus == 2) ~ x1 + x2 + x3, data=cov)

forestplotRegrObj (regr.obj = fit1, new_page=TRUE)

library(forestplot)
forestplotRegrObj (regr.obj = list(fit1, fit2),
    legend = c("Status = 1", "Status = 2"),
    legend_args = fpLegend(title="Type of regression"),
    new_page=TRUE)

modifyNameFunction <- function(x){
  if (x == "x1")
    return ("Covariate A")
  if (x == "x2")
    return (expression(paste("My \( \beta \)", beta[2])))
  return (x)
}
```

isFitCoxPH

forestplotRegrObj (regr_obj = list(fit1, fit2),
    col=fpColors(box=c("darkblue", "darkred")),
    variablesOfInterest.regexp = "(x2|x3)",
    legend = c("First model", "Second model"),
    legend_args = fpLegend(title = "Models"),
    rowname.fn = modifyNameFunction, new_page=TRUE)

par(org.par)

---

isFitCoxPH Functions for checking regression type

Description
The isFitCoxPH A simple check if object inherits either "coxph" or "crr" class indicating that it is a survival function.

Usage
isFitCoxPH(fit)
isFitLogit(fit)

Arguments
fit Regression object

Value
boolean Returns TRUE if the object is of that type otherwise it returns FALSE.

Examples
# simulated data to use
set.seed(10)
ds <- data.frame(
    ftime = rexp(200),
    fstatus = sample(0:1,200,replace=TRUE),
    x1 = runif(200),
    x2 = runif(200),
    x3 = runif(200))

library(survival)
library(rms)

dd <- datadist(ds)
options(datadist="dd")
s <- Surv(ds$ftime, ds$fstatus == 1)
isFitCoxPH

fit <- cph(s ~ x1 + x2 + x3, data=ds)

if (isFitCoxPH(fit))
  print("Correct, the cph is of cox PH hazard type")

fit <- coxph(s ~ x1 + x2 + x3, data=ds)
if (isFitCoxPH(fit))
  print("Correct, the coxph is of cox PH hazard type")

library(cmprsk)
set.seed(10)
ftime <- rexp(200)
fstatus <- sample(0:2,200,replace=TRUE)
cov <- matrix(runif(600),nrow=200)
dimnames(cov)[[2]] <- c('x1','x2','x3')
fit <- crr(ftime,fstatus,cov)

if (isFitCoxPH(fit))
  print(paste("Correct, the competing risk regression is",
    "considered a type of cox regression",
    "since it has a Hazard Ratio"))

# ** Borrowed code from the lrm example **

#Fit a logistic model containing predictors age, blood.pressure, sex
#and cholesterol, with age fitted with a smooth 5-knot restricted cubic
#spline function and a different shape of the age relationship for males
#and females.

n <- 1000 # define sample size
set.seed(17) # so can reproduce the results
age <- rnorm(n, 50, 10)
blood.pressure <- rnorm(n, 120, 15)
cholesterol <- rnorm(n, 200, 25)
sex <- factor(sample(c('female','male'), n,TRUE))
label(age) <- 'Age' # label is in Hmisc
label(cholesterol) <- 'Total Cholesterol'
label(blood.pressure) <- 'Systolic Blood Pressure'
label(sex) <- 'Sex'
units(cholesterol) <- 'mg/dl' # uses units.default in Hmisc
units(blood.pressure) <- 'mmHg'

#To use prop. odds model, avoid using a huge number of intercepts by
#grouping cholesterol into 40-tiles

# Specify population model for log odds that Y=1
L <- .4*(sex=='male') + .045*(age-50) +
    (log(cholesterol - 10)-5.2)*(-2*(sex=='female') + 2*(sex=='male'))

# Simulate binary y to have Prob(y=1) = 1/[1+exp(-L)]
y <- ifelse(runif(n) < plogis(L), 1, 0)
cholesterol[1:3] <- NA # 3 missings, at random
ddist <- datadist(age, blood.pressure, cholesterol, sex)
options(datadist='ddist')

fit_lrm <- lrm(y ~ blood.pressure + sex * (age + rcs(cholesterol,4)),
       x=TRUE, y=TRUE)

if (isFitLogit(fit_lrm) == TRUE)
   print("Correct, the lrm is a logistic regression")

fit_lm <- lm(blood.pressure ~ sex)
if (isFitLogit(fit_lm) == FALSE)
   print("Correct, the lm is not a logistic regression")

fit_glm_logit <- glm(y ~ blood.pressure + sex * (age + rcs(cholesterol,4)),
                     family = binomial())

if (isFitLogit(fit_glm_logit) == TRUE)
   print("Correct, the glm with a family of binomial is a logistic regression")

fit_glm <- glm(blood.pressure ~ sex)
if (isFitLogit(fit_glm) == FALSE)
   print("Correct, the glm without logit as a family is not a logistic regression")

---

plotHR

Plot a spline in a Cox regression model

Description

This function is a more specialized version of the termplot() function. It creates a plot with the spline against hazard ratio. The plot can additionally have indicator of variable density and have multiple lines.

