Package ‘survival’

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Title Survival Analysis
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LazyLoad Yes
ByteCompile Yes
Description Contains the core survival analysis routines, including
definition of Surv objects,
Kaplan-Meier and Aalen-Johansen (multi-state) curves, Cox models,
and parametric accelerated failure time models.
License LGPL (>= 2)
URL https://github.com/therneau/survival
NeedsCompilation yes
Author Terry M Therneau [aut, cre],
Thomas Lumley [ctb, trl] (original S->R port and R maintainer until 2009)
Repository CRAN
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aareg  Aalen’s additive regression model for censored data

Description

Returns an object of class "aareg" that represents an Aalen model.

Usage

aareg(formula, data, weights, subset, na.action,
qrtol=1e-07, nmin, dfbeta=FALSE, taper=1,
test = c('aalen', 'variance', 'nrisk'),
model=FALSE, x=FALSE, y=FALSE)

Arguments

formula a formula object, with the response on the left of a ‘~’ operator and the terms, separated by + operators, on the right. The response must be a Surv object. Due to a particular computational approach that is used, the model MUST include an intercept term. If "-1" is used in the model formula the program will ignore it.
data data frame in which to interpret the variables named in the formula, subset, and weights arguments. This may also be a single number to handle some special cases – see below for details. If data is missing, the variables in the model formula should be in the search path.
weights vector of observation weights. If supplied, the fitting algorithm minimizes the sum of the weights multiplied by the squared residuals (see below for additional technical details). The length of weights must be the same as the number of observations. The weights must be nonnegative and it is recommended that they be strictly positive, since zero weights are ambiguous. To exclude particular observations from the model, use the subset argument instead of zero weights.
subset expression specifying which subset of observations should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating the observation numbers to be included, or a character vector of the observation names that should be included. All observations are included by default.
na.action

a function to filter missing data. This is applied to the model frame after any subset argument has been applied. The default is na.fail, which returns an error if any missing values are found. An alternative is na.exclude, which deletes observations that contain one or more missing values.

qrtol

tolerance for detection of singularity in the QR decomposition

rmin

minimum number of observations for an estimate; defaults to 3 times the number of covariates. This essentially truncates the computations near the tail of the data set, when n is small and the calculations can become numerically unstable.

dfbeta

should the array of dfbeta residuals be computed. This implies computation of the sandwich variance estimate. The residuals will always be computed if there is a cluster term in the model formula.

taper

allows for a smoothed variance estimate. $\text{Var}(x)$, where $x$ is the set of covariates, is an important component of the calculations for the Aalen regression model. At any given time point $t$, it is computed over all subjects who are still at risk at time $t$. The taper argument allows smoothing these estimates, for example taper=1:10 would cause the variance estimate used at any event time to be a weighted average of the estimated variance matrices at the last 4 death times, with a weight of 1 for the current death time and decreasing to 1/4 for prior event times. The default value gives the standard Aalen model.

test

selects the weighting to be used, for computing an overall “average” coefficient vector over time and the subsequent test for equality to zero.

model, x, y

should copies of the model frame, the x matrix of predictors, or the response vector y be included in the saved result.

Details

The Aalen model assumes that the cumulative hazard $H(t)$ for a subject can be expressed as $a(t) + X B(t)$, where $a(t)$ is a time-dependent intercept term, $X$ is the vector of covariates for the subject (possibly time-dependent), and $B(t)$ is a time-dependent matrix of coefficients. The estimates are inherently non-parametric; a fit of the model will normally be followed by one or more plots of the estimates.

The estimates may become unstable near the tail of a data set, since the increment to $B$ at time $t$ is based on the subjects still at risk at time $t$. The tolerance and/or rmin parameters may act to truncate the estimate before the last death. The taper argument can also be used to smooth out the tail of the curve. In practice, the addition of a taper such as 1:10 appears to have little effect on death times when n is still reasonably large, but can considerably dampen wild oscillations in the tail of the plot.

Value

an object of class "aareg" representing the fit, with the following components:

n

vector containing the number of observations in the data set, the number of event times, and the number of event times used in the computation

times

vector of sorted event times, which may contain duplicates

nrisk

vector containing the number of subjects at risk, of the same length as times

coefficient

matrix of coefficients, with one row per event and one column per covariate
test.statistic  the value of the test statistic, a vector with one element per covariate

test.var      variance-covariance matrix for the test

test          the type of test; a copy of the test argument above

tweight       matrix of weights used in the computation, one row per event

call          a copy of the call that produced this result

References


See Also

print.aareg, summary.aareg, plot.aareg

Examples

# Fit a model to the lung cancer data set
lfit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data = lung, nmin = 1)

## Not run:
lfit
Call:
aareg(formula = Surv(time, status) ~ age + sex + ph.ecog, data = lung, nmin = 1)

n=227 (1 observations deleted due to missing values)
 138 out of 138 unique event times used

  slope  coef se(coef)  z  p
Intercept  5.26e-03 5.99e-03 4.74e-03 1.26 0.207000
  age  4.26e-05 7.02e-05 7.23e-05 0.97 0.332000
    sex -3.29e-03 -4.02e-03 1.22e-03 -3.30 0.000976
  ph.ecog 3.14e-03 3.80e-03 1.03e-03 3.70 0.000214

Chisq=26.73 on 3 df, p=6.7e-06; test weights=aalen

plot(lfit[4], ylim = c(-4,4))  # Draw a plot of the function for ph.ecog

## End(Not run)
lfit2 <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data = lung, nmin = 1, taper = 1:10)
## Not run: lines(lfit2[4], col=2)  # Nearly the same, until the last point

# A fit to the multiple-infection data set of children with
# Chronic Granulomatous Disease.  See section 8.5 of Therneau and Grambsch.
fita2 <- aareg(Surv(tstart, tstop, status) ~ treat + age + inherit + steroids + cluster(id), data = cgd)
aeqSurv

## Not run:

n = 203

69 out of 70 unique event times used

<table>
<thead>
<tr>
<th></th>
<th>slope</th>
<th>coef</th>
<th>se(coef)</th>
<th>robust se</th>
<th>z</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Intercept</td>
<td>0.004670</td>
<td>0.017800</td>
<td>0.002780</td>
<td>0.003910</td>
<td>4.55</td>
<td>5.3e-06</td>
</tr>
<tr>
<td>treatIFN-g</td>
<td>-0.002520</td>
<td>-0.010100</td>
<td>0.002290</td>
<td>0.003020</td>
<td>-3.36</td>
<td>7.87e-04</td>
</tr>
<tr>
<td>age</td>
<td>-0.000101</td>
<td>-0.000317</td>
<td>0.000115</td>
<td>0.000117</td>
<td>-2.70</td>
<td>6.84e-03</td>
</tr>
<tr>
<td>inheritautosomal</td>
<td>0.001330</td>
<td>0.003830</td>
<td>0.002800</td>
<td>0.002420</td>
<td>1.58</td>
<td>1.14e-01</td>
</tr>
<tr>
<td>steroids</td>
<td>0.004620</td>
<td>0.013200</td>
<td>0.010600</td>
<td>0.009700</td>
<td>1.36</td>
<td>1.73e-01</td>
</tr>
</tbody>
</table>

Chisq=16.74 on 4 df, p=0.0022; test weights=aalen

## End(Not run)

---

### aeqSurv

#### Adjudicate near ties in a Surv object

#### Description

The check for tied survival times can fail due to floating point imprecision, which can make actual ties appear to be distinct values. Routines that depend on correct identification of ties pairs will then give incorrect results, e.g., a Cox model. This function rectifies these.

#### Usage

```r
aeqSurv(x, tolerance = sqrt(.Machine$double.eps))
```

#### Arguments

- `x`: a Surv object
- `tolerance`: the tolerance used to detect values that will be considered equal

#### Details

This routine is called by both `survfit` and `coxph` to deal with the issue of ties that get incorrectly broken due to floating point imprecision. See the short vignette on tied times for a simple example. Use the `timefix` argument of `survfit` or `coxph.control` to control the option if desired.

The rule for ‘equality’ is identical to that used by the `all.equal` routine. Pairs of values that are within round off error of each other are replaced by the smaller value. An error message is generated if this process causes a 0 length time interval to be created.

#### Value

A Surv object identical to the original, but with ties restored.

#### Author(s)

Terry Therneau
See Also

survfit, coxph.control

agreg.fit Cox model fitting functions

Description

These are the functions called by coxph that do the actual computation. In certain situations, e.g. a simulation, it may be advantageous to call these directly rather than the usual coxph call using a model formula.

Usage

agreg.fit(x, y, strata, offset, init, control, weights, method, rownames, resid=TRUE)
coxph.fit(x, y, strata, offset, init, control, weights, method, rownames, resid=TRUE)

Arguments

x Matix of predictors. This should not include an intercept.
y a Surv object containing either 2 columns (coxph.fit) or 3 columns (agreg.fit).
strata a vector containing the stratification, or NULL
offset optional offset vector
init initial values for the coefficients
control the result of a call to coxph.control
weights optional vector of weights
method method for handling ties, one of "breslow" or "efron"
rownames this is only needed for a NULL model, in which case it contains the rownames (if any) of the original data.
resid compute and return residuals.

Details

This routine does no checking that arguments are the proper length or type. Only use it if you know what you are doing!
The resid and concordance arguments will save some compute time for calling routines that only need the likelihood, the generation of a permutation distribution for instance.

Value

a list containing results of the fit
Author(s)
Terry Therneau

See Also
coxph

aml
Acute Myelogenous Leukemia survival data

Description
Survival in patients with Acute Myelogenous Leukemia. The question at the time was whether the standard course of chemotherapy should be extended ('maintainance') for additional cycles.

Usage
aml
leukemia

Format

time: survival or censoring time
status: censoring status
x: maintenance chemotherapy given? (factor)

Source

anova.coxph
Analysis of Deviance for a Cox model.

Description
Compute an analysis of deviance table for one or more Cox model fits.

Usage
## S3 method for class 'coxph'
anova(object, ..., test = 'Chisq')
Arguments

- **object**: An object of class `coxph`
- ... Further `coxph` objects
- **test**: a character string. The appropriate test is a chi-square, all other choices result in no test being done.

Details

Specifying a single object gives a sequential analysis of deviance table for that fit. That is, the reductions in the model log-likelihood as each term of the formula is added in turn are given in as the rows of a table, plus the log-likelihoods themselves. A robust variance estimate is normally used in situations where the model may be mis-specified, e.g., multiple events per subject. In this case a comparison of partial-likelihood values does not make sense, and `anova` will refuse to print results.

If more than one object is specified, the table has a row for the degrees of freedom and loglikelihood for each model. For all but the first model, the change in degrees of freedom and loglik is also given. (This only make statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain test statistics (and P values) comparing the reduction in loglik for each row.

Value

An object of class "anova" inheriting from class "data.frame".

Warning

The comparison between two or more models by `anova` or will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values.

See Also

- `coxph`, `anova`.

Examples

```r
fit <- coxph(Surv(futime, fustat) ~ resid.ds *rx + ecog.ps, data = ovarian)
anova(fit)
fit2 <- coxph(Surv(futime, fustat) ~ resid.ds +rx + ecog.ps, data=ovarian)
anova(fit2, fit)
```
Description

The "assign" attribute on model matrices describes which columns come from which terms in the model formula. It has two versions. R uses the original version, but the alternate version found in S-plus is sometimes useful.

Usage

```r
## Default S3 method:
attrassign(object, tt, ...)
## S3 method for class 'lm'
attrassign(object, ...)
```

Arguments

- **object**: model matrix or linear model object
- **tt**: terms object
- **...**: ignored

Details

For instance consider the following

```r
survreg(Surv(time, status) ~ age + sex + factor(ph.ecog), lung)
```

R gives the compact for for assign, a vector (0, 1, 2, 3, 3, 3); which can be read as “the first column of the X matrix (intercept) goes with none of the terms, the second column of X goes with term 1 of the model equation, the third column of X with term 2, and columns 4-6 with term 3”.

The alternate (S-Plus default) form is a list

```
$\text{(Intercept)} 1
$\text{age} 2
$\text{sex} 3
$\text{factor(ph.ecog)} 4 5 6
```

Value

A list with names corresponding to the term names and elements that are vectors indicating which columns come from which terms

See Also

terms, model.matrix
Examples

```
formula <- Surv(time,status)-factor(ph.ecog)
fit <- terms(formula)
mf <- model.frame(tt,data=lung)
mm <- model.matrix(tt,mf)
## a few rows of data
mm[1:3,]
## old-style assign attribute
attr(mm,"assign")
## alternate style assign attribute
attrassign(mm,tt)
```

Description

Compute the predicted survival curve for a Cox model.

Usage

```
basehaz(fit, centered=TRUE)
```

Arguments

```
fit a coxph fit
centered if TRUE return data from a predicted survival curve at the mean values of the
covariates fit$mean, if FALSE return a prediction for all covariates equal to
zero.
```

Details

This function is simply an alias for `survfit`, which does the actual work and has a richer set of options. The alias exists only because some users look for predicted survival estimates under this name.

The function returns a data frame containing the `time`, `cumhaz` and optionally the `strata` (if the fitted Cox model used a strata statement), which are copied the `survfit` result. If there are factor variables in the model, then the default predictions at the "mean" are meaningless since they do not correspond to any possible subject; correct results require use of the `newdata` argument of `survfit`.

Results for all covariates =0 are normally only of use as a building block for further calculations.

Value

A data frame with variable names of `hazard`, `time` and optionally `strata`. The first is actually the cumulative hazard.

See Also

`survfit.coxph`
Description

Data on recurrences of bladder cancer, used by many people to demonstrate methodology for recurrent event modelling.

Bladder1 is the full data set from the study. It contains all three treatment arms and all recurrences for 118 subjects; the maximum observed number of recurrences is 9.

Bladder is the data set that appears most commonly in the literature. It uses only the 85 subjects with nonzero follow-up who were assigned to either thiotepa or placebo, and only the first four recurrences for any patient. The status variable is 1 for recurrence and 0 for everything else (including death for any reason). The data set is laid out in the competing risks format of the paper by Wei, Lin, and Weissfeld.

Bladder2 uses the same subset of subjects as bladder, but formatted in the (start, stop] or Anderson-Gill style. Note that in transforming from the WLW to the AG style data set there is a quite common programming mistake that leads to extra follow-up time for 12 subjects: all those with follow-up beyond their 4th recurrence. This "follow-up" is a side effect of throwing away all events after the fourth while retaining the last follow-up time variable from the original data. The bladder2 data set found here does not make this mistake, but some analyses in the literature have done so; it results in the addition of a small amount of immortal time bias and shrinks the fitted coefficients towards zero.

Usage

bladder1
bladder
bladderR

Format

bladder1

id: Patient id
treatment: Placebo, pyridoxine (vitamin B6), or thiotepa
number: Initial number of tumours (8=8 or more)
size: Size (cm) of largest initial tumour
recur: Number of recurrences
start,stop: The start and end time of each time interval
status: End of interval code, 0=censored, 1=recurrence,
2=death from bladder disease, 3=death other/unknown cause
rtumor: Number of tumors found at the time of a recurrence
rsize: Size of largest tumor at a recurrence
enum: Event number (observation number within patient)
cch

Fits proportional hazards regression model to case-cohort data

Description

Returns estimates and standard errors from relative risk regression fit to data from case-cohort studies. A choice is available among the Prentice, Self-Prentice and Lin-Ying methods for unstratified data. For stratified data the choice is between Borgan I, a generalization of the Self-Prentice estimator for unstratified case-cohort data, and Borgan II, a generalization of the Lin-Ying estimator.

Usage

cch(formula, data = sys.parent(), subcoh, id, stratum=NULL, cohort.size, method =c("Prentice","SelfPrentice","LinYing","I.Borgan","II.Borgan"), robust=FALSE)
**Arguments**

- **formula**: A formula object that must have a `Surv` object as the response. The `Surv` object must be of type "right", or of type "counting".
- **subcoh**: Vector of indicators for subjects sampled as part of the sub-cohort. Code 1 or TRUE for members of the sub-cohort, 0 or FALSE for others. If `data` is a data frame then `subcoh` may be a one-sided formula.
- **id**: Vector of unique identifiers, or formula specifying such a vector.
- **stratum**: A vector of stratum indicators or a formula specifying such a vector.
- **cohort.size**: Vector with size of each stratum original cohort from which subcohort was sampled.
- **data**: An optional data frame in which to interpret the variables occurring in the formula.
- **method**: Three procedures are available. The default method is "Prentice", with options for "SelfPrentice" or "LinYing".
- **robust**: For "LinYing" only, if robust=TRUE, use design-based standard errors even for phase I.

**Details**

Implements methods for case-cohort data analysis described by Therneau and Li (1999). The three methods differ in the choice of "risk sets" used to compare the covariate values of the failure with those of others at risk at the time of failure. "Prentice" uses the sub-cohort members "at risk" plus the failure if that occurs outside the sub-cohort and is score unbiased. "SelfPren" (Self-Prentice) uses just the sub-cohort members "at risk". These two have the same asymptotic variance-covariance matrix. "LinYing" (Lin-Ying) uses the all members of the sub-cohort and all failures outside the sub-cohort who are "at risk". The methods also differ in the weights given to different score contributions.

The `data` argument must not have missing values for any variables in the model. There must not be any censored observations outside the subcohort.

**Value**

An object of class "cch" incorporating a list of estimated regression coefficients and two estimates of their asymptotic variance-covariance matrix.

- **coef**: regression coefficients.
- **naive.var**: Self-Prentice model based variance-covariance matrix.
- **var**: Lin-Ying empirical variance-covariance matrix.

**Author(s)**

Norman Breslow, modified by Thomas Lumley
References


See Also
twophase and svycoxph in the "survey" package for more general two-phase designs. http://faculty.washington.edu/tlumley/survey/

Examples

```r
## The complete Wilms Tumor Data
## (Breslow and Chatterjee, Applied Statistics, 1999)
## subcohort selected by simple random sampling.
##
## subcoh <- nwtco$in.subcohort
## selcooh <- with(nwtco, rel==1|subcoh==1)
## ccoh.data <- nwtco[selcooh,]
## ccoh.data$subcohort <- subcoh[selcooh]
##
## ccoh.data$histol <- factor(ccoh.data$histol,labels=c("FH","UH"))
## ccoh.data$stage <- factor(ccoh.data$stage,labels=c("I","II","III","IV"))
## ccoh.data$age <- ccoh.data$age/12 # Age in years
##
## ## Standard case-cohort analysis: simple random subcohort
##
## fit.ccP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
## subcoh = ~subcohort, id=~seqno, cohort.size=4028)
##
## fit.ccP
##
## fit.ccSP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
## subcoh = ~subcohort, id=~seqno, cohort.size=4028, method="SelfPren")
```
`summary(fit.ccSP)`

```r
## (post-)stratified on instit
## stratsizes<-table(mwtco$instit)
fit.BI<- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
        subcoh =~subcohort, id=~seqno, stratum=~instit, cohort.size=stratsizes,
        method="I.Borgan")

summary(fit.BI)
```

---

**Chronic Granulotamous Disease data**

**Description**

Data are from a placebo controlled trial of gamma interferon in chronic granulotomous disease (CGD). Contains the data on time to serious infections observed through end of study for each patient.

**Usage**

`cgd`

**Format**

- **id** subject identification number
- **center** enrolling center
- **random** date of randomization
- **treatment** placebo or gamma interferon
- **sex** sex
- **age** age in years, at study entry
- **height** height in cm at study entry
- **weight** weight in kg at study entry
- **inherit** pattern of inheritance
- **steroids** use of steroids at study entry, 1=yes
- **propylac** use of prophylactic antibiotics at study entry
- **hos.cat** a categorization of the centers into 4 groups
- **tstart, tstop** start and end of each time interval
- **status** 1=the interval ends with an infection
- **enum** observation number within subject
Details

The cgdp data set is in the form found in the references, with one line per patient and no recoding of the variables. The cgd data set (this one) has been cast into (start, stop] format with one line per event, and covariates such as center recoded as factors to include meaningful labels.

Source

Fleming and Harrington, Counting Processes and Survival Analysis, appendix D.2.

See Also

link{cgdp}

---

### cgdp

*Chronic Granulotomous Disease data*

Description

Data are from a placebo controlled trial of gamma interferon in chronic granulotomous disease (CGD). Contains the data on time to serious infections observed through end of study for each patient.

Usage

cgdp

Format

id    subject identification number
center  enrolling center
random  date of randomization
treatment  placebo or gamma interferon
sex    sex
age    age in years, at study entry
height height in cm at study entry
weight weight in kg at study entry
inherit pattern of inheritance
steroids use of steroids at study entry, 1=yes
propylac use of prophylactic antibiotics at study entry
hos.cat a categorization of the centers into 4 groups
futime days to last follow-up
etime1-etime7 up to 7 infection times for the subject
Details
The cgdraw data set (this one) is in the form found in the references, with one line per patient and no recoding of the variables.
The cgd data set has been further processed so as to have one line per event, with covariates such as center recoded as factors to include meaningful labels.