Usage

plotHR(
   models,
   term = 1,
   se = TRUE,
   cntrst = ifelse(inherits(models, "rms") || inherits(models[[1]], "rms"), TRUE, FALSE),
   polygon_ci = TRUE,
   rug = "density",
   xlab = "",
   ylab = "Hazard Ratio",
   main = NULL,
   xlim = NULL,
   ylim = NULL,
   col.term = "#08519C",
   col.se = "#DEEBF7",
   col.dens = grey(0.9),
   lwd.term = 3,
lty.term = 1,
lwd.se = lwd.term,
lty.se = lty.term,
x.ticks = NULL,
y.ticks = NULL,
ylog = TRUE,
cex = 1,
y_axis_side = 2,
plot.bty = "n",
axes = TRUE,
alpha = 0.05,
...)

Arguments

models A single model or a list() with several models

term The term of interest. Can be either the name or the number of the covariate in the model.

se Boolean if you want the confidence intervals or not

cntrst By contrasting values you can have the median as a reference point making it easier to compare hazard ratios.

polygon_ci If you want a polygon as indicator for your confidence interval. This can also be in the form of a vector if you have several models. Sometimes you only want one model to have a polygon and the rest to be dotted lines. This gives the reader an indication of which model is important.

rug The rug is the density of the population along the spline variable. Often this is displayed as a jitter with bars that are thicker & more common when there are more observations in that area or a smooth density plot that looks like a mountain. Use "density" for the mountain view and "ticks" for the jitter format.

xlab The label of the x-axis

ylab The label of the y-axis

main The main title of the plot

xlim A vector with 2 elements containing the upper & the lower bound of the x-axis

ylim A vector with 2 elements containing the upper & the lower bound of the y-axis

col.term The color of the estimate line. If multiple lines you can have different colors by giving a vector.

col.se The color of the confidence interval. If multiple lines you can have different colors by giving a vector.

col.dens The color of the density plot. Ignored if you’re using jitter

lwd.term The width of the estimated line. If you have more than one model then provide the function with a vector if you want to have different lines for different width for each model.
The typeof the estimated line, see lty. If you have more than one model then provide the function with a vector if you want to have different line types for for each model.

The line width of your confidence interval. This is ignored if you're using polygons for all the confidence intervals.

The line type of your confidence interval. This is ignored if you're using polygons for all the confidence intervals.

The ticks for the x-axis if you desire other than the default.

The ticks for the y-axis if you desire other than the default.

Show a logarithmic y-axis. Not having a logarithmic axis might seem easier to understand but it's actually not really a good idea. The distance between HR 0.5 and 2.0 should be the same. This will only show on a logarithmic scale and therefore it is strongly recommended to use the logarithmic scale.

Increase if you want larger font size in the graph.

The side that the y axis is to be plotted, see axis() for details

Type of box that you want. See the bty description in graphical parameters (par). If bty is one of "o" (the default), "l", "7", "c", "u", or "]" the resulting box resembles the corresponding upper case letter. A value of "n" suppresses the box.

A boolean that is used to identify if axes are to be plotted

The alpha level for the confidence intervals

Any additional values that are to be sent to the plot() function

The function does not return anything

The function allows for plotting multiple splines in one graph. Sometimes you might want to show more than one spline for the same variable. This allows you to create that comparison.

Examples of a situation where I’ve used multiple splines in one plot is when I want to look at a variables behavior in different time periods. This is another way of looking at the proportional hazards assumption. The Schoenfeld residuals can be a little tricky to look at when you have the splines.

Another example of when I’ve used this is when I’ve wanted to plot adjusted and unadjusted splines. This can very nicely demonstrate which of the variable span is mostly confounded. For instance - younger persons may exhibit a higher risk for a procedure but when you put in your covariates you find that the increased hazard changes back to the basic

Reinhard Seifert, Max Gordon
Examples

library(survival)
library(rms)

# Get data for example
n <- 1000
set.seed(731)

age <- round(50 + 12*rnorm(n), 1)
label(age) <- "Age"

sex <- factor(sample(c("Male","Female"), n,
                      rep=TRUE, prob=c(.6, .4)))
cens <- 15*runif(n)

smoking <- factor(sample(c("Yes","No"), n,
                         rep=TRUE, prob=c(.2, .75)))

h <- .02*exp(.02*(age-50)+.1*((age-50)/10)^3+.8*(sex=="Female") + 2*(smoking=="Yes"))
dt <- -log(runif(n))/h
label(dt) <- 'Follow-up Time'

e <- ifelse(dt <= cens,1,0)
dt <- pmin(dt, cens)
units(dt) <- "Year"

# Add missing data to smoking
smoking[sample(1:n, round(n*0.05))] <- NA

# Create a data frame since plotHR will otherwise
# have a hard time getting the names of the variables
ds <- data.frame(
  dt = dt,
  e = e,
  age=age,
  smoking=smoking,
  sex=sex)

library(splines)
Srv <- Surv(dt,e)
fit.coxph <- coxph(Srv ~ bs(age, 3) + sex + smoking, data=ds)

org_par <- par(xaxs="i", ask=TRUE)
plotHR(fit.coxph, term="age", plot.bty="o", xlim=c(30, 70), xlab="Age")

dd <- datadist(ds)
options(datadist="dd")
fit.cph <- cph(Srv ~ rcs(age,4) + sex + smoking, data=ds, x=TRUE, y=TRUE)
plotHR(fit.cph, term=1, plot.bty="l", xlim=c(30, 70), xlab="Age")
plotHR(fit.cph, term="age", plot.bty="l", xlim=c(30, 70), ylog=FALSE, rug="ticks", xlab="Age")
unadjusted_fit <- cph(Srv ~ rcs(age, 4), data=ds, x=TRUE, y=TRUE)
plotHR(list(fit.cph, unadjusted_fit), term="age", xlab="Age", 
polygon_ci=c(TRUE, FALSE),
col.term = c("#08519C", "#77777799"),
col.se = c("#DEEBF7BB", grey(0.6)),
lty.term = c(1, 2),
plot.bty="l", xlim=c(30, 70))
par(org_par)

---

rob cov ali

Robust covariance matrix based upon the 'sandwich'-package

Description

This is an alternative to the 'rms'-package robust covariance matrix that uses the 'sandwich' package vcovHC() function instead of the 'rms'-built-in estimator. The advantage being that many more estimation types are available.

Usage

rob cov.ali(fit, type = "HC3", ...)

Arguments

fit The ols fit that
type a character string specifying the estimation type. See vcovHC() for options.
... You should specify type= followed by some of the alternative available for the vcovHC() function.

Value

model The fitted model with adjusted variance and df.residual set to NULL

Examples

# Generate some data
n <- 500
x1 <- runif(n)*2
x2 <- runif(n)
y <- x1^3 + x2 + rnorm(n)
library(rms)
library(sandwich)
dd <- datadist(x1, x2, y)
org.op <- options(datadist = "dd")

# Main function
f <- ols(y ~ rcs(x1, 3) + x2)
timeSplitter

Description

If we have a violation of the cox proportional hazards assumption we need to split an individual’s followup time into several. See vignette("timeSplitter",package="Greg") for a detailed description.

Usage

timeSplitter(
  data,
  by,
  time_var,
  event_var,
  event_start_status,
  time_related_vars,
  time_offset
)

Arguments

data The dataset that you want to split according to the time_var option.
by The time period that you want to split the dataset by. The size of the variable must be in proportion to the the time_var. The by variable can also be a vector for each time split, useful if the effect has large variations over time.
time_var The name of the main time variable in the dataset. This variable must be a numeric variable.
event_var The event variable
event_start_status The start status of the event status, e.g. "Alive"
timeSplitter


time_related_vars
A dataset often contains other variables that you want to update during the split, most commonly these are age or calendar time.

time_offset
If you want to skip the initial years you can offset the entire dataset by setting this variable. See detailed description below.

Details

Important note: The time variables must have the same time unit. I.e. function can not dedu if all variables are in years or if one happens to be in days.

Value

data.frame with the split data. The starting time for each period is named Start_time and the ending time is called Stop_time. Note that the resulting event_var will now contain the time-splitted eventvar.

The time_offset - details

Both time_var and other variables will be adjusted by the time_offset, e.g. if we the time scale is in years and we want to skip the first 4 years we set the time_offset = 4. In the outputted dataset the smallest time_var will be 0. Note: 0 will not be included as we generally want to look at those that survived the start date, e.g. if a patient dies on the 4-year mark we would not include him/her in our study.

Examples

test_data <- data.frame(
id = 1:4,
  time = c(4, 3.5, 1, 5),
  event = c(“alive”, “censored”, “dead”, “dead”),
  age = c(62.2, 55.3, 73.7, 46.3),
  date = as.Date(
    c(“2003-01-01”,
      “2010-04-01”,
      “2013-09-20”,
      “2002-02-23”)))

timeSplitter(test_data, .5,
  time_var = “time”,
  time_related_vars = c(“age”, “date”),
  event_var = “event”)
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