Source
Fleming and Harrington, Counting Processes and Survival Analysis, appendix D.2.

See Also
cgd

cipoisson

Confidence limits for the Poisson

Description
Confidence interval calculation for Poisson rates.

Usage
cipoisson(k, time = 1, p = 0.95, method = c("exact", "anscombe"))

Arguments
k Number of successes
time Total time on trial
p Probability level for the (two-sided) interval
method The method for computing the interval.

Details
The likelihood method is based on equation 10.10 of Feller, which relates poisson probabilities to tail area of the gamma distribution. The Anscombe approximation is based on the fact that sqrt(k + 3/8) is has a nearly constant variance of 1/4, along with a continuity correction.
There are many other proposed intervals: Patil and Kulkarni list and evaluate 19 different suggestions from the literature!. The exact intervals can be overly broad for very small values of k, many of the other approaches try to shrink the lengths, with varying success.

Value
a vector, matrix, or array. If both k and time are single values the result is a vector of length 2 containing the lower an upper limits. If either or both are vectors the result is a matrix with two columns. If k is a matrix or array, the result will be an array with one more dimension; in this case the dimensions and dimnames (if any) of k are preserved.
clogit

Conditional logistic regression

Description

Estimates a logistic regression model by maximising the conditional likelihood. Uses a model formula of the form case\-status~exposure+strata(matched\-set). The default is to use the exact conditional likelihood, a commonly used approximate conditional likelihood is provided for compatibility with older software.

Usage

clogit(formula, data, weights, subset, na.action, method=c("exact", "approximate", "efron", "breslow"), ...)

Arguments

formula Model formula
data data frame
weights optional, names the variable containing case weights
subset optional, subset the data
na.action optional na.action argument. By default the global option na.action is used.

References


See Also

ppois, qpois

Examples

cipoisson(4) # 95% confidence limit
# lower   upper
# 1.089865 10.24153
ppois(4, 10.24153) # chance of seeing 4 or fewer events with large rate
# [1] 0.02500096
1-ppois(3, 1.08986) # chance of seeing 4 or more, with a small rate
# [1] 0.02499961
**Details**

It turns out that the loglikelihood for a conditional logistic regression model = loglik from a Cox model with a particular data structure. Proving this is a nice homework exercise for a PhD statistics class; not too hard, but the fact that it is true is surprising.

When a well tested Cox model routine is available many packages use this ‘trick’ rather than writing a new software routine from scratch, and this is what the clogit routine does. In detail, a stratified Cox model with each case/control group assigned to its own stratum, time set to a constant, status of 1=case 0=control, and using the exact partial likelihood has the same likelihood formula as a conditional logistic regression. The clogit routine creates the necessary dummy variable of times (all 1) and the strata, then calls coxph.

The computation of the exact partial likelihood can be very slow, however. If a particular strata had say 10 events out of 20 subjects we have to add up a denominator that involves all possible ways of choosing 10 out of 20, which is $20!/(10!\cdot10!) = 184756$ terms. Gail et al describe a fast recursion method which partly ameliorates this; it was incorporated into version 2.36-11 of the survival package. The computation remains infeasible for very large groups of ties, say 100 ties out of 500 subjects, and may even lead to integer overflow for the subscripts – in this latter case the routine will refuse to undertake the task. The Efron approximation is normally a sufficiently accurate substitute.

Most of the time conditional logistic modeling is applied data with 1 case + k controls per set, in which case all of the approximations for ties lead to exactly the same result. The 'approximate' option maps to the Breslow approximation for the Cox model, for historical reasons.

Case weights are not allowed when the exact option is used, as the likelihood is not defined for fractional weights. Even with integer case weights it is not clear how they should be handled. For instance if there are two deaths in a strata, one with weight=1 and one with weight=2, should the likelihood calculation consider all subsets of size 2 or all subsets of size 3? Consequently, case weights are ignored by the routine in this case.

**Value**

An object of class "clogit", which is a wrapper for a "coxph" object.

**References**


**Author(s)**

Thomas Lumley
cluster

Identify clusters.

Description

This is a special function used in the context of survival models. It identifies correlated groups of observations, and is used on the right hand side of a formula. Using `cluster()` in a formula implies that robust sandwich variance estimators are desired.

Usage

```
cluster(x)
```

Arguments

- `x` A character, factor, or numeric variable.

Details

The function’s only action is semantic, to mark a variable as the cluster indicator. The resulting variance is what is known as the “working independence” variance in a GEE model. Note that one cannot use both a frailty term and a cluster term in the same model, the first is a mixed-effects approach to correlation and the second a GEE approach, and these don’t mix.

Value

```
x
```
See Also

coxph, survreg

Examples

marginal.model <- coxph(Surv(time, status) ~ rx + cluster(litter), rats,
subsetsex=='f'))
frailty.model <- coxph(Surv(time, status) ~ rx + frailty(litter), rats,
subsetsex=='f'))

---

Chemotherapy for Stage B/C colon cancer

Description

These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are two records per person, one for recurrence and one for death.

Usage

colon

Format

id: id
study: 1 for all patients
rx: Treatment - Obs(ervation), Lev(amisole), Lev(amisole)+5-FU
sex: 1=male
age: in years
obstruct: obstruction of colon by tumour
perfor: perforation of colon
adhere: adherence to nearby organs
nodes: number of lymph nodes with detectable cancer
time: days until event or censoring
status: censoring status
differ: differentiation of tumour (1=well, 2=moderate, 3=poor)
extent: Extent of local spread (1=submucosa, 2= muscle, 3=serosa, 4=contiguous structures)
surg: time from surgery to registration (0=short, 1=long)
node4: more than 4 positive lymph nodes
etype: event type: 1=recurrence, 2=death
Note

The study is originally described in Laurie (1989). The main report is found in Moertel (1990). This data set is closest to that of the final report in Moertel (1991). A version of the data with less follow-up time was used in the paper by Lin (1994).

References


---

concordance

**Compute the concordance statistic for data or a model**

**Description**

The concordance statistic compute the agreement between an observed response and a predictor. It is closely related to Kendall’s tau-a and tau-b, Goodman’s gamma, and Somers’ d, all of which can also be calculated from the results of this function.

**Usage**

concordance(object, ...)

```
## S3 method for class 'formula'
concordance(object, data, weights, subset, na.action,
            cluster, ymin, ymax, timewt= c("n", "S", "S/G", "n/G", "n/G2", "I"),
            influence=0, ranks = FALSE, reverse=FALSE, timefix=TRUE, ...)
```

```
## S3 method for class 'lm'
concordance(object, ..., newdata, cluster, ymin, ymax,
             influence=0, ranks=FALSE, timefix=TRUE)
```

```
## S3 method for class 'coxph'
concordance(object, ..., newdata, cluster, ymin, ymax,
             timewt= c("n", "S", "S/G", "n/G", "n/G2", "I"), influence=0,
             ranks=FALSE, timefix=TRUE)
```

```
## S3 method for class 'survreg'
concordance(object, ..., newdata, cluster, ymin, ymax,
             ...)
```
Arguments

object
- a fitted model or a formula. The formula should be of the form \( y \sim x \) or \( y \sim x + \text{strata}(z) \) with a single numeric or survival response and a single predictor. Counts of concordant, discordant and tied pairs are computed separately per stratum, and then added.

data
- a data.frame in which to interpret the variables named in the formula, or in the subset and the weights argument. Only applicable if object is a formula.

weights
- optional vector of case weights. Only applicable if object is a formula.

subset
- expression indicating which subset of the rows of data should be used in the fit. Only applicable if object is a formula.

na.action
- a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is options()$na.action. Only applicable if object is a formula.

... multiple fitted models are allowed. Only applicable if object is a model object.

newdata
- optional, a new data frame in which to evaluate (but not refit) the models

cluster
- optional grouping vector for calculating the robust variance

ymin, ymax
- compute the concordance over the restricted range ymin <= y <= ymax. (For survival data this is a time range.)

timewt
- the weighting to be applied. The overall statistic is a weighted mean over event times.

influence
- 1 = return the dfbeta vector, 2 = return the full influence matrix, 3 = return both

ranks
- if TRUE, return a data frame containing the individual ranks that make up the overall score.

reverse
- if TRUE then assume that larger x values predict smaller response values y; a proportional hazards model is the common example of this.

timefix
- if the response is a Surv object, correct for possible rounding error; otherwise this argument has no effect. See the vignette on tied times for more explanation.

Details

At each event time, compute the rank of the subject who had the event as compared to all others with a longer survival, where the rank is value between 0 and 1. The concordance is a weighted mean of these values, determined by the timewt option. For uncensored data each unique response value is compared to all those which are larger.

Using the default value for timewt, this gives the area under the receiver operating curve (AUC) for a binary response, Harrell’s c-statistic when the response is a survival time, and \((d+1)/2\) when y is continuous, where d is Somers’ d.
Value

An object of class concordance containing the following components:

- **concordance**: the estimated concordance value or values
- **count**: a vector containing the number of concordant pairs, discordant, tied on x but not y, tied on y but not x, and tied on both x and y
- **n**: the number of observations
- **var**: a vector containing the estimated variance of the concordance based on the infinitesimal jackknife (IJ) method. If there are multiple models it contains the estimated variance/covariance matrix.
- **cvar**: a vector containing the estimated variance(s) of the concordance values, based on the variance formula for the associated score test from a proportional hazards model. (This was the primary variance used in the `survConcordance` function.)
- **dfbeta**: optional, the vector of leverage estimates for the concordance
- **influence**: optional, the matrix of leverage values for each of the counts, one row per observation
- **ranks**: optional, a data frame containing the Somers’ d rank at each event time, along with the time weight, case weight of the observation with an event, and variance (contribution to the proportional hazards model information matrix). A weighted mean of the ranks equals Somer’s d.

Author(s)

Terry Therneau

See Also

- coxph

Examples

```r
fit1 <- coxph(Surv(ptime, pstat) ~ age + sex + mspike, mgus2)
concordance(fit1, timewt="n")

# logistic regression
fit2 <- glm(pstat ~ age + sex + mspike, binomial, data= mgus2)
concordance(fit2)  # equal to the AUC
```

Description

Test the proportional hazards assumption for a Cox regression model fit (coxph).
Usage

\texttt{cox.zph(fit, transform="km", global=TRUE)}

Arguments

- \texttt{fit} \hspace{1cm} the result of fitting a Cox regression model, using the \texttt{coxph} function.
- \texttt{transform} \hspace{1cm} a character string specifying how the survival times should be transformed before the test is performed. Possible values are "km", "rank", "identity" or a function of one argument.
- \texttt{global} \hspace{1cm} should a global chi-square test be done, in addition to the per-variable tests.

Value

an object of class "cox.zph", with components:

- \texttt{table} \hspace{1cm} a matrix with one row for each variable, and optionally a last row for the global test. Columns of the matrix contain the correlation coefficient between transformed survival time and the scaled Schoenfeld residuals, a chi-square, and the two-sided p-value. For the global test there is no appropriate correlation, so an NA is entered into the matrix as a placeholder.
- \texttt{x} \hspace{1cm} the transformed time axis.
- \texttt{y} \hspace{1cm} the matrix of scaled Schoenfeld residuals. There will be one column per variable and one row per event. The row labels contain the original event times (for the identity transform, these will be the same as \texttt{x}).
- \texttt{call} \hspace{1cm} the calling sequence for the routine.

The computations require the original \texttt{x} matrix of the Cox model fit. Thus it saves time if the \texttt{x=TRUE} option is used in \texttt{coxph}. This function would usually be followed by both a plot and a print of the result. The plot gives an estimate of the time-dependent coefficient $\beta(t)$. If the proportional hazards assumption is true, $\beta(t)$ will be a horizontal line. The printout gives a test for slope=0.

References


See Also

\texttt{coxph}, \texttt{Surv}.

Examples

\begin{verbatim}
fit <- coxph(Surv(futime, fustat) ~ age + ecog.ps, 
data=ovarian)

 temp <- cox.zph(fit)

 print(temp) \hspace{1cm} # display the results
 plot(temp) \hspace{1cm} # plot curves
\end{verbatim}
**coxph**

*Fit Proportional Hazards Regression Model*

**Description**

Fits a Cox proportional hazards regression model. Time dependent variables, time dependent strata, multiple events per subject, and other extensions are incorporated using the counting process formulation of Andersen and Gill.

**Usage**

```r
coxph(formula, data = , weights, subset, 
   na.action, init, control, 
   ties = c("efron", "breslow", "exact"), 
   singular.ok = TRUE, robust = FALSE, 
   model = FALSE, x = FALSE, y = TRUE, tt, method, ...)
```

**Arguments**

- **formula**: a formula object, with the response on the left of a ~ operator, and the terms on the right. The response must be a survival object as returned by the `Surv` function.
- **data**: a data.frame in which to interpret the variables named in the `formula`, or in the `subset` and the `weights` argument.
- **weights**: vector of case weights, see the note below. For a thorough discussion of these see the book by Therneau and Grambsch.
- **subset**: expression indicating which subset of the rows of `data` should be used in the fit. All observations are included by default.
- **na.action**: a missing-data filter function. This is applied to the `model.frame` after any subset argument has been used. Default is `options()$na.action`.
- **init**: vector of initial values of the iteration. Default initial value is zero for all variables.
- **control**: Object of class `coxph.control` specifying iteration limit and other control options. Default is `coxph.control(...)`.
- **ties**: a character string specifying the method for tie handling. If there are no tied death times all the methods are equivalent. Nearly all Cox regression programs use the Breslow method by default, but not this one. The Efron approximation is used as the default here, it is more accurate when dealing with tied death times, and is as efficient computationally. The "exact partial likelihood" is equivalent to a conditional logistic model, and is appropriate when the times are a small set of discrete values. See further below.
- **singular.ok**: logical value indicating how to handle collinearity in the model matrix. If `TRUE`, the program will automatically skip over columns of the X matrix that are linear combinations of earlier columns. In this case the coefficients for such columns will be NA, and the variance matrix will contain zeros. For ancillary calculations, such as the linear predictor, the missing coefficients are treated as zeros.
robust   this argument has been deprecated, use a cluster term in the model instead. (The two options accomplish the same goal – creation of a robust variance – but the second is more flexible).
model   logical value: if TRUE, the model frame is returned in component model.
x   logical value: if TRUE, the x matrix is returned in component x.
y   logical value: if TRUE, the response vector is returned in component y.

Details
The proportional hazards model is usually expressed in terms of a single survival time value for each person, with possible censoring. Andersen and Gill reformulated the same problem as a counting process; as time marches onward we observe the events for a subject, rather like watching a Geiger counter. The data for a subject is presented as multiple rows or "observations'', each of which applies to an interval of observation (start, stop).

The routine internally scales and centers data to avoid overflow in the argument to the exponential function. These actions do not change the result, but lead to more numerical stability. However, arguments to offset are not scaled since there are situations where a large offset value is a purpose-fully used. In general, however, users should not avoid very large numeric values for an offset due to possible loss of precision in the estimates.

Value
an object of class coxph representing the fit. See coxph.object for details.

Side Effects
Depending on the call, the predict, residuals, and survfit routines may need to reconstruct the x matrix created by coxph. It is possible for this to fail, as in the example below in which the predict function is unable to find tform.

```r
tfun <- function(tform) coxph(tform, data=lung)
fit <- tfun(Surv(time, status) ~ age)
predict(fit)
```

In such a case add the model=TRUE option to the coxph call to obviate the need for reconstruction, at the expense of a larger fit object.

Case weights
Case weights are treated as replication weights, i.e., a case weight of 2 is equivalent to having 2 copies of that subject's observation. When computers were much smaller grouping like subjects together was a common trick to used to conserve memory. Setting all weights to 2 for instance will give the same coefficient estimate but halve the variance. When the Efron approximation for
ties (default) is employed replication of the data will not give exactly the same coefficients as the weights option, and in this case the weighted fit is arguably the correct one.

When the model includes a cluster term or the robust=TRUE option the computed variance treats any weights as sampling weights; setting all weights to 2 will in this case give the same variance as weights of 1.

Special terms

There are three special terms that may be used in the model equation. A strata term identifies a stratified Cox model; separate baseline hazard functions are fit for each strata. The cluster term is used to compute a robust variance for the model. The term + cluster(id) where each value of id is unique is equivalent to specifying the robust=TRUE argument. If the id variable is not unique, it is assumed that it identifies clusters of correlated observations. The robust estimate arises from many different arguments and thus has had many labels. It is variously known as the Huber sandwich estimator, White's estimate (linear models/econometrics), the Horvitz-Thompson estimate (survey sampling), the working independence variance (generalized estimating equations), the infinitesimal jackknife, and the Wei, Lin, Weissfeld (WLW) estimate.

A time-transform term allows variables to vary dynamically in time. In this case the tt argument will be a function or a list of functions (if there are more than one tt() term in the model) giving the appropriate transform. See the examples below.

Convergence

In certain data cases the actual MLE estimate of a coefficient is infinity, e.g., a dichotomous variable where one of the groups has no events. When this happens the associated coefficient grows at a steady pace and a race condition will exist in the fitting routine: either the log likelihood converges, the information matrix becomes effectively singular, an argument to exp becomes too large for the computer hardware, or the maximum number of interactions is exceeded. (Nearly always the first occurs.) The routine attempts to detect when this has happened, not always successfully. The primary consequence for the user is that the Wald statistic = coefficient/se(coefficient) is not valid in this case and should be ignored; the likelihood ratio and score tests remain valid however.

Ties

There are three possible choices for handling tied event times. The Breslow approximation is the easiest to program and hence became the first option coded for almost all computer routines. It then ended up as the default option when other options were added in order to "maintain backwards compatibility". The Efron option is more accurate if there are a large number of ties, and it is the default option here. In practice the number of ties is usually small, in which case all the methods are statistically indistinguishable.

Using the "exact partial likelihood" approach the Cox partial likelihood is equivalent to that for matched logistic regression. (The clogit function uses the coxph code to do the fit.) It is technically appropriate when the time scale is discrete and has only a few unique values, and some packages refer to this as the "discrete" option. There is also an "exact marginal likelihood" due to Prentice which is not implemented here.

The calculation of the exact partial likelihood is numerically intense. Say for instance 180 subjects are at risk on day 7 of which 15 had an event; then the code needs to compute sums over all 180-choose-15 > 10^43 different possible subsets of size 15. There is an efficient recursive algorithm
for this task, but even with this the computation can be insufferably long. With (start, stop) data it is much worse since the recursion needs to start anew for each unique start time.

A second issue is that of artificial ties due to floating-point imprecision. See the vignette on this topic for a full explanation or the `timefix` option in `coxph.control`. Users may need to add `timefix=FALSE` for simulated data sets.

**Penalized regression**

`coxph` can maximise a penalised partial likelihood with arbitrary user-defined penalty. Supplied penalty functions include ridge regression (`ridge`), smoothing splines (`pspline`), and frailty models (`frailty`).

**References**


**See Also**

`coxph.object`, `coxph.control`, `cluster`, `strata`, `Surv`, `survfit`, `pspline`, `ridge`.

**Examples**

```r
# Create the simplest test data set
test1 <- list(time=c(4,3,1,2,2,3),
              status=c(1,1,1,0,1,1,0),
              x=c(0,2,1,1,1,0,0),
              sex=c(0,0,0,0,1,1,1))
# Fit a stratified model
coxph(Surv(time, status) ~ x + strata(sex), test1)
# Create a simple data set for a time-dependent model
test2 <- list(start=c(1,2,5,2,1,7,3,4,8,8),
              stop=c(2,3,6,7,8,9,9,9,14,17),
              event=c(1,1,1,1,1,1,0,0,0,0),
              x=c(1,0,0,1,0,1,1,1,0,0))
summary(coxph(Surv(start, stop, event) ~ x, test2))

# Create a simple data set for a time-dependent model
#
test2 <- list(start=c(1, 2, 5, 2, 1, 7, 3, 4, 8, 8),
              stop =c(2, 3, 6, 7, 8, 9, 9, 9, 14,17),
              event=c(1, 1, 1, 1, 1, 1, 1, 0, 0, 0),
              x =c(1, 0, 0, 1, 0, 1, 1, 1, 0, 0 ) )

summary( coxph( Surv(start, stop, event) ~ x, test2))
# Fit a stratified model, clustered on patients
```
bladder1 <- bladder[bladder$enum < 5, ]
coxph(Surv(stop, event) ~ (rx + size + number) * strata(enum) + cluster(id), bladder1)

# Fit a time transform model using current age
coxph(Surv(time, status) ~ ph.ecog + tt(age), data=lung,
       tt=function(x,t,...) pspline(x + t/365.25))

coxph.control  

**Ancillary arguments for controlling coxph fits**

**Description**

This is used to set various numeric parameters controlling a Cox model fit. Typically it would only be used in a call to coxph.

**Usage**

```r
coxph.control(eps = 1e-09, toler.chol = .Machine$double.eps^0.75,
iter.max = 20, toler.inf = sqrt(eps), outer.max = 10, timefix=TRUE)
```

**Arguments**

- **eps**: Iteration continues until the relative change in the log partial likelihood is less than eps. Must be positive.
- **toler.chol**: Tolerance for detection of singularity during a Cholesky decomposition of the variance matrix, i.e., for detecting a redundant predictor variable.
- **iter.max**: Maximum number of iterations to attempt for convergence.
- **toler.inf**: Tolerance criteria for the warning message about a possible infinite coefficient value.
- **outer.max**: For a penalized coxph model, e.g. with pspline terms, there is an outer loop of iteration to determine the penalty parameters; maximum number of iterations for this outer loop.
- **timefix**: Resolve any near ties in the time variables.

**Details**

See the vignette "Roundoff error and tied times" for a more detailed explanation of the `timefix` option. In short, when time intervals are created via subtraction then two time intervals that are actually identical can appear to be different due to floating point round off error, which in turn can make coxph and survfit results dependent on things such as the order in which operations were done or the particular computer that they were run on. Such cases are unfortunately not rare in practice. The `timefix=TRUE` option adds logic similar to `all.equal` to ensure reliable results. In analysis of simulated data sets, however, where often by definition there can be no duplicates, the option will often need to be set to `FALSE` to avoid spurious merging of close numeric values.
Value

a list containing the values of each of the above constants

See Also

coxph

description

Returns the individual contributions to the first and second derivative matrix, at each unique event time.

Usage

coxph.detail(object, riskmat=FALSE)

Arguments

object 
a Cox model object, i.e., the result of coxph.

riskmat 
include the at-risk indicator matrix in the output?

details

This function may be useful for those who wish to investigate new methods or extensions to the Cox model. The example below shows one way to calculate the Schoenfeld residuals.

Value

a list with components

time 
the vector of unique event times

nevent 
the number of events at each of these time points.

means 
a matrix with one row for each event time and one column for each variable in the Cox model, containing the weighted mean of the variable at that time, over all subjects still at risk at that time. The weights are the risk weights \( \exp(x \times \%\% \text{fit$coeff}) \).

nrisk 
number of subjects at risk.

score 
the contribution to the score vector (first derivative of the log partial likelihood) at each time point.

imat 
the contribution to the information matrix (second derivative of the log partial likelihood) at each time point.
hazard  the hazard increment. Note that the hazard and variance of the hazard are always for some particular future subject. This routine uses object$mean as the future subject.

varhaz  the variance of the hazard increment.

x,y  copies of the input data.

strata  only present for a stratified Cox model, this is a table giving the number of time points of component time that were contributed by each of the strata.

riskmat  a matrix with one row for each time and one column for each observation containing a 0/1 value to indicate whether that observation was (1) or was not (0) at risk at the given time point.

See Also

coxph, residuals.coxph

Examples

fit <- coxph(Surv(futime,fustat) ~ age + rx + ecog.ps, ovarian, x=TRUE)
fitd <- coxph.detail(fit)
# There is one Schoenfeld residual for each unique death. It is a
# vector (covariates for the subject who died) - (weighted mean covariate
# vector at that time). The weighted mean is defined over the subjects
# still at risk, with exp(x beta) as the weight.

events <- fit$y[,2]==1
etime <- fit$y[events,1]  # the event times --- may have duplicates
indx <- match(etime, fitd$time)
schoen <- fit$x[events,] - fitd$means[indx,]

coxph.object  Proportional Hazards Regression Object

Description

This class of objects is returned by the coxph class of functions to represent a fitted proportional hazards model. Objects of this class have methods for the functions print, summary, residuals, predict and survfit.

Arguments

coefficients  the vector of coefficients. If the model is over-determined there will be missing values in the vector corresponding to the redundant columns in the model matrix.

var  the variance matrix of the coefficients. Rows and columns corresponding to any missing coefficients are set to zero.

naive.var  this component will be present only if the robust option was true. If so, the var component will contain the robust estimate of variance, and this component will contain the ordinary estimate.
loglik  a vector of length 2 containing the log-likelihood with the initial values and with
the final values of the coefficients.

score  value of the efficient score test, at the initial value of the coefficients.

rscore  the robust log-rank statistic, if a robust variance was requested.

wald.test  the Wald test of whether the final coefficients differ from the initial values.

iter  number of iterations used.

linear.predictors  the vector of linear predictors, one per subject. Note that this vector has been
centered, see predict.coxph for more details.

residuals  the martingale residuals.

means  vector of column means of the X matrix. Subsequent survival curves are ad-
justed to this value.

n  the number of observations used in the fit.

nevent  the number of events (usually deaths) used in the fit.

concordance  a vector of length 6, containing the number of pairs that are concordant, discord-
ant, tied on x, tied on y, and tied on both, followed by the standard error of the
concordance statistic.

first  the first derivative vector at the solution.

weights  the vector of case weights, if one was used.

method  the method used for handling tied survival times.

na.action  the na.action attribute, if any, that was returned by the na.action routine.

The object will also contain the following, for documentation see the lm object:
terms, assign, formula, call, and, optionally, x, y, and/or frame.

Components

The following components must be included in a legitimate coxph object.

See Also

coxph, coxph.detail, cox.zph, residuals.coxph, survfit, survreg.

coxph.wtest  Compute a quadratic form

Description

This function is used internally by several survival routines. It computes a simple quadratic form,
while properly dealing with missings.

Usage

coxph.wtest(var, b, toler.chol = 1e-09)
Arguments

var  variance matrix
b    vector
toler.chol  tolerance for the internal cholesky decomposition

Details

Compute $b^T V^{-1} b$. Equivalent to $\text{sum}(b * \text{solve}(V,b))$, except for the case of redundant covariates in the original model, which lead to NA values in $V$ and $b$.

Value

a real number

Author(s)

Terry Therneau

---

diabetic  

Ddiabetic retinopathy

Description

Partial results from a trial of laser coagulation for the treatment of diabetic retinopathy.

Usage

data("diabetic")

Format

A data frame with 394 observations on the following 8 variables.

id  subject id
laser  laser type: xenon or argon
age  age at diagnosis
eye  a factor with levels of left right
trt  treatment: 0 = no treatment, 1= laser
risk  risk group of 6-12
time  time to event or last follow-up
status  status of 0= censored or 1 = visual loss
Details

The 197 patients in this dataset were a 50% random sample of the patients with "high-risk" diabetic retinopathy as defined by the Diabetic Retinopathy Study (DRS). Each patient had one eye randomized to laser treatment and the other eye received no treatment. For each eye, the event of interest was the time from initiation of treatment to the time when visual acuity dropped below 5/200 two visits in a row. Thus there is a built-in lag time of approximately 6 months (visits were every 3 months). Survival times in this dataset are therefore the actual time to blindness in months, minus the minimum possible time to event (6.5 months). Censoring was caused by death, dropout, or end of the study.

References

Huster, Brookmeyer and Self, Biometrics, 1989.

Examples

# juvenile diabetes is defined as and age less than 20
juvenile <- 1*(diabetic$age < 20)
coxph(Surv(time, status) ~ trt + juvenile + cluster(id),
     data= diabetic)

---
dsurvreg

Distributions available in survreg.

Description

Density, cumulative distribution function, quantile function and random generation for the set of distributions supported by the survreg function.

Usage

dsurvreg(x, mean, scale=1, distribution='weibull', parms)
p survreg(q, mean, scale=1, distribution='weibull', parms)
q survreg(p, mean, scale=1, distribution='weibull', parms)
r survreg(n, mean, scale=1, distribution='weibull', parms)

Arguments

x vector of quantiles. Missing values (NAs) are allowed.
q vector of quantiles. Missing values (NAs) are allowed.
p vector of probabilities. Missing values (NAs) are allowed.
n number of random deviates to produce
mean vector of linear predictors for the model. This is replicated to be the same length as p, q or n.
scale

vector of (positive) scale factors. This is replicated to be the same length as p, q or n.

distribution

character string giving the name of the distribution. This must be one of the elements of survreg.distributions

pars

optional parameters, if any, of the distribution. For the t-distribution this is the degrees of freedom.

Details

Elements of q or p that are missing will cause the corresponding elements of the result to be missing.

The location and scale values are as they would be for survreg. The label "mean" was an unfortunate choice (made in mimicry of qnorm); since almost none of these distributions are symmetric it will not actually be a mean, but corresponds instead to the linear predictor of a fitted model.

Translation to the usual parameterization found in a textbook is not always obvious. For example, the Weibull distribution is fit using the Extreme value distribution along with a log transformation. Letting \( F(t) = 1 - \exp[-(at)^p] \) be the cumulative distribution of the Weibull using a standard parameterization in terms of \( a \) and \( p \), the survreg location corresponds to \(-\log(a)\) and the scale to \(1/p\) (Kalbfleisch and Prentice, section 2.2.2).

Value

density (dsurvreg), probability (psurvreg), quantile (qsurvreg), or for the requested distribution with mean and scale parameters mean and sd.

References


See Also

survreg, Normal

Examples

```r
# List of distributions available
names(survreg.distributions)

# Not run:
[1] "extreme"    "logistic"   "gaussian"   "weibull"   "exponential"
[6] "rayleigh"   "loggaussian" "lognormal" "loglogistic" "t"

# End(Not run)
# Compare results
all.equal(dsurvreg(1:10, 2, 5, dist='lognormal'), dlnorm(1:10, 2, 5))

# Hazard function for a Weibull distribution
x <- seq(.1, 3, length=30)
 haz <- dsurvreg(x, 2, 3)/ (1-psurvreg(x, 2, 3))
# Not run:
plot(x, haz, log='xy', ylab="Hazard") # line with slope (1/scale -1)
```
The Fine-Gray model can be fit by first creating a special data set, and then fitting a weighted Cox model to the result. This routine creates the data set.

### Usage

```r
finegray(formula, data, subset, na.action = na.pass, etype, prefix="fg", count, id, timefix=TRUE)
```

### Arguments

- **formula**: a standard model formula, with survival on the left and covariates on the right.
- **data**: an optional data frame, list or environment (or object coercible by `as.data.frame` to a data frame) containing the variables in the model.
- **subset**: an optional vector specifying a subset of observations to be used in the fitting process.
- **na.action**: a function which indicates what should happen when the data contain NAs. The default is set by the `na.action` setting of options.
- **etype**: the event type for which a data set will be generated. The default is to use whichever is listed first in the multi-state survival object.
- **prefix**: the routine will add 4 variables to the data set: a start and end time for each interval, status, and a weight for the interval. The default names of these are "fgstart", "fgstop", "fgstatus", and "fgwt"; the `prefix` argument determines the initial portion of the new names.
- **count**: a variable name in the output data set for an optional variable that will contain the the replication count for each row of the input data. If a row is expanded into multiple lines it will contain 1, 2, etc.
- **id**: optional, the variable name in the data set which identifies subjects.
- **timefix**: process times through the `aeqSurv` function to eliminate potential roundoff issues.

### Details

The function expects a multi-state survival expression or variable as the left hand side of the formula, e.g. `Surv(atime, astat)` where `astat` is a factor whose first level represents censoring and remaining levels are states. The output data set will contain simple survival data (status = 0 or 1) for a single endpoint of interest. In the output data set subjects who did not experience the event of interest become censored subjects whose times are artificially extended over multiple intervals,
with a decreasing case weight from interval to interval. The output data set will normally contain many more rows than the input.

Time dependent covariates are allowed, but not (currently) delayed entry. If there are time dependent covariates, e.g., the input data set had \( \text{Surv(entry, exit, stat)} \) as the left hand side, then an \texttt{id} statement is required. The program does data checks in this case, and needs to know which rows belong to each subject.

See the competing risks vignette for more details.

**Value**

a data frame

**Author(s)**

Terry Therneau

**References**


**See Also**

coxph, aeqSurv

**Examples**

```r
# Treat time to death and plasma cell malignancy as competing risks
etime <- with(mgus2, ifelse(pstat==0, futime, ptime))
event <- with(mgus2, ifelse(pstat==0, 2*death, 1))
event <- factor(event, 0:2, labels=c("censor", "pcm", "death"))

# FG model for PCM
pdata <- finegray(Surv(etime, event) ~ ., data=mgus2)
fgfit <- coxph(Surv(fgstart, fgstop, fgstatus) ~ age + sex,
               weight=fgwt, data=pdata)

# Compute the weights separately by sex
adata <- finegray(Surv(etime, event) ~ . + strata(sex),
                 data=mgus2, na.action=na.pass)
```
Assay of serum free light chain for 7874 subjects.

Description

This is a stratified random sample containing 1/2 of the subjects from a study of the relationship between serum free light chain (FLC) and mortality. The original sample contains samples on approximately 2/3 of the residents of Olmsted County aged 50 or greater.

Usage

data(flchain)

Format

A data frame with 7874 persons containing the following variables.

- **age**: age in years
- **sex**: F=female, M=male
- **sample.yr**: the calendar year in which a blood sample was obtained
- **kappa**: serum free light chain, kappa portion
- **lambda**: serum free light chain, lambda portion
- **flc.grp**: the FLC group for the subject, as used in the original analysis
- **creatinine**: serum creatinine
- **mgus**: 1 if the subject had been diagnosed with monoclonal gammapothy (MGUS)
- **futime**: days from enrollment until death. Note that there are 3 subjects whose sample was obtained on their death date.
- **death**: 0=alive at last contact date, 1=dead
- **chapter**: for those who died, a grouping of their primary cause of death by chapter headings of the International Code of Diseases ICD-9

Details

In 1995 Dr. Robert Kyle embarked on a study to determine the prevalence of monoclonal gammapathy of undetermined significance (MGUS) in Olmsted County, Minnesota, a condition which is normally only found by chance from a test (serum electrophoresis) which is ordered for other causes. Later work suggested that one component of immunoglobulin production, the serum free light chain, might be a possible marker for immune disregulation. In 2010 Dr. Angela Dispenzieri and colleagues assayed FLC levels on those samples from the original study for which they had patient permission and from which sufficient material remained for further testing. They found that elevated FLC levels were indeed associated with higher death rates.

Patients were recruited when they came to the clinic for other appointments, with a final random sample of those who had not yet had a visit since the study began. An interesting side question is whether there are differences between early, mid, and late recruits.
This data set contains an age and sex stratified random sample that includes 7874 of the original 15759 subjects. The original subject identifiers and dates have been removed to protect patient identity. Subsampling was done to further protect this information.

Source

The primary investigator (A Dispenzieri) and statistician (T Therneau) for the study.

References


Examples

data(flchain)
age.grp <- cut(flchain$age, c(49,54, 59,64, 69,74,79, 89, 110),
    labels= paste(c(50,55,60,65,70,75,80,90),
                      c(54,59,64,69,74,79,89,109), sep='-'))
table(flchain$sex, age.grp)

---

frailty

Describe

The frailty function allows one to add a simple random effects term to a Cox or survreg model.

Usage

frailty(x, distribution="gamma", ...)
frailty.gamma(x, sparse = (nclass > 5), theta, df, eps = 1e-05,
   method = c("em","aic", "df", "fixed"), ...)
frailty.gaussian(x, sparse = (nclass > 5), theta, df,
    method =c("reml","aic", "df", "fixed"), ...)
frailty.t(x, sparse = (nclass > 5), theta, df, eps = 1e-05, tdf = 5,
   method = c("aic", "df", "fixed"), ...)
Arguments

- **x**
  - the variable to be entered as a random effect. It is always treated as a factor.
- **distribution**
  - either the gamma, gaussian or t distribution may be specified. The routines frailty.gamma, frailty.gaussian and frailty.t do the actual work.
- **...**
  - Arguments for specific distribution, including (but not limited to)
- **sparse**
  - cutoff for using a sparse coding of the data matrix. If the total number of levels of x is larger than this value, then a sparse matrix approximation is used. The correct cutoff is still a matter of exploration: if the number of levels is very large (thousands) then the non-sparse calculation may not be feasible in terms of both memory and compute time. Likewise, the accuracy of the sparse approximation appears to be related to the maximum proportion of subjects in any one class, being best when no one class has a large membership.
- **theta**
  - if specified, this fixes the variance of the random effect. If not, the variance is a parameter, and a best solution is sought. Specifying this implies method = 'fixed'.
- **df**
  - if specified, this fixes the degrees of freedom for the random effect. Specifying this implies method = 'df'. Only one of theta or df should be specified.
- **method**
  - the method used to select a solution for theta, the variance of the random effect. The fixed corresponds to a user-specified value, and no iteration is done. The df selects the variance such that the degrees of freedom for the random effect matches a user specified value. The aic method seeks to maximize Akaike’s information criteria 2*(partial likelihood - df). The em and reml methods are specific to Cox models with gamma and gaussian random effects, respectively. Please see further discussion below.
- **tdf**
  - the degrees of freedom for the t-distribution.
- **eps**
  - convergence criteria for the iteration on theta.

Details

The frailty plugs into the general penalized modeling framework provided by the coxph and survreg routines. This framework deals with likelihood, penalties, and degrees of freedom; these aspects work well with either parent routine.

Therneau, Grambsch, and Pankratz show how maximum likelihood estimation for the Cox model with a gamma frailty can be accomplished using a general penalized routine, and Ripatti and Palmgren work through a similar argument for the Cox model with a gaussian frailty. Both of these are specific to the Cox model. Use of gamma/ml or gaussian/reml with survreg does not lead to valid results.

The extensible structure of the penalized methods is such that the penalty function, such as frailty or pspine, is completely separate from the modeling routine. The strength of this is that a user can plug in any penalization routine they choose. A weakness is that it is very difficult for the modeling routine to know whether a sensible penalty routine has been supplied.

Note that use of a frailty term implies a mixed effects model and use of a cluster term implies a GEE approach; these cannot be mixed.

The coxme package has superseded this method. It is faster, more stable, and more flexible.
Value

this function is used in the model statement of either coxph or survreg. It’s results are used internally.

References


See Also

coxph, survreg

Examples

# Random institutional effect
coxph(Surv(time, status) ~ age + frailty(inst, df=4), lung)

# Litter effects for the rats data
rfit2a <- survreg(Surv(time, status) ~ rx +
 frailty.gaussian(litter, df=13, sparse=FALSE), rats,
subset = (sex=='f'))
rfit2b <- survreg(Surv(time, status) ~ rx +
 frailty.gaussian(litter, df=13, sparse=TRUE), rats,
subset = (sex=='f'))

Description

The data come from a field engineering study of the time to failure of diesel generator fans. The ultimate goal was to decide whether or not to replace the working fans with a higher quality fan to prevent future failures. Seventy generators were studied. For each one, the number of hours of running time from its first being put into service until fan failure or until the end of the study (whichever came first) was recorded.

Usage

data("genfan")

Format

A data frame with 70 observations on the following 2 variables.

hours  hours of service
status  1=failure, 0=censored
heart

References

---

Stanford Heart Transplant data

**Description**
Survival of patients on the waiting list for the Stanford heart transplant program.

**Usage**
- heart
- jasa
- jasa1

**Format**

<table>
<thead>
<tr>
<th>Format</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>jasa</td>
<td>original data</td>
</tr>
<tr>
<td>birth.dt</td>
<td>birth date</td>
</tr>
<tr>
<td>accept.dt</td>
<td>acceptance into program</td>
</tr>
<tr>
<td>tx.date</td>
<td>transplant date</td>
</tr>
<tr>
<td>fu.date</td>
<td>end of followup</td>
</tr>
<tr>
<td>fustat</td>
<td>dead or alive</td>
</tr>
<tr>
<td>surgery</td>
<td>prior bypass surgery</td>
</tr>
<tr>
<td>age</td>
<td>age (in years)</td>
</tr>
<tr>
<td>futime</td>
<td>followup time</td>
</tr>
<tr>
<td>wait.time</td>
<td>time before transplant</td>
</tr>
<tr>
<td>transplant</td>
<td>transplant indicator</td>
</tr>
<tr>
<td>mismatch</td>
<td>mismatch score</td>
</tr>
<tr>
<td>hla.a2</td>
<td>particular type of mismatch</td>
</tr>
<tr>
<td>mscore</td>
<td>another mismatch score</td>
</tr>
<tr>
<td>reject</td>
<td>rejection occurred</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Format</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>jasa1, heart</td>
<td>processed data</td>
</tr>
<tr>
<td>start, stop, event</td>
<td>Entry and exit time and status for this interval of time</td>
</tr>
<tr>
<td>age</td>
<td>age-48 years</td>
</tr>
<tr>
<td>year</td>
<td>year of acceptance (in years after 1 Nov 1967)</td>
</tr>
<tr>
<td>surgery</td>
<td>prior bypass surgery 1=yes</td>
</tr>
<tr>
<td>transplant</td>
<td>received transplant 1=yes</td>
</tr>
<tr>
<td>id</td>
<td>patient id</td>
</tr>
</tbody>
</table>
is.ratetable

Source


See Also

stanford2

is.ratetable(x, verbose=FALSE)

Arguments

x the object to be verified.

verbose if TRUE and the object is not a ratetable, then return a character string describing the way(s) in which x fails to be a proper ratetable object.

Details

Rate tables are used by the pyears and survexp functions, and normally contain death rates for some population, categorized by age, sex, or other variables. They have a fairly rigid structure, and the verbose option can help in creating a new rate table.

Value

returns TRUE if x is a ratetable, and FALSE or a description if it is not.

See Also

pyears, survexp.

Examples

is.ratetable(survexp.us) # True
is.ratetable(cancer) # False
Kidney catheter data

Description

Data on the recurrence times to infection, at the point of insertion of the catheter, for kidney patients using portable dialysis equipment. Catheters may be removed for reasons other than infection, in which case the observation is censored. Each patient has exactly 2 observations.

This data has often been used to illustrate the use of random effects (frailty) in a survival model. However, one of the males (id 21) is a large outlier, with much longer survival than his peers. If this observation is removed no evidence remains for a random subject effect.

Format

<table>
<thead>
<tr>
<th>patient</th>
<th>id</th>
</tr>
</thead>
<tbody>
<tr>
<td>time</td>
<td>time</td>
</tr>
<tr>
<td>status</td>
<td>event status</td>
</tr>
<tr>
<td>age</td>
<td>in years</td>
</tr>
<tr>
<td>sex</td>
<td>1=male, 2=female</td>
</tr>
<tr>
<td>disease</td>
<td>disease type (0=GN, 1=AN, 2=PKD, 3=Other)</td>
</tr>
<tr>
<td>frail</td>
<td>frailty estimate from original paper</td>
</tr>
</tbody>
</table>

Note

The original paper ignored the issue of tied times and so is not exactly reproduced by the survival package.

Source


Examples

```r
kfit <- coxph(Surv(time, status)~ age + sex + disease + frailty(id), kidney)
kfit0 <- coxph(Surv(time, status)~ age + sex + disease, kidney)
kfitm1 <- coxph(Surv(time, status) ~ age + sex + disease + frailty(id, dist='gauss'), kidney)
```
levels.Surv

Return the states of a multi-state Surv object

Description
For a multi-state Surv object, this will return the names of the states.

Usage
```r
## S3 method for class 'Surv'
levels(x)
```

Arguments
- `x`: a Surv object

Value
for a multi-state Surv object, the vector of state names (excluding censoring); or NULL for an ordinary Surv object

Examples
```r
y1 <- Surv(c(1, 5, 9, 17, 21, 30),
           factor(c(0, 1, 2, 1, 0, 2), 0:2, c("censored", "progression", "death")))
levels(y1)

y2 <- Surv(1:6, rep(0:1, 3))
y2
levels(y2)
```

lines.survfit

Add Lines or Points to a Survival Plot

Description
Often used to add the expected survival curve(s) to a Kaplan-Meier plot generated with `plot.survfit`.

Usage
```r
## S3 method for class 'survfit'
lines(x, type="s", pch=3, col=1, lty=1,
      lwd=1, cex=1, mark.time=FALSE,
      xscale=1, firstx=0, firsty=1, xmax, fun, conf.int=FALSE,
      conf.times, conf.cap=.005, conf.offset=.012, mark, ...)
## S3 method for class 'survexp'
```
```
lines(x, type="1", ...)  
## S3 method for class 'survfit'
points(x, xscale, xmax, fun, censor=FALSE, col=1, pch, ...)
```

### Arguments

- **x**: a survival object, generated from the `survfit` or `survexp` functions.
- **type**: the line type, as described in `lines`. The default is a step function for `survfit` objects, and a connected line for `survexp` objects. All other arguments for `lines.survexp` are identical to those for `lines.survfit`.
- **col, lty, lwd, cex**: vectors giving the mark symbol, color, line type, line width and character size for the added curves. Of this set only color is applicable to `points`.
- **pch**: plotting characters for points, in the style of `matplot`, i.e., either a single string of characters of which the first will be used for the first curve, etc; or a vector of characters or integers, one element per curve.
- **mark**: a historical alias for `pch`.
- **censor**: should censoring times be displayed for the `points` function?
- **xscale**: this parameter is no longer necessary and is ignored. See the note in `plot.survfit`.
- **firstx, firsty**: the starting point for the survival curves. If either of these is set to `NA` or `< blank >` the plot will start at the first time point of the curve.
- **xmax**: the maximum horizontal plot coordinate. This shortens the curve before plotting it, so unlike using the `xlim` graphical parameter, warning messages about out of bounds points are not generated.
- **fun**: an arbitrary function defining a transformation of the survival curve. For example `fun=log` is an alternative way to draw a log-survival curve (but with the axis labeled with log(S) values). Four often used transformations can be specified with a character argument instead: "log" is the same as using the `log=T` option, "event" plots cumulative events (f(y) = 1-y), "cumhaz" plots the cumulative hazard function (f(y) = -log(y)) and "cloglog" creates a complimentary log-log survival plot (f(y) = log(-log(y))) along with log scale for the x-axis.
- **conf.int**: if TRUE, confidence bands for the curves are also plotted. If set to "only", then only the CI bands are plotted, and the curve itself is left off. This can be useful for fine control over the colors or line types of a plot.
- **conf.times**: optional vector of times at which to place a confidence bar on the curve(s). If present, these will be used instead of confidence bands.
- **conf.cap**: width of the horizontal cap on top of the confidence bars; only used if `conf.times` is used. A value of 1 is the width of the plot region.
conf.offset the offset for confidence bars, when there are multiple curves on the plot. A value of 1 is the width of the plot region. If this is a single number then each curve’s bars are offset by this amount from the prior curve’s bars, if it is a vector the values are used directly.

Details

When the `survfit` function creates a multi-state survival curve the resulting object has class ‘survfitms’. The only difference in the plots is that that it defaults to a curve that goes from lower left to upper right (starting at 0), where survival curves default to starting at 1 and going down. All other options are identical.

Value

a list with components x and y, containing the coordinates of the last point on each of the curves (but not of the confidence limits). This may be useful for labeling.

Side Effects

one or more curves are added to the current plot.

See Also

`lines`, `par`, `plot.survfit`, `survfit`, `survexp`.

Examples

```r
fit <- survfit(Surv(time, status==2) ~ sex, pbc, subset=1:312)
plot(fit, mark.time=FALSE, xscale=365.25,
     xlab='Years', ylab='Survival')
lines(fit[1], lwd=2)  # darken the first curve and add marks

# Add expected survival curves for the two groups,
# based on the US census data
# The data set does not have entry date, use the midpoint of the study
efit <- survexp(~sex, data=pbc, times= (0:24)*182, ratetable=survexp.us,
                    rmap=list(sex=sex, age=age*365.35, year=as.Date('1979/01/01')))
temp <- lines(efit, lty=2, lwd=2:1)
text(temp, c("Male", "Female"), adj= -.1) # labels just past the ends
title(main="Primary Biliary Cirrhosis, Observed and Expected")
```
Description

Intergenerational occupational mobility data with covariates.

Usage

data(logan)

Format

A data frame with 838 observations on the following 4 variables.

- **occupation**: subject's occupation, a factor with levels farm, operatives, craftsmen, sales, and professional
- **focc**: father's occupation
- **education**: total years of schooling, 0 to 20
- **race**: levels of non-black and black

Source

General Social Survey data, see the web site for detailed information on the variables. [http://www3.norc.org/GSS+Website](http://www3.norc.org/GSS+Website).

References


---

**logLik.coxph**

*logLik method for a Cox model*

Description

The logLik function for survival models

Usage

```r
## S3 method for class 'coxph'
logLik(object, ...)
## S3 method for class 'survreg'
logLik(object, ...)
```
Arguments

object the result of a coxph or survreg fit

... optional arguments for other instances of the method

Details

The logLik function is used by summary functions in R such as AIC. For a Cox model, this method returns the partial likelihood. The number of degrees of freedom (df) used by the fit and the effective number of observations (nobs) are added as attributes. Per Raftery and others, the effective number of observations is the taken to be the number of events in the data set.

For a survreg model the proper value for the effective number of observations is still an open question (at least to this author). For right censored data the approach of logLik.coxph is the possible the most sensible, but for interval censored observations the result is unclear. The code currently does not add a nobs attribute.

Value

an object of class logLik

Author(s)

Terry Therneau

References


See Also

logLik

lung

NCCTG Lung Cancer Data

Description

Survival in patients with advanced lung cancer from the North Central Cancer Treatment Group. Performance scores rate how well the patient can perform usual daily activities.

Usage

lung cancer
lung

Format
Description

Natural history of 241 subjects with monoclonal gammopathy of undetermined significance (MGUS).

Usage

mgus
mgus1

Format

mgus: A data frame with 241 observations on the following 12 variables.

id: subject id
age: age in years at the detection of MGUS
sex: male or female
dxyr: year of diagnosis
pcdx: for subjects who progress to a plasma cell malignancy
the subtype of malignancy: multiple myeloma (MM) is the
most common, followed by amyloidosis (AM), macroglobulinemia (MA), and other lymphoproliferative disorders (LP)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pctime</td>
<td>days from MGUS until diagnosis of a plasma cell malignancy</td>
</tr>
<tr>
<td>futime</td>
<td>days from diagnosis to last follow-up</td>
</tr>
<tr>
<td>death</td>
<td>1= follow-up is until death</td>
</tr>
<tr>
<td>alb</td>
<td>albumin level at MGUS diagnosis</td>
</tr>
<tr>
<td>creat</td>
<td>creatinine at MGUS diagnosis</td>
</tr>
<tr>
<td>hgb</td>
<td>hemoglobin at MGUS diagnosis</td>
</tr>
<tr>
<td>mspike</td>
<td>size of the monoclonal protein spike at diagnosis</td>
</tr>
</tbody>
</table>

mgus1: The same data set in start,stop format. Contains the id, age, sex, and laboratory variable described above along with

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>start, stop</td>
<td>sequential intervals of time for each subject</td>
</tr>
<tr>
<td>status</td>
<td>=1 if the interval ends in an event</td>
</tr>
<tr>
<td>event</td>
<td>a factor containing the event type: censor, death, or plasma cell malignancy</td>
</tr>
<tr>
<td>enum</td>
<td>event number for each subject: 1 or 2</td>
</tr>
</tbody>
</table>

Details

Plasma cells are responsible for manufacturing immunoglobulins, an important part of the immune defense. At any given time there are estimated to be about $10^6$ different immunoglobulins in the circulation at any one time. When a patient has a plasma cell malignancy the distribution will become dominated by a single isotype, the product of the malignant clone, visible as a spike on a serum protein electrophoresis. Monoclonal gammopathy of underdetermined significance (MGUS) is the presence of such a spike, but in a patient with no evidence of overt malignancy. This data set of 241 sequential subjects at Mayo Clinic was the groundbreaking study defining the natural history of such subjects. Due to the diligence of the principle investigator 0 subjects have been lost to follow-up.

Three subjects had MGUS detected on the day of death. In data set mgus1 these subjects have the time to MGUS coded as .5 day before the death in order to avoid tied times.

These data sets were updated in Jan 2015 to correct some small errors.

Source

Mayo Clinic data courtesy of Dr. Robert Kyle.

References


Examples

```r
# Create the competing risk curves for time to first of death or PCM
sfit <- survfit(Surv(start, stop, event) ~ sex, mgus1, subset=(enum==1))
print(sfit)  # the order of printout is the order in which they plot
```
plot(sfit, xscale=365.25, lty=c(2,1,2,1), col=c(1,1,2,2),
xlab="Years after MGUS detection", ylab="Proportion")
legend(0, .8, c("Death/male", "Death/female", "PCM/male", "PCM/female"),
  lty=c(1,1,2,2), col=c(2,1,2,1), bty='n')
title("Curves for the first of plasma cell malignancy or death")
# The plot shows that males have a higher death rate than females (no
# surprise) but their rates of conversion to PCM are essentially the same.

---

### mgus2

#### Monoclonal gammopathy data

**Description**

Natural history of 1341 sequential patients with monoclonal gammopathy of undetermined significance (MGUS).

**Usage**

```r
data("mgus2")
```

**Format**

A data frame with 1384 observations on the following 10 variables.

- **id** subject identifier
- **age** age at diagnosis, in years
- **sex** a factor with levels F M
- **hgb** hemoglobin
- **creat** creatinine
- **mspike** size of the monoclonal serum spike
- **ptime** time until progression to a plasma cell malignancy (PCM) or last contact, in months
- **pstat** occurrence of PCM: 0=no, 1=yes
- **futime** time until death or last contact, in months
- **death** occurrence of death: 0=no, 1=yes

**Details**

This is a larger follow-on study of the condition also found in data set mgus.

**Source**

Mayo Clinic data courtesy of Dr. Robert Kyle. All patient identifiers have been removed, age rounded to the nearest year, and follow-up times rounded to the nearest month.
References


model.frame.coxph

Model.frame method for coxph objects

Description

Recreate the model frame of a coxph fit.

Usage

## S3 method for class 'coxph'
model.frame(formula, ...)

Arguments

formula the result of a coxph fit
... other arguments to model.frame

Details

For details, see the manual page for the generic function. This function would rarely be called by a user, it is mostly used inside functions like residual that need to recreate the data set from a model in order to do further calculations.

Value

the model frame used in the original fit, or a parallel one for new data.

Author(s)

Terry Therneau

See Also

model.frame
Description

Reconstruct the model matrix for a cox model.

Usage

### S3 method for class 'coxph'

model.matrix(object, data=NULL, contrast.arg =

object$contrasts, ...)

Arguments

- `object`: the result of a coxph model
- `data`: optional, a data frame from which to obtain the data
- `contrast.arg`: optional, a contrasts object describing how factors should be coded
- `...`: other possible argument to `model.frame`

Details

When there is a `data` argument this function differs from most of the other `model.matrix` methods in that the response variable for the original formula is not required to be in the data.

If the data frame contains a `terms` attribute then it is assumed to be the result of a call to `model.frame`, otherwise a call to `model.frame` is applied with the data as an argument.

Value

The model matrix for the fit

Author(s)

Terry Therneau

See Also

model.matrix

Examples

```r
fit1 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung)
xfit <- model.matrix(fit1)

fit2 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung, x=TRUE)
all.equal(model.matrix(fit1), fit2$x)
```
Description

This simulated data set is based on a trial in acute myeloid leukemia.

Format

A data frame with 646 observations on the following 9 variables.

- id: subject identifier, 1-646
- trt: treatment arm A or B
- futime: time to death or last follow-up
- death: 1 if futime is a death, 0 for censoring
- txtime: time to hematopoietic stem cell transplant
- crtime: time to complete response
- rltime: time to relapse of disease

Details

This data set is used to illustrate multi-state survival curves. The correlation between within-subject event times strongly resembles that from an actual trial, but none of the actual data values are from that source.

Examples

```r
coxph(Surv(futime, death) ~ trt, data=myeloid)
# See the mstate vignette for a more complete analysis
```

Description

Find the index of the closest value in data set 2, for each entry in data set one.

Usage

```r
neardate(id1, id2, y1, y2, best = c("after", "prior"),
nomatch = NA_integer_)
```
Arguments

id1 vector of subject identifiers for the index group
id2 vector of identifiers for the reference group
y1 normally a vector of dates for the index group, but any orderable data type is allowed
y2 reference set of dates
best if best='prior' find the index of the first y2 value less than or equal to the target y1 value, for each subject. If best='after' find the first y2 value which is greater than or equal to the target y1 value, for each subject.
nomatch the value to return for items without a match

Details

This routine is closely related to match and to findInterval, the first of which finds exact matches and the second closest matches. This finds the closest matching date within sets of exactly matching identifiers. Closest date matching is often needed in clinical studies. For example data set 1 might contain the subject identifier and the date of some procedure and data set 2 has the dates and values for laboratory tests, and the query is to find the first test value after the intervention but no closer than 7 days.

The id1 and id2 arguments are similar to match in that we are searching for instances of id1 that will be found in id2, and the result is the same length as id1. However, instead of returning the first match with idR this routine returns the one that best matches with respect to y1.

The y1 and y2 arguments need not be dates, the function works for any data type such that the expression cHy1L yRI gives a sensible, sortable result. Be careful about matching Date and DateTime values and the impact of time zones, however, see as.POSIXct. If y1 and y2 are not of the same class the user is on their own. Since there exist pairs of unmatched data types where the result could be sensible, the routine will in this case proceed under the assumption that "the user knows what they are doing". Caveat emptor.

Value

the index of the matching observations in the second data set, or the nomatch value for no successful match

Author(s)

Terry Therneau

See Also

match, findInterval

Examples

data1 <- data.frame(id = 1:10,
entry.dt = as.Date(paste("2011", 1:10, "5", sep='-')))
temp1 <- c(1,4,5,1,3,6,9, 2,7,8,12,4,6,7,10,12,3)
data2 <- data.frame(id = c(1,1,1,2,2,4,4,5,5,5,6,8,8,9,10,10,12),
    lab.dt = as.Date(paste("2011", templ, "1", sep='-')),
  chol = round(runif(17, 130, 280)))

#first cholesterol on or after enrollment
indx1 <- neardate(data1$id, data2$id, data1$entry.dt, data2$lab.dt)
data2_indx1, "chol"]

# Closest one, either before or after.
# indx2 <- neardate(data1$id, data2$id, data1$entry.dt, data2$lab.dt,
    best="prior")
ifelse(is.na(indx1), indx2, # none after, take before
    ifelse(is.na(indx2), indx1, #none before
        ifelse(abs(data2$lab.dt[indx2] - data1$entry.dt) <
            abs(data2$lab.dt[indx1] - data1$entry.dt), indx2, indx1)))

# closest date before or after, but no more than 21 days prior to index
indx2 <- ifelse(data1$entry.dt - data2$lab.dt[indx2] >21, NA, indx2)
ifelse(is.na(indx1), indx2, # none after, take before
    ifelse(is.na(indx2), indx1, #none before
        ifelse(abs(data2$lab.dt[indx2] - data1$entry.dt) <
            abs(data2$lab.dt[indx1] - data1$entry.dt), indx2, indx1)))

---

nwtco | Data from the National Wilm’s Tumor Study

**Description**

Measurement error example. Tumor histology predicts survival, but prediction is stronger with central lab histology than with the local institution determination.

**Usage**

nwtco

**Format**

A data frame with 4028 observations on the following 9 variables.

- **seqno**: id number
- **instit**: Histology from local institution
- **histol**: Histology from central lab
- **stage**: Disease stage
- **study**: study
- **rel**: indicator for relapse
- **edrel**: time to relapse
- **age**: age in months
- **in.subcohort**: Included in the subcohort for the example in the paper
### References


### Examples

```r
with(nwtco, table(instit,histol))
anova(coxph(Surv(edrel,rel)~histol+instit,data=nwtco))
anova(coxph(Surv(edrel,rel)~instit+histol,data=nwtco))
```

<table>
<thead>
<tr>
<th>ovarian</th>
<th>Ovarian Cancer Survival Data</th>
</tr>
</thead>
</table>

### Description

Survival in a randomised trial comparing two treatments for ovarian cancer

### Usage

```r
ovarian
```

### Format

- `futime`: survival or censoring time
- `fustat`: censoring status
- `age`: in years
- `resid.ds`: residual disease present (1=no,2=yes)
- `rx`: treatment group
- `ecog.ps`: ECOG performance status (1 is better, see reference)

### Source

Terry Therneau

### References

Description

This data is from the Mayo Clinic trial in primary biliary cirrhosis (PBC) of the liver conducted between 1974 and 1984. A total of 424 PBC patients, referred to Mayo Clinic during that ten-year interval, met eligibility criteria for the randomized placebo controlled trial of the drug D-penicillamine. The first 312 cases in the data set participated in the randomized trial and contain largely complete data. The additional 112 cases did not participate in the clinical trial, but consented to have basic measurements recorded and to be followed for survival. Six of those cases were lost to follow-up shortly after diagnosis, so the data here are on an additional 106 cases as well as the 312 randomized participants.

A nearly identical data set found in appendix D of Fleming and Harrington; this version has fewer missing values.

Usage

Format

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>age</td>
<td>in years</td>
</tr>
<tr>
<td>albumin</td>
<td>serum albumin (g/dl)</td>
</tr>
<tr>
<td>alk.phos</td>
<td>alkaline phosphotase (U/liter)</td>
</tr>
<tr>
<td>ascites</td>
<td>presence of ascites</td>
</tr>
<tr>
<td>ast</td>
<td>aspartate aminotransferase, once called SGOT (U/ml)</td>
</tr>
<tr>
<td>bili</td>
<td>serum bilirubin (mg/dl)</td>
</tr>
<tr>
<td>chol</td>
<td>serum cholesterol (mg/dl)</td>
</tr>
<tr>
<td>copper</td>
<td>urine copper (ug/day)</td>
</tr>
<tr>
<td>edema</td>
<td>0 no edema, 0.5 untreated or successfully treated, 1 edema despite diuretic therapy</td>
</tr>
<tr>
<td>hepato</td>
<td>presence of hepatomegaly or enlarged liver</td>
</tr>
<tr>
<td>id</td>
<td>case number</td>
</tr>
<tr>
<td>platelet</td>
<td>platelet count</td>
</tr>
<tr>
<td>protime</td>
<td>standardised blood clotting time</td>
</tr>
<tr>
<td>sex</td>
<td>m/f</td>
</tr>
<tr>
<td>spiders</td>
<td>blood vessel malformations in the skin</td>
</tr>
<tr>
<td>stage</td>
<td>histologic stage of disease (needs biopsy)</td>
</tr>
<tr>
<td>status</td>
<td>status at endpoint, 0/1/2 for censored, transplant, dead</td>
</tr>
<tr>
<td>time</td>
<td>number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986</td>
</tr>
<tr>
<td>trt</td>
<td>1/2/NA for D-penicillmain, placebo, not randomised</td>
</tr>
<tr>
<td>trig</td>
<td>triglycerides (mg/dl)</td>
</tr>
</tbody>
</table>
Source


See Also

pbcseq

---

**pbcseq**

*Mayo Clinic Primary Biliary Cirrhosis, sequential data*

### Description

This data is a continuation of the PBC data set, and contains the follow-up laboratory data for each study patient. An analysis based on the data can be found in Murtagh, et. al.

The primary PBC data set contains only baseline measurements of the laboratory parameters. This data set contains multiple laboratory results, but only on the 312 randomized patients. Some baseline data values in this file differ from the original PBC file, for instance, the data errors in prothrombin time and age which were discovered after the original analysis (see Fleming and Harrington, figure 4.6.7).

One "feature" of the data deserves special comment. The last observation before death or liver transplant often has many more missing covariates than other data rows. The original clinical protocol for these patients specified visits at 6 months, 1 year, and annually thereafter. At these protocol visits lab values were obtained for a large pre-specified battery of tests. "Extra" visits, often undertaken because of worsening medical condition, did not necessarily have all this lab work. The missing values are thus potentially informative.

### Usage

pbc

### Format

- **id**: case number
- **age**: in years
- **sex**: m/f
- **trt**: 1/2/NA for D-penicillmain, placebo, not randomised
- **time**: number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986
- **status**: status at endpoint, 0/1/2 for censored, transplant, dead
- **day**: number of days between enrollment and this visit date
- **albumin**: serum albumin (mg/dl)
- **alk.phos**: alkaline phosphatase (U/liter)
ascites: presence of ascites
ast: aspartate aminotransferase, once called SGOT (U/ml)
bili: serum bilirubin (mg/dl)
chol: serum cholesterol (mg/dl)
copper: urine copper (ug/day)
edema: 0 no edema, 0.5 untreated or successfully treated
head: 1 edema despite diuretic therapy
hepato: presence of hepatomegaly or enlarged liver
platelet: platelet count
protime: standardised blood clotting time
spiders: blood vessel malformations in the skin
stage: histologic stage of disease (needs biopsy)
trig: triglycerides (mg/dl)

Source


References


See Also

pbc

Examples

# Create the start-stop-event triplet needed for coxph
first <- with(pbcseq, c(TRUE, diff(id) != 0)) # first id for each subject
last <- c(first[-1], TRUE) # last id

time1 <- with(pbcseq, ifelse(first, 0, day))
time2 <- with(pbcseq, ifelse(last, futime, c(day[-1], 0)))
event <- with(pbcseq, ifelse(last, status, 0))

fit1 <- coxph(Surv(time1, time2, event) ~ age + sex + log(bili), pbcseq)
**Description**

Plot the estimated coefficient function(s) from a fit of Aalen’s additive regression model.

**Usage**

```r
## S3 method for class 'aareg'
plot(x, se=TRUE, maxtime, type='s', ...)```

**Arguments**

- `x`  
  the result of a call to the `aareg` function
- `se`  
  if TRUE, standard error bands are included on the plot
- `maxtime`  
  upper limit for the x-axis.
- `type`  
  graphical parameter for the type of line, default is "steps".
- `...`  
  other graphical parameters such as line type, color, or axis labels.

**Side Effects**

A plot is produced on the current graphical device.

**References**


**See Also**

`aareg`

---

**Description**

Displays a graph of the scaled Schoenfeld residuals, along with a smooth curve.

**Usage**

```r
## S3 method for class 'cox.zph'
plot(x, resid=TRUE, se=TRUE, df=4, nsmo=40, var,
     xlab="Time", ylab, lty=1:2, col=1, lwd=1, ...)```
Arguments

- **x**: result of the `cox.zph` function.
- **resid**: a logical value, if TRUE the residuals are included on the plot, as well as the smooth fit.
- **se**: a logical value, if TRUE, confidence bands at two standard errors will be added.
- **df**: the degrees of freedom for the fitted natural spline, df=2 leads to a linear fit.
- **nsmo**: number of points to use for the lines
- **var**: the set of variables for which plots are desired. By default, plots are produced in turn for each variable of a model. Selection of a single variable allows other features to be added to the plot, e.g., a horizontal line at zero or a main title. This has been superseded by a subscripting method; see the example below.
- **xlab**: label for the x-axis of the plot
- **ylab**: optional label for the y-axis of the plot. If missing a default label is provided. This can be a vector of labels.
- **lty, col, lwd**: line type, color, and line width for the overlaid curve. Each of these can be a vector of length 2, in which case the second element is used for the confidence interval.
- **...**: additional graphical arguments passed to the `plot` function.

Side Effects

a plot is produced on the current graphics device.

See Also

- `coxph`, `cox.zph`.

Examples

```r
vfit <- coxph(Surv(time, status) ~ trt + factor(celltype) + karno + age, data=veteran, x=TRUE)
temp <- cox.zph(vfit)
plot(temp, var=5)  # Look at Karnofsy score, old way of doing plot
plot(temp[,5])     # New way with subscripting
abline(0, 0, lty=3)  # Add the linear fit as well
abline(lm(temp$var[5] - temp$x)$coefficients, lty=4, col=3)
title(main="VA Lung Study")
```
plot.survfit

Plot method for survfit objects

Description

A plot of survival curves is produced, one curve for each strata. The log=T option does extra work to avoid log(0), and to try to create a pleasing result. If there are zeros, they are plotted by default at 0.8 times the smallest non-zero value on the curve(s).

Curves are plotted in the same order as they are listed by print (which gives a 1 line summary of each). This will be the order in which col, lty, etc are used.

Usage

```r
## S3 method for class 'survfit'
plot(x, conf.int=, mark.time=FALSE,
    pch=3, col=1, lty=1, lwd=1, cex=1, log=FALSE, xscale=1, yscale=1,
    firstx=0, firsty=1, xmax, ymin=0, fun,
    xlab=", ylab="", xaxs="S", conf.times, conf.cap=.005,
    conf.offset=.012, mark, ...)
```

Arguments

- `x`: an object of class survfit, usually returned by the survfit function.
- `conf.int`: determines whether confidence intervals will be plotted. The default is to do so if there is only 1 curve, i.e., no strata.
- `mark.time`: controls the labeling of the curves. If set to FALSE, no labeling is done. If TRUE, then curves are marked at each censoring time. If mark is a numeric vector then curves are marked at the specified time points.
- `pch`: vector of characters which will be used to label the curves. The points help file contains examples of the possible marks. A single string such as "abcd" is treated as a vector c("a", "b", "c", "d"). The vector is reused cyclically if it is shorter than the number of curves. If it is present this implies mark.time = TRUE.
- `col`: a vector of integers specifying colors for each curve. The default value is 1.
- `lty`: a vector of integers specifying line types for each curve. The default value is 1.
- `lwd`: a vector of numeric values for line widths. The default value is 1.
- `cex`: a numeric value specifying the size of the marks. This is not treated as a vector; all marks have the same size.
- `log`: a logical value, if TRUE the y axis will be on a log scale. Alternately, one of the standard character strings "x", "y", or "xy" can be given to specific logarithmic horizontal and/or vertical axes.
- `yscale`: a numeric value used to multiply the labels on the y axis. A value of 100, for instance, would be used to give a percent scale. Only the labels are changed, not the actual plot coordinates, so that adding a curve with "lines(surv.exp(...))", say, will perform as it did without the yscale argument.
xscale  a numeric value used like yscale for labels on the x axis. A value of 365.25 will give labels in years instead of the original days.

firstx, firsty  the starting point for the survival curves. If either of these is set to NA the plot will start at the first time point of the curve. By default, the plot program obeys tradition by having the plot start at (0,0).

If start.time argument is used in survfit, firstx is set to that value.

xmax  the maximum horizontal plot coordinate. This can be used to shrink the range of a plot. It shortens the curve before plotting it, so that unlike using the xlim graphical parameter, warning messages about out of bounds points are not generated.

ymin  lower boundary for y values. Survival curves are most often drawn in the range of 0-1, even if none of the curves approach zero. The parameter is ignored if the fun argument is present, or if it has been set to NA.

fun  an arbitrary function defining a transformation of the survival curve. For example fun=log is an alternative way to draw a log-survival curve (but with the axis labeled with log(S) values), and fun=sqrt would generate a curve on square root scale. Five often used transformations can be specified with a character argument instead: "S" gives the usual survival curve, "log" is the same as using the log=T option, "event" or "F" plots the empirical CDF \( F(t) = 1 - S(t) \) (\( f(y) = 1-y \)), "cumhaz" plots the cumulative hazard function (\( f(y) = -\log(y) \)), and "cloglog" creates a complimentary log-log survival plot (\( f(y) = \log(-\log(y)) \) along with log scale for the x-axis). The terms "identity" and "surv" are allowed as synonyms for type="S".

xlab  label given to the x-axis.

ylab  label given to the y-axis.

xaxs  either "S" for a survival curve or a standard x axis style as listed in par. Survival curves are usually displayed with the curve touching the y-axis, but not touching the bounding box of the plot on the other 3 sides. Type "S" accomplishes this by manipulating the plot range and then using the "i" style internally.

conf.times  optional vector of times at which to place a confidence bar on the curve(s). If present, these will be used instead of confidence bands.

conf.cap  width of the horizontal cap on top of the confidence bars; only used if conf.times is used. A value of 1 is the width of the plot region.

conf.offset  the offset for confidence bars, when there are multiple curves on the plot. A value of 1 is the width of the plot region. If this is a single number then each curve's bars are offset by this amount from the prior curve's bars, if it is a vector the values are used directly.

mark  a historical alias for pch

...  for future methods

Details

When the survfit function creates a multi-state survival curve the resulting object also has class ‘survfitms’. Competing risk curves are a common case. The only difference in the plots is that
multi-state defaults to a curve that goes from lower left to upper right (starting at 0), where survival
curves by default start at 1 and go down. All other options are identical.
When the conf.times argument is used, the confidence bars are offset by conf.offset units to
avoid overlap. The bar on each curve are the confidence interval for the time point at which the bar
is drawn, i.e., different time points for each curve. If curves are steep at that point, the visual impact
can sometimes substantially differ for positive and negative values of conf.offset.

Value

A list with components x and y, containing the coordinates of the last point on each of the curves
(but not the confidence limits). This may be useful for labeling.

Note

In prior versions the behavior of xscale and yscale differed: the first changed the scale both for
the plot and for all subsequent actions such as adding a legend, whereas yscale affected only the
axis label. This was normalized in version 2-36.4, and both parameters now only affect the labeling.

See Also

points.survfit, lines.survfit, par, survfit

Examples

leukemia.surv <- survfit(Surv(time, status) ~ x, data = aml)
plot(leukemia.surv, lty = 2:3)
legend(100, .9, c("Maintenance", "No Maintenance"), lty = 2:3)
title("Kaplan-Meier Curves\nfor AML Maintenance Study")
lsurv2 <- survfit(Surv(time, status) ~ x, aml, type='fleming')
plot(lsurv2, lty=2:3, fun="cumhaz",
xlab="Months", ylab="Cumulative Hazard")

predict.coxph

Predictions for a Cox model

Description

Compute fitted values and regression terms for a model fitted by coxph

Usage

# S3 method for class 'coxph'
predict(object, newdata,
type=c("lp", "risk", "expected", "terms", "survival"),
se.fit=FALSE, na.action=na.pass, terms=names(object$assign), collapse,
reference=c("strata", "sample"), ...)
Arguments

object: the results of a coxph fit.
newdata: Optional new data at which to do predictions. If absent predictions are for the
data frame used in the original fit. When coxph has been called with a formula
argument created in another context, i.e., coxph has been called within another
function and the formula was passed as an argument to that function, there can
be problems finding the data set. See the note below.
type: the type of predicted value. Choices are the linear predictor ("lp"), the risk
score exp(lp) ("risk"), the expected number of events given the covariates and
follow-up time ("expected"), and the terms of the linear predictor ("terms").
The survival probability for a subject is equal to exp(-expected).
se.fit: if TRUE, pointwise standard errors are produced for the predictions.
na.action: applies only when the newdata argument is present, and defines the missing
value action for the new data. The default is to include all observations. When
there is no newdata, then the behavior of missing is dictated by the na.action
option of the original fit.
terms: if type="terms", this argument can be used to specify which terms should be
included; the default is all.
collapse: optional vector of subject identifiers. If specified, the output will contain one
entry per subject rather than one entry per observation.
reference: reference for centering predictions, see details below
...: For future methods

Details

The Cox model is a relative risk model; predictions of type "linear predictor", "risk", and "terms"
are all relative to the sample from which they came. By default, the reference value for each of
these is the mean covariate within strata. The primary underlying reason is statistical: a Cox model
only predicts relative risks between pairs of subjects within the same strata, and hence the addition
of a constant to any covariate, either overall or only within a particular stratum, has no effect on
the fitted results. Using the reference="strata" option causes this to be true for predictions as
well. (There have been occasional requests for reference="zero", i.e., a hypothetical subject with
all covariates equal to zero, in order to match certain other packages' results. The issue is that the
results are often silly, e.g., risk relative to a subject with height, weight, or blood pressure of zero.)

When the results of predict are used in further calculations it may be desirable to use a fixed
reference level. Use of reference="sample" will use the overall means, and agrees with the
linear.predictors component of the coxph object (which uses the overall mean for backwards
compatibility with older code). Predictions of type="terms" are almost invariably passed forward
to further calculation, so for these we default to using the sample as the reference.

Predictions of type "expected" incorporate the baseline hazard and are thus absolute instead of
relative; the reference option has no effect on these. These values depend on the follow-up time
for the future subjects as well as covariates so the newdata argument needs to include both the right
and left hand side variables from the formula. (The status variable will not be used, but is required
since the underlying code needs to reconstruct the entire formula.)

Models that contain a frailty term are a special case: due to the technical difficulty, when there is
a newdata argument the predictions will always be for a random effect of zero.
Value

A vector or matrix of predictions, or a list containing the predictions (element "fit") and their standard errors (element "se.fit") if the se.fit option is TRUE.

Note

Some predictions can be obtained directly from the coxph object, and for others it is necessary for the routine to have the entirety of the original data set, e.g., for type = terms or if standard errors are requested. This extra information is saved in the coxph object if model=TRUE, if not the original data is reconstructed. If it is known that such residuals will be required overall execution will be slightly faster if the model information is saved.

In some cases the reconstruction can fail. The most common is when coxph has been called inside another function and the formula was passed as one of the arguments to that enclosing function. Another is when the data set has changed between the original call and the time of the prediction call. In each of these the simple solution is to add model=TRUE to the original coxph call.

See Also

predict.coxph, termplot

Examples

```r
options(na.action=na.exclude) # retain NA in predictions
fit <- coxph(Surv(time, status) ~ age + ph.ecog + strata(inst), lung)
#lung data set has status coded as 1/2
mresid <- (lung$status-1) - predict(fit, type='expected') #Martingale resid
predict(fit,type="lp")
predict(fit,type="expected")
predict(fit,type="risk",se.fit=TRUE)
predict(fit,type="terms",se.fit=TRUE)

# For someone who demands reference='zero'
pzero <- function(fit)
  predict(fit, reference="sample") + sum(coef(fit) * fit$means, na.rm=TRUE)
```

---

**predict.survreg**

**Predicted Values for a 'survreg' Object**

**Description**

Predicted values for a survreg object

**Usage**

```r
## S3 method for class 'survreg'
predict(object, newdata, type=c("response", "link", "lp", "linear", "terms", "quantile", "uquantile"), se.fit=FALSE, terms=NULL, p=c(0.1, 0.9), na.action=na.pass, ...)
```
Arguments

- `object`: result of a model fit using the `survreg` function.
- `newdata`: data for prediction. If absent predictions are for the subjects used in the original fit.
- `type`: the type of predicted value. This can be on the original scale of the data (response), the linear predictor ("linear", with "lp" as an allowed abbreviation), a predicted quantile on the original scale of the data ("quantile"), a quantile on the linear predictor scale ("quantile"), or the matrix of terms for the linear predictor ("terms"). At this time "link" and linear predictor ("lp") are identical.
- `se.fit`: if TRUE, include the standard errors of the prediction in the result.
- `terms`: subset of terms. The default for residual type "terms" is a matrix with one column for every term (excluding the intercept) in the model.
- `p`: vector of percentiles. This is used only for quantile predictions.
- `na.action`: applies only when the `newdata` argument is present, and defines the missing value action for the new data. The default is to include all observations.
- ... for future methods

Value

a vector or matrix of predicted values.

References


See Also

`survreg`, `residuals.survreg`

Examples

```r
# Draw figure 1 from Escobar and Meeker, 1992.
fit <- survreg(Surv(time, status) ~ age + I(age^2), data=stanford2, dist='lognormal')
with(stanford2, plot(age, time, xlab='Age', ylab='Days',
xlim=c(0,65), ylim=c(.1, 10^5), log='y', type='n'))
with(stanford2, points(age, time, pch=c(2,4)[status+1], cex=.7))
pred <- predict(fit, newdata=list(age=1:65), type='quantile',
               p=c(.1, .5, .9))
matlines(1:65, pred, lty=c(2,1,2), col=1)

# Predicted Weibull survival curve for a lung cancer subject with
# ECOG score of 2
lfit <- survreg(Surv(time, status) ~ ph.ecog, data=lung)
pct <- 1:98/100  # The 100th percentile of predicted survival is at +infinity
ptime <- predict(lfit, newdata=data.frame(ph.ecog=2), type='quantile',
```
print.aareg

p=pct, se=TRUE)
matplot(cbind(ptime$fit, ptime$fit + 2*ptime$se.fit,
ptime$fit - 2*ptime$se.fit)/30.5, 1-pct,
           xlab="Months", ylab="Survival", type='l', lty=c(1,2,2), col=1)

print.aareg

Print an aareg object

Description
Print out a fit of Aalen’s additive regression model

Usage
## S3 method for class 'aareg'
print(x, maxtime, test=c("aalen", "nrisk"),scale=1,...)

Arguments
x
the result of a call to the aareg function
maxtime
the upper time point to be used in the test for non-zero slope
test
the weighting to be used in the test for non-zero slope. The default weights are
based on the variance of each coefficient, as a function of time. The alternative
weight is proportional to the number of subjects still at risk at each time point.
scale
scales the coefficients. For some data sets, the coefficients of the Aalen model
will be very small (10^-4); this simply multiplies the printed values by a constant,
say 1e6, to make the printout easier to read.
... for future methods

Details
The estimated increments in the coefficient estimates can become quite unstable near the end of
follow-up, due to the small number of observations still at risk in a data set. Thus, the test for slope
will sometimes be more powerful if this last ‘tail’ is excluded.

Value
the calling argument is returned.

Side Effects
the results of the fit are displayed.

References
8:907-925.
print.summary.coxph

See Also

aareg

print.summary.coxph  Print method for summary.coxph objects

Description

Produces a printed summary of a fitted coxph model

Usage

## S3 method for class 'summary.coxph'
print(x, digits=max(getOption("digits") - 3, 3),
      signif.stars = getOption("show.signif.stars"), ...)

Arguments

  x             the result of a call to summary.coxph
  digits        significant digits to print
  signif.stars  Show stars to highlight small p-values
  ...           For future methods

print.summary.survexp  Print Survexp Summary

Description

Prints the results of summary.survexp

Usage

## S3 method for class 'summary.survexp'
print(x, digits = max(options()$digits - 4, 3), ...)

Arguments

  x               an object of class summary.survexp.
  digits          the number of digits to use in printing the result.
  ...             For future methods

Value

  x, with the invisible flag set to prevent further printing.
Author(s)

Terry Therneau

See Also

link{summary.survexp}, survexp

print.summary.survfit  Print Survfit Summary

Description

Prints the result of summary.survfit.

Usage

```r
## S3 method for class 'summary.survfit'
print(x, digits = max(options()$digits-4, 3), ...)
```

Arguments

- `x`: an object of class "summary.survfit", which is the result of the summary.survfit function.
- `digits`: the number of digits to use in printing the numbers.
- `...`: for future methods

Value

`x`, with the invisible flag set to prevent printing.

Side Effects

prints the summary created by summary.survfit.

See Also

options.print.summary.survfit.
print.survfit

Print a Short Summary of a Survival Curve

Description

Print number of observations, number of events, the restricted mean survival and its standard error, and the median survival with confidence limits for the median.

Usage

```r
## S3 method for class 'survfit'
print(x, scale=1, digits = max(options()$digits - 4, 3),
     print.rmean=getOption("survfit.print.rmean"),
     rmean = getOption('survfit.rmean'),...)
```

Arguments

- `x` the result of a call to the `survfit` function.
- `scale` a numeric value to rescale the survival time, e.g., if the input data to `survfit` were in days, `scale=365` would scale the printout to years.
- `digits` Number of digits to print
- `print.rmean,rmean` Options for computation and display of the restricted mean.
- `...` for future results

Details

The mean and its variance are based on a truncated estimator. That is, if the last observation(s) is not a death, then the survival curve estimate does not go to zero and the mean is undefined. There are four possible approaches to resolve this, which are selected by the `rmean` option. The first is to set the upper limit to a constant, e.g., `rmean=365`. In this case the reported mean would be the expected number of days, out of the first 365, that would be experienced by each group. This is useful if interest focuses on a fixed period. Other options are "none" (no estimate), "common" and "individual". The "common" option uses the maximum time for all curves in the object as a common upper limit for the auc calculation. For the "individual" options the mean is computed as the area under each curve, over the range from 0 to the maximum observed time for that curve. Since the end point is random, values for different curves are not comparable and the printed standard errors are an underestimate as they do not take into account this random variation. This option is provided mainly for backwards compatibility, as this estimate was the default (only) one in earlier releases of the code. Note that SAS (as of version 9.3) uses the integral up to the last event time of each individual curve; we consider this the worst of the choices and do not provide an option for that calculation.

The median and its confidence interval are defined by drawing a horizontal line at 0.5 on the plot of the survival curve and its confidence bands. The intersection of the line with the lower CI band defines the lower limit for the median’s interval, and similarly for the upper band. If any of the intersections is not a point the we use the center of the intersection interval, e.g., if the survival
curve were exactly equal to 0.5 over an interval. When data is uncensored this agrees with the usual definition of a median.

Value

x, with the invisible flag set to prevent printing. (The default for all print functions in R is to return the object passed to them; print.survfit complies with this pattern. If you want to capture these printed results for further processing, see the table component of summary.survfit.)

Side Effects

The number of observations, the number of events, the median survival with its confidence interval, and optionally the restricted mean survival (rmean) and its standard error, are printed. If there are multiple curves, there is one line of output for each.

References


See Also

summary.survfit, quantile.survfit

---

pspline

Smoothing splines using a pspline basis

Description

Specifies a penalised spline basis for the predictor. This is done by fitting a comparatively small set of splines and penalising the integrated second derivative. Traditional smoothing splines use one basis per observation, but several authors have pointed out that the final results of the fit are indistinguishable for any number of basis functions greater than about 2-3 times the degrees of freedom. Eilers and Marx point out that if the basis functions are evenly spaced, this leads to significant computational simplification, they refer to the result as a p-spline.

Usage

pspline(x, df=4, theta, nterm=2.5 * df, degree=3, eps=0.1, method, Boundary.knots=range(x), intercept=FALSE, penalty=TRUE, combine, ...)

psplineinverse(x)
Arguments

x for psline: a covariate vector. The function does not apply to factor variables. For psplineinverse x will be the result of a pspline call.
df the desired degrees of freedom. One of the arguments df or theta’ must be given, but not both. If df=0, then the AIC = (loglik -df) is used to choose an "optimal" degrees of freedom. If AIC is chosen, then an optional argument ‘caic=T’ can be used to specify the corrected AIC of Hurvich et. al.
theta roughness penalty for the fit. It is a monotone function of the degrees of freedom, with theta=1 corresponding to a linear fit and theta=0 to an unconstrained fit of nterm degrees of freedom.
nterm number of splines in the basis
degree degree of splines
esps accuracy for df
method the method for choosing the tuning parameter theta. If theta is given, then 'fixed' is assumed. If the degrees of freedom is given, then 'df' is assumed. If method='aic' then the degrees of freedom is chosen automatically using Akaike's information criterion.
... optional arguments to the control function
Boundary.knots the spline is linear beyond the boundary knots. These default to the range of the data.
intercept if TRUE, the basis functions include the intercept.
penalty if FALSE a large number of attributes having to do with penalized fits are excluded. This is useful to create a pspline basis matrix for other uses.
combine an optional vector of increasing integers. If two adjacent values of combine are equal, then the corresponding coefficients of the fit are forced to be equal. This is useful for monotone fits, see the vignette for more details.

Value

Object of class pspline, coxph.penalty containing the spline basis, with the appropriate attributes to be recognized as a penalized term by the coxph or survreg functions.

For psplineinverse the original x vector is reconstructed.

References


See Also

coxph,survreg,ridge,frailty
Examples

```r
lfit6 <- survreg(Surv(time, status)-pspline(age, df=2), cancer)
plot(cancer$age, predict(lfit6), xlab='Age', ylab="Spline prediction")
title("Cancer Data")
fit0 <- coxph(Surv(time, status) ~ ph.ecog + age, cancer)
fit1 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,3), cancer)
fit3 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,8), cancer)
```

```
pyears | Person Years
-------|---------------------

Description

This function computes the person-years of follow-up time contributed by a cohort of subjects, stratified into subgroups. It also computes the number of subjects who contribute to each cell of the output table, and optionally the number of events and/or expected number of events in each cell.

Usage

```
pyears(formula, data, weights, subset, na.action, rmap,
      ratetable, scale=365.25, expect=c('event', 'pyears'),
      model=FALSE, x=FALSE, y=FALSE, data.frame=FALSE)
```

Arguments

- **formula**: a formula object. The response variable will be a vector of follow-up times for each subject, or a Surv object containing the survival time and an event indicator. The predictors consist of optional grouping variables separated by + operators (exactly as in survfit), time-dependent grouping variables such as age (specified with tcut), and optionally a ratetable term. This latter matches each subject to his/her expected cohort.
- **data**: a data frame in which to interpret the variables named in the formula, or in the subset and the weights argument.
- **weights**: case weights.
- **subset**: expression saying that only a subset of the rows of the data should be used in the fit.
- **na.action**: a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()$na.action.
- **rmap**: an optional list that maps data set names to the ratetable names. See the details section below.
- **ratetable**: a table of event rates, such as survexp.uswhite.
- **scale**: a scaling for the results. As most rate tables are in units/day, the default value of 365.25 causes the output to be reported in years.
should the output table include the expected number of events, or the expected
number of person-years of observation. This is only valid with a rate table.

If any of these is true, then the model frame, the model matrix, and/or the vector
of response times will be returned as components of the final result.

Details

Because `pyears` may have several time variables, it is necessary that all of them be in the same
units. For instance, in the call

```r
py <- pyears(futime ~ rx, rmap=list(age=age, sex=sex, year=entry.dt),
             ratetable=survexp.us)
```

the natural unit of the ratetable is hazard per day, it is important that `futime`, `age` and `entry.dt` all
be in days. Given the wide range of possible inputs, it is difficult for the routine to do sanity checks
of this aspect.

The ratetable being used may have different variable names than the user’s data set, this is dealt
with by the `rmap` argument. The rate table for the above calculation was `survexp.us`, a call to
`summary(survexp.us)` reveals that it expects to have variables `age = age in days, sex, and year` =
the date of study entry, we create them in the `rmap` line. The `sex` variable is not mapped, therefore
the code assumes that it exists in `mydata` in the correct format. (Note: for factors such as sex, the
program will match on any unique abbreviation, ignoring case.)

A special function `tcut` is needed to specify time-dependent cutpoints. For instance, assume that
age is in years, and that the desired final arrays have as one of their margins the age groups 0-2, 2-10,
10-25, and 25+. A subject who enters the study at age 4 and remains under observation for 10 years
will contribute follow-up time to both the 2-10 and 10-25 subsets. If `cut(age, c(0, 2, 10, 25, 100))`
were used in the formula, the subject would be classified according to his starting age only. The
`tcut` function has the same arguments as `cut`, but produces a different output object which allows
the `pyears` function to correctly track the subject.

The results of `pyears` are normally used as input to further calculations. The `print` routine, there-
fore, is designed to give only a summary of the table.

Value

a list with components:

- `pyears` an array containing the person-years of exposure. (Or other units, depending
  on the rate table and the scale). The dimension and dimnames of the array
  correspond to the variables on the right hand side of the model equation.
- `n` an array containing the number of subjects who contribute time to each cell of
  the `pyears` array.
- `event` an array containing the observed number of events. This will be present only if
  the response variable is a `Surv` object.
- `expected` an array containing the expected number of events (or person years if `expect ="pyears")`. This will be present only if there was a `ratetable` term.
if the data.frame option was set, a data frame containing the variables n, event, pyears and event that supplants the four arrays listed above, along with variables corresponding to each dimension. There will be one row for each cell in the arrays.

offtable the number of person-years of exposure in the cohort that was not part of any cell in the pyears array. This is often useful as an error check; if there is a mismatch of units between two variables, nearly all the person years may be off table.

tcut whether the call included any time-dependent cutpoints.

summary a summary of the rate-table matching. This is also useful as an error check.

call an image of the call to the function.

observations the number of observations in the input data set, after any missings were removed.

na.action the na.action attribute contributed by an na.action routine, if any.

See Also
ratetable, survexp, Surv.

Examples

# Look at progression rates jointly by calendar date and age
#
temp.yr <- tcut(mgus$dxyr, 55:92, labels=as.character(55:91))
temp.age <- tcut(mgus$age, 34:101, labels=as.character(34:100))
ptime <- ifelse(is.na(mgus$pctime), mgus$futime, mgus$pctime)
pstat <- ifelse(is.na(mgus$pctime), 0, 1)
pfit <- pyears(Surv(ptime/365.25, pstat) - temp.yr + temp.age + sex, mgus,
data.frame=TRUE)

# Turn the factor back into numerics for regression
tdata <- pfit$data
tdata$age <- as.numeric(as.character(tdata$temp.age))
tdata$year<- as.numeric(as.character(tdata$temp.yr))
fit1 <- glm(event ~ year + age + sex + offset(log(pyears)),
data=tdata, family=poisson)

## Not run:
# fit a gam model

gfit.m <- gam(y ~ s(age) + s(year) + offset(log(time)),
             family = poisson, data = tdata)

## End(Not run)

# Example #2 Create the hearta data frame:
hearta <- by(heart, heart$id,
        function(x)x[x$stop == max(x$stop),])

hearta <- do.call("rbind", hearta)
# Produce pyears table of death rates on the surgical arm
# The first is by age at randomization, the second by current age

fit1 <- pyears(Surv(stop/365.25, event) ~ cut(age + 48, c(0,50,60,70,100)) + surgery, data = hearta, scale = 1)
quantile.survfit

Quantiles from a survfit object

Description

Retrieve quantiles and confidence intervals for them from a survfit object.

Usage

## S3 method for class 'survfit'
quantile(x, probs = c(0.25, 0.5, 0.75), conf.int = TRUE,
          tolerance = sqrt(.Machine$double.eps), ...)

## S3 method for class 'survfitms'
quantile(x, probs = c(0.25, 0.5, 0.75), conf.int = TRUE,
          tolerance = sqrt(.Machine$double.eps), ...)

Arguments

- **x**: a result of the survfit function
- **probs**: numeric vector of probabilities with values in [0,1]
- **conf.int**: should lower and upper confidence limits be returned?
- **tolerance**: tolerance for checking that the survival curve exactly equals one of the quantiles
- ... optional arguments for other methods

Details

The kth quantile for a survival curve $S(t)$ is the location at which a horizontal line at height $p = 1-k$ intersects the plot of $S(t)$. Since $S(t)$ is a step function, it is possible for the curve to have a horizontal segment at exactly 1-k, in which case the midpoint of the horizontal segment is returned. This mirrors the standard behavior of the median when data is uncensored. If the survival curve does not fall to 1-k, then that quantile is undefined.

In order to be consistent with other quantile functions, the argument prob of this function applies to the cumulative distribution function $F(t) = 1 - S(t)$.

Confidence limits for the values are based on the intersection of the horizontal line at 1-k with the upper and lower limits for the survival curve. Hence confidence limits use the same p-value as was in effect when the curve was created, and will differ depending on the conf.type option of survfit. If the survival curves have no confidence bands, confidence limits for the quantiles are not available.

When a horizontal segment of the survival curve exactly matches one of the requested quantiles the returned value will be the midpoint of the horizontal segment; this agrees with the usual definition

```r
fit2 <- pyears(Surv(stop/365.25, event) ~ tcut(age + 48, c(0, 50, 60, 70, 100)) + 
                surgery, data = hearta, scale = 1)
fit1$event/fit1$pyears  # death rates on the surgery and non-surg arm

fit2$event/fit2$pyears  # death rates on the surgery and non-surg arm
```
of a median for uncensored data. Since the survival curve is computed as a series of products, however, there may be round off error. Assume for instance a sample of size 20 with no tied times and no censoring. The survival curve after the 10th death is \((19/20)(18/19)(17/18) \ldots (10/11) = 10/20\), but the computed result will not be exactly 0.5. Any horizontal segment whose absolute difference with a requested percentile is less than tolerance is considered to be an exact match.

Value

The quantiles will be a vector if the survfit object contains only a single curve, otherwise it will be a matrix or array. In this case the last dimension will index the quantiles.

If confidence limits are requested, then result will be a list with components quantile, lower, and upper, otherwise it is the vector or matrix of quantiles.

Author(s)

Terry Therneau

See Also

survfit, print.survfit, qsurvreg

Examples

```r
fit <- survfit(Surv(time, status) ~ ph.ecog, data=lung)
quantile(fit)

cfit <- coxph(Surv(time, status) ~ age + strata(ph.ecog), data=lung)
csurv <- survfit(cfit, newdata=data.frame(age=c(40, 60, 80)),
                 conf.type ="none")
temp <- quantile(csurv, 1:5/10)
temp[2,3,] # quantiles for second level of ph.ecog, age=80
quantile(csurv[2,3], 1:5/10) # quantiles of a single curve, same result
```

ratetable

Description

Description of the rate tables used by expected survival routines.

Details

A rate table contains event rates per unit time for some particular endpoint. Death rates are the most common use, the survexp.us table, for instance, contains death rates for the United States by year of age, sex, and calendar year.

A rate table is structured as a multi-way array with the following attributes:

- **dim** the dimensions of the array

Rate table structure
**dimnames** a named list of dimnames. The names are used to match user data to the dimensions, e.g., see the `rmap` argument in the `pyears` example. If a dimension is categorical, such as `sex` in `survexp.us`, then the dimname itself is matched against user’s data values. The matching ignores case and allows abbreviations, e.g., "M", "Male", and "m" all successfully match the `survexp.us` dimname of `sex=c("male", "female")`.

**type** a vector giving the type of each dimension, which will be 1= categorical, 2= continuous, 3= date, 4= calendar year of a US rate table. If `type` is 3 or 4, then the corresponding cutpoints must be one of the calendar date types: Date, POSIXt, date, or chron. This allows the code to properly match user data to the ratetable. (The published US decennial rate tables’ definition is that a subject does not begin to experience a new years’ death rate on Jan 1, but rather on their next birthday. The actual impact of this delay on any given subjects’ calculation is negligible, but the code has always tried to be correct.)

**cutpoints** a list with one element per dimension. If `type`=1 then the corresponding list element should be NULL, otherwise it should be a vector of length `dim[i]` containing the starting point of the interval to which the corresponding row/col of the array applies. Cutpoints must be in the same units as the underlying table, e.g., the `survexp.us` table contains death rates per day, so the age cutpoint vector contains age in days while `year` contains a vector of Dates. Cutpoints do not need to be evenly spaced: the `survexp.us` table, for instance, originally had age divided up as 0-1 days, 1-7 days, 7-28 days, 28 days - 1 year, 2, 3, … 119 years. (Changes in the source of the tables made it difficult to continue splitting out the first year.)

**summary** an optional summarization function. If present, it will be called with a numeric matrix that has one column per dimension and one row per observation. The function returns a character string giving a summary of the data. This is used by some routines to print an informative message, and provides one way to inform users of a data mistake, e.g., if the printout states that all subjects are between 0.14 and 0.23 years old it is likely that the user’s age variable was in years when it should have been in days.

**dimid** optional attribute containing the names of the dimnames. If the dimnames list itself has names, this attribute will be ignored.

**See Also**

`survexp`, `pyears`, `survexp.us`

---

**ratetableDate**

*Convert date objects to ratetable form*

**Description**

This method converts dates from various forms into the internal form used in `ratetable` objects.

**Usage**

`ratetableDate(x)`
Arguments

x       a date. The function currently has methods for Date, date, POSIXt, timeDate, and chron objects.

Details

This function is useful for those who create new ratetables, but is normally invisible to users. It is used internally by the survexp and pyears functions to map the various date formats; if a new method is added then those routines will automatically be adapted to the new date type.

Value

a numeric vector, the number of days since 1/1/1960.

Author(s)

Terry Therneau

See Also

pyears, survexp

---

Description

Census data sets for the expected survival and person years functions.

Details

survexp.us  total United States population, by age and sex, 1940 to 2012.
survexp.usr United States population, by age, sex and race, 1940 to 2014. Race is white, nonwhite, or black. For 1960 and 1970 the black population values were not reported separately, so the nonwhite values were used.
survexp.mn  total Minnesota population, by age and sex, 1970 to 2013.

Each of these tables contains the daily hazard rate for a matched subject from the population, defined as $-\log(1 - q)/365.25$ where $q$ is the 1 year probability of death as reported in the original tables from the US Census. For age 25 in 1970, for instance, $p = 1 - q$ is the probability that a subject who becomes 25 years of age in 1970 will achieve his/her 26th birthday. The tables are recast in terms of hazard per day for computational convenience.

Each table is stored as an array, with additional attributes, and can be subset and manipulated as standard R arrays. See the help page for ratetable for details.

All numeric dimensions of a rate table must be in the same units. The survexp.us rate table contains daily hazard rates, the age cutpoints are in days, and the calendar year cutpoints are a Date.
See Also

ratetable, survexp, pyears

Examples

survexp.uswhite <- survexp.usr[, "white", ]

rats

Rat treatment data from Mantel et al

Description

Rat treatment data from Mantel et al. Three rats were chosen from each of 100 litters, one of which was treated with a drug, and then all followed for tumor incidence.

Usage

rats

Format

<table>
<thead>
<tr>
<th></th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>litter</td>
<td>litter number from 1 to 100</td>
</tr>
<tr>
<td>rx</td>
<td>treatment,(1=drug, 0=control)</td>
</tr>
<tr>
<td>time</td>
<td>time to tumor or last follow-up</td>
</tr>
<tr>
<td>status</td>
<td>event status, 1=tumor and 0=censored</td>
</tr>
<tr>
<td>sex</td>
<td>male or female</td>
</tr>
</tbody>
</table>

Note

Since only 2/150 of the male rats have a tumor, most analyses use only females (odd numbered litters), e.g. Lee et al.

Source


References

rats2  Rat data from Gail et al.

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
stop: exit time
status: event status, 1=tumor, 0=censored

Source


residuals.coxph  Calculate Residuals for a 'coxph' Fit

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

Usage

## S3 method for class 'coxph'
residuals(object,
         type=c("martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", "scaledsch", "partial"),
         collapse=FALSE, weighted=FALSE, ...)

residuals

Rat data from Gail et al.

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
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status: event status, 1=tumor, 0=censored

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Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
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status: event status, 1=tumor, 0=censored

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         collapse=FALSE, weighted=FALSE, ...)

residuals

Rat data from Gail et al.

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
stop: exit time
status: event status, 1=tumor, 0=censored

Source


residuals.coxph  Calculate Residuals for a 'coxph' Fit

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

Usage

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         type=c("martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", "scaledsch", "partial"),
         collapse=FALSE, weighted=FALSE, ...)

residuals

Rat data from Gail et al.

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
stop: exit time
status: event status, 1=tumor, 0=censored

Source


residuals.coxph  Calculate Residuals for a 'coxph' Fit

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

Usage

## S3 method for class 'coxph'
residuals(object,
         type=c("martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", "scaledsch", "partial"),
         collapse=FALSE, weighted=FALSE, ...)

residuals

Rat data from Gail et al.

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
stop: exit time
status: event status, 1=tumor, 0=censored

Source


residuals.coxph  Calculate Residuals for a 'coxph' Fit

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

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## S3 method for class 'coxph'
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         type=c("martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", "scaledsch", "partial"),
         collapse=FALSE, weighted=FALSE, ...)

residuals

Rat data from Gail et al.

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
stop: exit time
status: event status, 1=tumor, 0=censored

Source


residuals.coxph  Calculate Residuals for a 'coxph' Fit

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

Usage

## S3 method for class 'coxph'
residuals(object,
         type=c("martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", "scaledsch", "partial"),
         collapse=FALSE, weighted=FALSE, ...)

residuals

Rat data from Gail et al.

Description

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

Usage

rats2

Format

rat: id
trt: treatment,(1=drug, 0=control)
observation: within rat
start: entry time
stop: exit time
status: event status, 1=tumor, 0=censored

Source


residuals.coxph  Calculate Residuals for a 'coxph' Fit

Description

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

Usage

## S3 method for class 'coxph'
residuals(object,
         type=c("martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", "scaledsch", "partial"),
         collapse=FALSE, weighted=FALSE, ...)

residuals
residuals.coxph

## S3 method for class 'coxph.null'
residuals(object,
  type=c("martingale", "deviance", "score", "schoenfeld"),
  collapse=FALSE, weighted=FALSE, ...)

### Arguments

- **object**: an object inheriting from class `coxph`, representing a fitted Cox regression model. Typically this is the output from the `coxph` function.
- **type**: character string indicating the type of residual desired. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", and "scaledsch". Only enough of the string to determine a unique match is required.
- **collapse**: vector indicating which rows to collapse (sum) over. In time-dependent models more than one row data can pertain to a single individual. If there were 4 individuals represented by 3, 1, 2 and 4 rows of data respectively, then collapse=c(1,1,1,2,3,3,4,4,4) could be used to obtain per subject rather than per observation residuals.
- **weighted**: if TRUE and the model was fit with case weights, then the weighted residuals are returned.
- **...**: other unused arguments

### Value

For martingale and deviance residuals, the returned object is a vector with one element for each subject (without collapse). For score residuals it is a matrix with one row per subject and one column per variable. The row order will match the input data for the original fit. For Schoenfeld residuals, the returned object is a matrix with one row for each event and one column per variable. The rows are ordered by time within strata, and an attribute `strata` is attached that contains the number of observations in each strata. The scaled Schoenfeld residuals are used in the `coxph` function.

The score residuals are each individual’s contribution to the score vector. Two transformations of this are often more useful: `dfbeta` is the approximate change in the coefficient vector if that observation were dropped, and `dfbetas` is the approximate change in the coefficients, scaled by the standard error for the coefficients.

### NOTE

For deviance residuals, the status variable may need to be reconstructed. For score and Schoenfeld residuals, the X matrix will need to be reconstructed.

### References


### See Also

coxph
Examples

```r
fit <- coxph(Surv(start, stop, event) ~ (age + surgery)* transplant,
               data=heart)
mresid <- resid(fit, collapse=heart$id)
```

residuals.survreg  \hspace{1cm} \textit{Compute Residuals for 'survreg' Objects}

Description

This is a method for the function \texttt{residuals} for objects inheriting from class survreg.

Usage

```r
## S3 method for class 'survreg'
residuals(object, type=c("response", "deviance", "dfbeta", "dfbetas",
"working", "ldcase", "ldresp", "ldshape", "matrix"), rsigma=TRUE,
collapse=FALSE, weighted=FALSE, ...)
```

Arguments

- \texttt{object} an object inheriting from class survreg.
- \texttt{type} type of residuals, with choices of "response", "deviance", "dfbeta", "dfbetas",
  "working", "ldcase", "ldresp", "ldshape", and "matrix".
- \texttt{rsigma} include the scale parameters in the variance matrix, when doing computations.
  (I can think of no good reason not to).
- \texttt{collapse} optional vector of subject groups. If given, this must be of the same length as
  the residuals, and causes the result to be per group residuals.
- \texttt{weighted} give weighted residuals? Normally residuals are unweighted.
- \texttt{...} other unused arguments

Value

A vector or matrix of residuals is returned. Response residuals are on the scale of the original
data, working residuals are on the scale of the linear predictor, and deviance residuals are on log-
likelihood scale. The dfbeta residuals are a matrix, where the ith row gives the approximate change
in the coefficients due to the addition of subject i. The dfbetas matrix contains the dfbeta residuals,
with each column scaled by the standard deviation of that coefficient.

The matrix type produces a matrix based on derivatives of the log-likelihood function. Let \( L \) be
the log-likelihood, \( p \) be the linear predictor \( X \beta \), and \( s \) be \( \log(\sigma) \). Then the 6 columns of the matrix
are \( L, dL/dp, \partial^2 L/\partial p^2, dL/ds, \partial^2 L/\partial s^2 \) and \( \partial^2 L/\partial p \partial s \). Diagnostics based on these quantities
are discussed in the book and article by Escobar and Meeker. The main ones are the likelihood
displacement residuals for perturbation of a case weight (ldcase), the response value (ldresp),
and the shape.
For a transformed distribution such as the log-normal or Weibull, matrix residuals are based on the log-likelihood of the transformed data log(y). For a monotone function f the density of f(X) is the density of X divided by the derivative of f (the Jacobian), so subtract log(derivative) from each uncensored observation’s loglik value in order to match the loglik component of the result. The other columns of the matrix residual are unchanged by the transformation.

References


See Also

predict.survreg

Examples

fit <- survreg(Surv(futime, death) ~ age + sex, mgus2)
summary(fit)  # age and sex are both important

rr <- residuals(fit, type='matrix')
sum(rr[,1]) - with(mgus2, sum(log(futime[death==1])))  # loglik

plot(mgus2$age, rr[,2], col= (1+mgus2$death))  # ldresp

retinopathy

Diabetic Retinopathy

Description

A trial of laser coagulation as a treatment to delay diabetic retinopathy.

Usage

data("retinopathy")

Format

A data frame with 394 observations on the following 9 variables.

id  numeric subject id
laser type of laser used: xenon argon
eye which eye was treated: right left
age age at diagnosis of diabetes
type type of diabetes: juvenile adult, (diagnosis before age 20)
trt 0 = control eye, 1 = treated eye
futime  time to loss of vision or last follow-up
status  0 = censored, 1 = loss of vision in this eye
risk   a risk score for the eye. This high risk subset is defined as a score of 6 or greater in at least one eye.

Details

The 197 patients in this dataset were a 50% random sample of the patients with "high-risk" diabetic retinopathy as defined by the Diabetic Retinopathy Study (DRS). Each patient had one eye randomized to laser treatment and the other eye received no treatment, and has two observations in the data set. For each eye, the event of interest was the time from initiation of treatment to the time when visual acuity dropped below 5/200 two visits in a row. Thus there is a built-in lag time of approximately 6 months (visits were every 3 months). Survival times in this dataset are the actual time to vision loss in months, minus the minimum possible time to event (6.5 months). Censoring was caused by death, dropout, or end of the study.

References


Examples

```r
coxph(Surv(futime, status) ~ type + trt + cluster(id), retinopathy)
```

rhDNase  

rhDNASE data set

Description

Results of a randomized trial of rhDNase for the treatment of cystic fibrosis.

Format

A data frame with 767 observations on the following 8 variables.

  id  subject id
  inst enrolling institution
  trt  treatment arm: 0=placebo, 1=rhDNase
  entry.dt  date of entry into the study
  end.dt  date of last follow-up
  fev  forced expiratory volume at enrollment, a measure of lung capacity
  ivstart  days from enrollment to the start of IV antibiotics
  ivstop  days from enrollment to the cessation of IV antibiotics
Details

In patients with cystic fibrosis, extracellular DNA is released by leukocytes that accumulate in the airways in response to chronic bacterial infection. This excess DNA thickens the mucus, which then cannot be cleared from the lung by the cilia. The accumulation leads to exacerbations of respiratory symptoms and progressive deterioration of lung function. At the time of this study more than 90% of cystic fibrosis patients eventually died of lung disease.

Deoxyribonuclease I (DNase I) is a human enzyme normally present in the mucus of human lungs that digests extracellular DNA. Genentech, Inc. cloned a highly purified recombinant DNase I (rhDNase or Pulmozyme) which when delivered to the lungs in an aerosolized form cuts extracellular DNA, reducing the viscoelasticity of airway secretions and improving clearance. In 1992 the company conducted a randomized double-blind trial comparing rhDNase to placebo. Patients were then monitored for pulmonary exacerbations, along with measures of lung volume and flow. The primary endpoint was the time until first pulmonary exacerbation; however, data on all exacerbations were collected for 169 days.

The definition of an exacerbation was an infection that required the use of intravenous (IV) antibiotics. Subjects had 0–5 such episodes during the trial, those with more than one have multiple rows in the data set, those with none have NA for the IV start and end times. A few subjects were infected at the time of enrollment, subject 173 for instance has a first infection interval of -21 to 7. We do not count this first infection as an "event", and the subject first enters the risk set at day 7. Subjects who have an event are not considered to be at risk for another event during the course of antibiotics, nor for an additional 6 days after they end. (If the symptoms reappear immediately after cessation then from a medical standpoint this would not be a new infection.)

This data set reproduces the data in Therneau and Grambsch, is does not exactly reproduce those in Therneau and Hamilton due to data set updates.

References


T. M. Therneau and S.A. Mamliton, rhDNase as an example of recurrent event analysis, Statistics in Medicine, 16:2029-2047, 1997.

Examples

# Build the start-stop data set for analysis, and # replicate line 2 of table 8.13
first <- subset(rhDNase, !duplicated(id)) # first row for each subject
dnase <- tmerge(first, first, id=id, tstop=as.numeric(entry.dt - end.dt))

# Subjects whose fu ended during the 6 day window are the reason for # this next line
temp.end <- with(rhDNase, pmin(ivstart+6, end.dt-entry.dt))
dnase <- tmerge(dnase, rhDNase, id=id,
              infect=event(ivstart),
              end= event(temp.end))

# toss out the non-at-risk intervals, and extra variables
# 3 subjects had an event on their last day of fu, infect=1 and end=1
dnase <- subset(dnase, (infect==1 & end==0), c(id:trt, fev:infect))
agfit <- coxph(Surv(tstart, tstop, infect) ~ trt + fev + cluster(id), data=dnase)

ridge

Ridge regression

Description

When used in a coxph or survreg model formula, specifies a ridge regression term. The likelihood is penalised by \( \theta/2 \) time the sum of squared coefficients. If scale=\( T \) the penalty is calculated for coefficients based on rescaling the predictors to have unit variance. If df is specified then \( \theta \) is chosen based on an approximate degrees of freedom.

Usage

ridge(..., theta, df=nvar/2, eps=0.1, scale=TRUE)

Arguments

... predictors to be ridged
theta penalty is \( \theta/2 \) time sum of squared coefficients
df Approximate degrees of freedom
eps Accuracy required for df
scale Scale variables before applying penalty?

Value

An object of class coxph.penalty containing the data and control functions.

Note

If the expression ridge(x1, x2, x3, ...) is too many characters long then the internal terms() function will add newlines to the variable name and then the coxph routine simply gets lost. (Some labels will have the newline and some won’t.) One solution is to bundle all of the variables into a single matrix and use that matrix as the argument to ridge so as to shorten the call, e.g. mdta$many <- as.matrix(mydata[,5:53]).

References

Gray (1992) "Flexible methods of analysing survival data using splines, with applications to breast cancer prognosis" JASA 87:942–951

See Also
coxph,survreg,pspline,frailty
Examples

coxph(Surv(futime, fustat) ~ rx + ridge(age, ecog.ps, theta=1), ovarian)

lfit0 <- survreg(Surv(time, status) ~1, cancer)
lfit1 <- survreg(Surv(time, status) ~ age + ridge(ph.ecog, theta=5), cancer)
lfit2 <- survreg(Surv(time, status) ~ sex + ridge(age, ph.ecog, theta=1), cancer)
lfit3 <- survreg(Surv(time, status) ~ sex + age + ph.ecog, cancer)

solder

Data from a soldering experiment

Description

In 1988 an experiment was designed and implemented at one of AT&T’s factories to investigate alternatives in the "wave soldering" procedure for mounting electronic components to printed circuit boards. The experiment varied a number of factors relevant to the process. The response, measured by eye, is the number of visible solder skips.

Usage

data("solder")

Format

A data frame with 900 observations on the following 6 variables.

Opening   the amount of clearance around the mounting pad (3 levels)
Solder     the amount of solder (Thick or Thin)
Mask      type and thickness of the material used for the solder mask (A1.5, A3, A6, B3, B6)
PadType  the geometry and size of the mounting pad (10 levels)
Panel   each board was divided into 3 panels
skips   the number of skips

Details

This data set is used as a detailed example in chapter 1 of Chambers and Hastie. Observations 1-360 and 541-900 form a balanced design of 3*2*10*3= 180 observations for four of the pad types (A1.5, A3, B3, B6), while rows 361-540 match 3 of the 6 Solder*Opening combinations with pad type A6 and the other 3 with pad type A3.

References

Examples

data(solder)
# The balanced subset used by Chambers and Hastie
# contains the first 180 of each mask and deletes mask A6.
index <- 1 + (1:nrow(solder)) - match(solder$Mask, solder$Mask)
solder.balance <- droplevels(subset(solder, Mask != "A6" & index <= 180))

stanford2 More Stanford Heart Transplant data

Description

This contains the Stanford Heart Transplant data in a different format. The main data set is in heart.

Usage

stanford2

Format

id: ID number
time: survival or censoring time
status: censoring status
age: in years
t5: T5 mismatch score

Source


See Also

predict.survreg, heart

statefig Draw a state space figure.

Description

For multi-state survival models it is useful to have a figure that shows the states and the possible transitions between them. This function creates a simple "box and arrows" figure. It's goal was simplicity.
Usage

statefig(layout, connect, margin = 0.03, box = TRUE, cex = 1, col = 1, lwd=1, lty=1, bcol=col, acol=col, alwd=lwd, alty=lty, offset=0)

Arguments

layout describes the layout of the boxes on the page. See the detailed description below.
connect a square matrix with one row for each state. If connect[i,j] != 0 then an
arrow is drawn from state i to state j. The row names of the matrix are used as
the labels for the states.
margin the fraction of white space between the label and the surrounding box, and be-
tween the box and the arrows, as a function of the plot region size.
box should boxes be drawn? TRUE or FALSE.
cex, col, lty, lwd default graphical parameters used for the text and boxes. The last 3 can be a
vector of values.
bcol color for the box, if it differs from that used for the text.
acol, alwd, alty color, line type and line width for the arrows.
offset used to slight offset the arrows between two boxes x and y if there is a transition
in both directions. The default of 0 leads to a double headed arrow in this case – to arrows are drawn but they coincide.

Details

The arguments for color, line type and line width can all be vectors, in which case they are recycled
as needed. Boxes and text are drawn in the order of the rownames of connect, and arrows are
drawn in the usual R matrix order.

The layout argument is normally a vector of integers, e.g., the vector (1, 3, 2) describes a layout
with 3 columns. The first has a single state, the second column has 3 states and the third has 2. The
coordinates of the plotting region are 0 to 1 for both x and y. Within a column the centers of the
boxes are evenly spaced, with 1/2 a space between the boxes and the margin, e.g., 4 boxes would be
at 1/8, 3/8, 5/8 and 7/8. If layout were a 1 column matrix with values of (1, 3, 2) then the layout
will have three rows with 1, 3, and 2 boxes per row, respectively. Alternatively, the user can supply
a 2 column matrix that directly gives the centers.

The values of the connect matrix should be 0 for pairs of states that do not have a transition and
values between 0 and 2 for those that do. States are connected by an arc that passes through the
centers of the two boxes and a third point that is between them. Specifically, consider a line segment
joining the two centers and erect a second segment at right angles to the midpoint of length d times
the distance from center to midpoint. The arc passes through this point. A value of d=0 gives a
straight line, d=1 a right hand half circle centered on the midpoint and d=-1 a left hand half circle.
The connect matrix contains values of d+1 with -1 < d < 1.

The connecting arrow are drawn from (center of box 1 + offset) to (center of box 2 + offset), where
the the amount of offset (white space) is determined by the box and margin parameters. If a pair of
states are too close together this can result in an arrow that points the wrong way.
Value

a matrix containing the centers of the boxes, with the invisible attribute set.

Note

The goal of this function is to make “good enough” figures as simply as possible, and thereby to encourage users to draw them. The layout argument was inspired by the diagram package, which can draw more complex and well decorated figures, e.g., many different shapes, shading, multiple types of connecting lines, etc., but at the price of greater complexity.

Because curved lines are drawn as a set of short line segments, line types have almost no effect for that case.

Author(s)

Terry Therneau

Examples

# Draw a simple competing risks figure
states <- c("Entry", "Complete response", "Relapse", "Death")
connect <- matrix(0, 4, 4, dimnames=list(states, states))
connect[1, -1] <- c(1.1, 1, 0.9)
statefig(c(1, 3), connect)

---

strata

Identify Stratification Variables

Description

This is a special function used in the context of the Cox survival model. It identifies stratification variables when they appear on the right hand side of a formula.

Usage

strata(..., na.group=FALSE, shortlabel, sep=' ', ')

Arguments

... any number of variables. All must be the same length.
na.group a logical variable, if TRUE, then missing values are treated as a distinct level of each variable.
shortlabel if TRUE omit variable names from resulting factor labels. The default action is to omit the names if all of the arguments are factors, and none of them was named.
sep the character used to separate groups, in the created label
Details

When used outside of a coxph formula the result of the function is essentially identical to the interaction function, though the labels from strata are often more verbose.

Value

a new factor, whose levels are all possible combinations of the factors supplied as arguments.

See Also

coxph, interaction

Examples

```r
a <- factor(rep(1:3, 4), labels=c("low", "medium", "high"))
b <- factor(rep(1:4, 3))
levels(strata(b))
levels(strata(a,b,shortlabel=TRUE))

coxph(Surv(futime, fustat) ~ age + strata(rx), data=ovarian)
```
Details

It is not uncommon for the very right-hand tail of the plot to have large outlying values, particularly for the standard error. The `maxtime` parameter can then be used to truncate the range so as to avoid these. This gives an updated value for the test statistics, without refitting the model.

The slope is based on a weighted linear regression to the cumulative coefficient plot, and may be a useful measure of the overall size of the effect. For instance when two models include a common variable, "age" for instance, this may help to assess how much the fit changed due to the other variables, in lieu of overlaying the two plots. (Of course the plots are often highly non-linear, so it is only a rough substitute). The slope is not directly related to the test statistic, as the latter is invariant to any monotone transformation of time.

Value

A list is returned with the following components:

- `table`: a matrix with rows for the intercept and each covariate, and columns giving a slope estimate, the test statistic, its standard error, the z-score and a p-value.
- `test`: the time weighting used for computing the test statistics.
- `test.statistic`: the vector of test statistics.
- `test.var`: the model-based variance matrix for the test statistic.
- `test.var2`: optionally, a robust variance matrix for the test statistic.
- `chisq`: the overall test (ignoring the intercept term) for significance of any variable.
- `n`: a vector containing the number of observations, the number of unique death times used in the computation, and the total number of unique death times.

See Also

`aareg`, `plot.aareg`

Examples

```r
afit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung, dfbeta=TRUE)
summary(afit)
```

```
Not run:
# Not run:
slope  test se(test) robust se  z   p
Intercept 5.05e-03  1.9  1.54   1.55 1.23 0.219000
age  4.01e-05 109.0 110.0 110.00  1.82 0.307000
sex -3.16e-03 -19.5  5.90  5.95 -3.28 0.001030
ph.ecog 3.01e-03  33.2  9.18  9.17  3.62 0.000299

Chisq=22.84 on 3 df, p=4.4e-05; test weights=aalen
```

```
# End(Not run)

summary(afit, maxtime=600)
```

```
# Not run:
```
summary.coxph

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slope  test se(test) robust se  z  p
Intercept 4.16e-03 2.13 1.48 1.47 1.450 0.146000
age 2.82e-05 85.80 106.00 100.00 0.857 0.392000
sex -2.54e-03 -20.60 5.61 5.63 -3.660 0.000256
ph.ecog 2.47e-03 31.60 8.91 8.67 3.640 0.000271

Chisq=27.08 on 3 df, p=5.7e-06; test weights=aalen

## End(Not run)

## Summary method for Cox models

**Description**

Produces a summary of a fitted coxph model

**Usage**

```
## S3 method for class 'coxph'
summary(object, conf.int=0.95, scale=1,...)
```

**Arguments**

- `object` the result of a coxph fit
- `conf.int` level for computation of the confidence intervals. If set to FALSE no confidence intervals are printed
- `scale` vector of scale factors for the coefficients, defaults to 1. The printed coefficients, se, and confidence intervals will be associated with one scale unit.
- `...` for future methods

**Value**

An object of class `summary.coxph`.

**See Also**

coxph, print.coxph

**Examples**

```
fit <- coxph(Surv(time, status) ~ age + sex, lung)
summary(fit)
## Not run:
Call:
coxph(formula = Surv(time, status) ~ age + sex, data = lung)

n= 228
```
```
coef exp(coef) se(coef)   z    p
age   0.017    1.017    0.00922  1.85 0.0650
sex  -0.513    0.599    0.16745 -3.06 0.0022

exp(coef) exp(-coef) lower .95 upper .95
age   1.017    0.983    0.999  1.036
sex   0.599    1.670    0.431  0.831

Rsquare= 0.06  (max possible= 0.999 )
Likelihood ratio test= 14.1 on 2 df,  p=0.000857
Wald test       = 13.5 on 2 df,  p=0.000119
Score (logrank) test = 13.7 on 2 df,  p=0.00105

## End(Not run)
```

### summary.pyears

**Summary function for pyears objects**

#### Description

Create a printable table of a person-years result.

#### Usage

```r
## S3 method for class 'pyears'
summary(object, header = TRUE, call = header, n = TRUE,
event = TRUE, pyears = TRUE, expected = TRUE, rate = FALSE, rr = expected,
ci.r = FALSE, ci.rr = FALSE, totals=FALSE, legend = TRUE, vline = FALSE,
vertical= TRUE, nastring=".", conf.level = 0.95,
scale = 1, ...)
```

#### Arguments

- `object`: a pyears object
- `header`: print out a header giving the total number of observations, events, person-years, and total time (if any) omitted from the table
- `call`: print out a copy of the call
- `n, event, pyears, expected`: logical arguments: should these elements be printed in the table?
- `rate, ci.r`: logical arguments: should the incidence rate and/or its confidence interval be given in the table?
- `rr, ci.rr`: logical arguments: should the hazard ratio and/or its confidence interval be given in the table?
- `totals`: should row and column totals be added?
- `legend`: should a legend be included in the printout?
should vertical lines be included in the printed tables?

when there is only a single predictor, should the table be printed with the predictor on the left (vertical=TRUE) or across the top (vertical=FALSE)?

what to use for missing values in the table. Some of these are structural, e.g., risk ratios for a cell with no follow-up time.

certainty level for any confidence intervals

a scaling factor for printed rates

optional arguments which will be passed to the format function; common choices would be digits=2 or nsmall=1.

Details

The `pyears` function is often used to create initial descriptions of a survival or time-to-event variable; the type of material that is often found in “table 1” of a paper. The summary routine prints this information out using one of pandoc table styles. A primary reason for choosing this style is that Rstudio is then able to automatically render the results in multiple formats: html, rtf, latex, etc.

If the `pyears` call has only a single covariate then the table will have that covariate as one margin and the statistics of interest as the other. If the `pyears` call has two predictors then those two predictors are used as margins of the table, while each cell of the table contains the statistics of interest as multiple rows within the cell. If there are more than two predictors then multiple tables are produced, in the same order as the standard R printout for an array.

The "N" entry of a pyears object is the number of observations which contributed to a particular cell. When the original call includes `tcut` objects then a single observation may contribute to multiple cells.

Value

a copy of the object

Notes

The pandoc system has four table types: with or without vertical bars, and with single or multiple rows of data in each cell. This routine produces all 4 styles depending on options, but currently not all of them are recognized by the Rstudio-pandoc pipeline. (And we don’t yet see why.)

Author(s)

Terry Therneau and Elizabeth Atkinson

See Also

`cipoisson`, `pyears`, `format`
summary.survexp

Summary function for a survexp object

Description

Returns a list containing the values of the survival at specified times.

Usage

## S3 method for class 'survexp'
summary(object, times, scale = 1, ...)

Arguments

- object: the result of a call to the survexp function
- times: vector of times; the returned matrix will contain 1 row for each time. Missing values are not allowed.
- scale: numeric value to rescale the survival time, e.g., if the input data to survfit were in days, scale = 365.25 would scale the output to years.
- ...: For future methods

Details

A primary use of this function is to retrieve survival at fixed time points, which will be properly interpolated by the function.

Value

a list with the following components:

- surv: the estimate of survival at time t.
- time: the timepoints on the curve.
- n.risk: In expected survival each subject from the data set is matched to a hypothetical person from the parent population, matched on the characteristics of the parent population. The number at risk is the number of those hypothetical subject who are still part of the calculation.

Author(s)

Terry Therneau

See Also

survexp
**Summary of a Survival Curve**

**Description**

Returns a list containing the survival curve, confidence limits for the curve, and other information.

**Usage**

```r
## S3 method for class 'survfit'
summary(object, times, censored=FALSE, scale=1,
        extend=FALSE, rmean=getOption('survfit.rmean'), ...)
```

**Arguments**

- `object`: the result of a call to the `survfit` function.
- `times`: vector of times; the returned matrix will contain 1 row for each time. The vector will be sorted into increasing order; missing values are not allowed. If `censored=TRUE`, the default `times` vector contains all the unique times in `fit`, otherwise the default `times` vector uses only the event (death) times.
- `censored`: logical value: should the censoring times be included in the output? This is ignored if the `times` argument is present.
- `scale`: numeric value to rescale the survival time, e.g., if the input data to `survfit` were in days, `scale = 365.25` would scale the output to years.
- `extend`: logical value: if TRUE, prints information for all specified `times`, even if there are no subjects left at the end of the specified `times`. This is only valid if the `times` argument is present.
- `rmean`: Show restricted mean: see `print.survfit` for details
- `...`: for future methods

**Value**

A list with the following components:

- `surv`: the estimate of survival at time t+0.
- `time`: the timepoints on the curve.
- `n.risk`: the number of subjects at risk at time t-0 (but see the comments on weights in the `survfit` help file).
- `n.event`: if the `times` argument is missing, then this column is the number of events that occurred at time t. Otherwise, it is the cumulative number of events that have occurred since the last time listed until time t+0.
n.entered

This is present only for counting process survival data. If the times argument is missing, this column is the number of subjects that entered at time t. Otherwise, it is the cumulative number of subjects that have entered since the last time listed until time t.

n.exit.censored

if the times argument is missing, this column is the number of subjects that left without an event at time t. Otherwise, it is the cumulative number of subjects that have left without an event since the last time listed until time t+0. This is only present for counting process survival data.

std.err

the standard error of the survival value.

cnf.int

level of confidence for the confidence intervals of survival.

lower

lower confidence limits for the curve.

upper

upper confidence limits for the curve.

strata

indicates stratification of curve estimation. If strata is not NULL, there are multiple curves in the result and the surv, time, n.risk, etc. vectors will contain multiple curves, pasted end to end. The levels of strata (a factor) are the labels for the curves.

call

the statement used to create the fit object.

na.action

same as for fit, if present.

table

table of information that is returned from print.survfit function.

type

type of data censoring. Passed through from the fit object.

See Also

survfit, print.summary.survfit

Examples

summary( survfit( Surv(futime, fustat)-1, data=ovarian))
summary( survfit( Surv(futime, fustat)-rx, data=ovarian))

Create a Survival Object

Create a survival object, usually used as a response variable in a model formula. Argument matching is special for this function, see Details below.

Usage

Surv(time, time2, event,
    type=c('right', 'left', 'interval', 'counting', 'interval2', 'mstate'),
    origin=0)

is.Surv(x)
Arguments

- **time**: for right censored data, this is the follow up time. For interval data, the first argument is the starting time for the interval.

- **event**: The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For interval censored data, the status indicator is 0=right censored, 1=event at time, 2=left censored, 3=interval censored. For multiple endpoint data the event variable will be a factor, whose first level is treated as censoring. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.

- **time2**: ending time of the interval for interval censored or counting process data only. Intervals are assumed to be open on the left and closed on the right, [{start, end}].

- **type**: character string specifying the type of censoring. Possible values are "right", "left", "counting", "interval", "interval2" or "mstate".

- **origin**: for counting process data, the hazard function origin. This option was intended to be used in conjunction with a model containing time dependent strata in order to align the subjects properly when they cross over from one strata to another, but it has rarely proven useful.

- **x**: any R object.

Details

When the `type` argument is missing the code assumes a type based on the following rules:

- If there are two unnamed arguments, they will match `time` and `event` in that order. If there are three unnamed arguments they match `time`, `time2` and `event`.
- If the event variable is a factor then type `mstate` is assumed. Otherwise type `right` if there is no `time2` argument, and type `counting` if there is.

As a consequence the `type` argument will normally be omitted.

When the survival type is "mstate" then the status variable will be treated as a factor. The first level of the factor is taken to represent censoring and remaining ones a transition to the given state. (If the status variable is a factor then `mstate` is assumed.)

Interval censored data can be represented in two ways. For the first use `type = "interval"` and the codes shown above. In that usage the value of the `time2` argument is ignored unless `event=3`. The second approach is to think of each observation as a time interval with (-infinity, t) for left censored, (t, infinity) for right censored, (t1, t2) for exact and (t1, t2) for an interval. This is the approach used for type = `interval2`. Infinite values can be represented either by actual infinity (Inf) or NA. The second form has proven to be the more useful one.

Presently, the only methods allowing interval censored data are the parametric models computed by `survreg` and survival curves computed by `survfit`; for both of these, the distinction between open and closed intervals is unimportant. The distinction is important for counting process data and the Cox model.

The function tries to distinguish between the use of 0/1 and 1/2 coding for censored data via the condition if \( \max(\text{status}) = 2 \). If 1/2 coding is used and all the subjects are censored, it will guess
wrong. In any questionable case it is safer to use logical coding, e.g., \( \text{Surv}(\text{time}, \text{status}=3) \) would indicate that a 3 is the code for an event. For multi-state survival the status variable will be a factor, whose first level is assumed to correspond to censoring.

Surv objects can be subscripted either as a vector, e.g. \( x[1:3] \) using a single subscript, in which case the drop argument is ignored and the result will be a survival object; or as a matrix by using two subscripts. If the second subscript is missing and drop=F (the default), the result of the subscripting will be a Surv object, e.g., \( x[1:3,, \text{drop}=\text{F}] \), otherwise the result will be a matrix (or vector), in accordance with the default behavior for subscripting matrices.

**Value**

An object of class Surv. There are methods for print, is.na, and subsetting survival objects. Surv objects are implemented as a matrix of 2 or 3 columns that has further attributes. These include the type (left censored, right censored, counting process, etc.) and labels for the states for multi-state objects. Any attributes of the input arguments are also preserved in inputAttributes. This may be useful for other packages that have attached further information to data items such as labels; none of the routines in the survival package make use of these values, however.

In the case of is.Surv, a logical value TRUE if \( x \) inherits from class "Surv", otherwise an FALSE.

**See Also**

coxph, survfit, survreg.

**Examples**

```r
with(lung, Surv(time, status))
Surv(heart$start, heart$stop, heart$event)
```

---

**Surv-methods**

**Methods for Surv objects**

**Description**

The list of methods that apply to Surv objects

**Usage**

```r
## S3 method for class 'Surv'
anyDuplicated(x, ...)
## S3 method for class 'Surv'
as.character(x, ...)
## S3 method for class 'Surv'
as.data.frame(x, ...)
## S3 method for class 'Surv'
as.integer(x, ...)
## S3 method for class 'Surv'
as.matrix(x, ...)
```
Surv-methods

```r
## S3 method for class 'Surv'
as.numeric(x, ...)  ## S3 method for class 'Surv'
c(...)  ## S3 method for class 'Surv'
duplicated(x, ...)  ## S3 method for class 'Surv'
format(x, ...)  ## S3 method for class 'Surv'
head(x, ...)  ## S3 method for class 'Surv'
is.na(x)  ## S3 method for class 'Surv'
length(x)  ## S3 method for class 'Surv'
mean(x, ...)  ## S3 method for class 'Surv'
median(x, ...)  ## S3 method for class 'Surv'
names(x)  ## S3 replacement method for class 'Surv'
names(x) <- value  ## S3 method for class 'Surv'
quantile(x, probs, na.rm=FALSE, ...)  ## S3 method for class 'Surv'
plot(x, ...)  ## S3 method for class 'Surv'
rep(x, ...)  ## S3 method for class 'Surv'
rep.int(x, ...)  ## S3 method for class 'Surv'
rep_len(x, ...)  ## S3 method for class 'Surv'
rev(x)  ## S3 method for class 'Surv'
t(x)  ## S3 method for class 'Surv'
tail(x, ...)  ## S3 method for class 'Surv'
unique(x, ...)
```

Arguments

- `x` a `Surv` object
- `probs` a vector of probabilities
- `na.rm` remove missing values from the calculation
- `value` a character vector of up to the same length as x, or NULL
- `...` other arguments to the method
Details

These functions extend the standard methods to Surv objects. The arguments and results from these are mostly as expected, with the following further details:

- The as.character function uses "5+" for right censored at time 5, "5-" for left censored at time 5, "[2,7]" for an observation that was interval censored between 2 and 7, "(1,6]" for a counting process data denoting an observation which was at risk from time 1 to 6, with an event at time 6, and "(1,6+]" for an observation over the same interval but not ending with an event. For a multi-state survival object the type of event is appended to the event time using ":type".
- The print and format methods make use of as.character.
- The as.numeric and as.integer methods perform these actions on the survival times, but do not affect the censoring indicator.
- The as.matrix and t methods return a matrix.
- The length of a Surv object is the number of survival times it contains, not the number of items required to encode it, e.g., x <- Surv(1:4, 5:9, c(1,0,1,0)); length(x) has a value of 4. Likewise names(x) will be NULL or a vector of length 4. (For technical reasons, any names are actually stored in the rownames attribute of the object.)
- For a multi-state survival object levels returns the names of the endpoints, otherwise it is NULL.
- The median, quantile and plot methods first construct a survival curve using survfit, then apply the appropriate method to that curve.
- The concatenation method c() is asymmetric, its first argument determines the execution path. For instance c(Surv(1:4), Surv(5:6)) will concatenate the two objects, c(Surv(1:4), 5:6) will give an error, and c(5:6, Surv(1:4)) is equivalent to c(5:6, as.vector(Surv(1:4))).

See Also

Surv

---

**survConcordance**

Compute a concordance measure.

Description

This function computes the concordance between a right-censored survival time and a single continuous covariate

Usage

survConcordance(formula, data, weights, subset, na.action)
survConcordance.fit(y, x, strata, weight)
Arguments

- `formula`: a formula with a survival time on the left and a single covariate on the right, along with an optional `strata()` term. The left hand term can also be a numeric vector.
- `data`: a data frame
- `weights`, `subset`, `na.action`: as for `coxph`
- `x, y, strata, weight`: predictor, response, strata, and weight vectors for the direct call

Details

The `survConcordance` function computes the result but does no data checking whatsoever. It is intended as a hook for other packages that wish to compute concordance, and the data has already been assembled and verified.

Concordance is defined as \( \text{Pr(} \text{agreement}) \) for any two randomly chosen observations, where in this case agreement means that the observation with the shorter survival time of the two also has the larger risk score. The predictor (or risk score) will often be the result of a Cox model or other regression.

For continuous covariates concordance is equivalent to Kendall's tau, and for logistic regression is equivalent to the area under the ROC curve. A value of 1 signifies perfect agreement, .6-.7 is a common result for survival data, .5 is an agreement that is no better than chance, and .3-.4 is the performance of some stock market analysts.

The computation involves all \( n(n-1)/2 \) pairs of data points in the sample. For survival data, however, some of the pairs are incomparable. For instance a pair of times \((5+, 8)\), the first being a censored value. We do not know whether the first survival time is greater than or less than the second. Among observations that are comparable, pairs may also be tied on survival time (but only if both are uncensored) or on the predictor. The final concordance is \( (\text{agree + tied}/2)/(\text{agree + disagree + tied}) \).

There is, unfortunately, one aspect of the formula above that is unclear. Should the count of ties include observations that are tied on survival time \( y \), tied on the predictor \( x \), or both? By default the concordance only counts ties in \( x \), treating tied survival times as incomparable; this agrees with the AUC calculation used in logistic regression. The Goodman-Kruskal Gamma statistic is \( (\text{agree}-\text{disagree})/(\text{agree} + \text{disagree}) \), ignoring ties. It ranges from -1 to +1 similar to a correlation coefficient. Kendall’s tau uses ties of both types. All of the components are returned in the result, however, so people can compute other combinations if interested. (If two observations have the same survival and the same \( x \), they are counted in the tied survival time category).

The algorithm is based on a balanced binary tree, which allows the computation to be done in \( O(n \log n) \) time.

Value

an object containing the concordance, followed by the number of pairs that agree, disagree, are tied, and are not comparable.
survdiff

Test Survival Curve Differences

Description

Tests if there is a difference between two or more survival curves using the $G^p$ family of tests, or for a single curve against a known alternative.

Usage

survdiff(formula, data, subset, na.action, rho=0, timefix=TRUE)

Arguments

- formula: a formula expression as for other survival models, of the form \( \text{Surv}(\text{time}, \text{status}) \sim \text{predictors} \). For a one-sample test, the predictors must consist of a single offset\((sp)\) term, where \(sp\) is a vector giving the survival probability of each subject. For a \(k\)-sample test, each unique combination of predictors defines a subgroup. A strata term may be used to produce a stratified test. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the strata function with its na.group=T argument.
- data: an optional data frame in which to interpret the variables occurring in the formula.
- subset: expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.
**survdiff**

na.action a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is options$na.action.

rho a scalar parameter that controls the type of test.

timefix process times through the aeqSurv function to eliminate potential roundoff issues.

**Value**

a list with components:

- **n** the number of subjects in each group.
- **obs** the weighted observed number of events in each group. If there are strata, this will be a matrix with one column per stratum.
- **exp** the weighted expected number of events in each group. If there are strata, this will be a matrix with one column per stratum.
- **chisq** the chisquare statistic for a test of equality.
- **var** the variance matrix of the test.
- **strata** optionally, the number of subjects contained in each stratum.

**METHOD**

This function implements the G-rho family of Harrington and Fleming (1982), with weights on each death of $S(t)^\rho$, where $S(t)$ is the Kaplan-Meier estimate of survival. With $\rho = 0$ this is the log-rank or Mantel-Haenszel test, and with $\rho = 1$ it is equivalent to the Peto & Peto modification of the Gehan-Wilcoxon test.

If the right hand side of the formula consists only of an offset term, then a one sample test is done. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the factor function with its exclude argument.

**References**


**Examples**

```r
# Two-sample test
survdiff(Surv(futime, fustat) ~ rx, data=ovarian)

# Stratified 7-sample test
survdiff(Surv(time, status) ~ pat.karno + strata(inst), data=lung)

# Expected survival for heart transplant patients based on
# US mortality tables
expect <- survexp(futime ~ 1, data=jasa, cohort=FALSE,
                  rmap= list(age=(accept.dt - birth.dt), sex=1, year=accept.dt),
                  ratetable=survexp.us)
```
## Compute Expected Survival

### Description

Returns either the expected survival of a cohort of subjects, or the individual expected survival for each subject.

### Usage

```r
survexp(formula, data, weights, subset, na.action, rmap, times, 
method=c("ederer", "hakulinen", "conditional", "individual.h", "individual.s"), 
cohort=TRUE, conditional=FALSE, 
ratetable=survexp::survexp.us, scale=1, 
se.fit, model=FALSE, x=FALSE, y=FALSE)
```

### Arguments

- **formula**: formula object. The response variable is a vector of follow-up times and is optional. The predictors consist of optional grouping variables separated by the `+` operator (as in `survfit`), and is often `~1`, i.e., expected survival for the entire group.
- **data**: data frame in which to interpret the variables named in the formula, subset and weights arguments.
- **weights**: case weights. This is most useful when conditional survival for a known population is desired, e.g., the data set would contain all unique age/sex combinations and the weights would be the proportion of each.
- **subset**: expression indicating a subset of the rows of data to be used in the fit.
- **na.action**: function to filter missing data. This is applied to the model frame after subset has been applied. Default is `options()$na.action`.
- **rmap**: an optional list that maps data set names to the ratetable names. See the details section below.
- **times**: vector of follow-up times at which the resulting survival curve is evaluated. If absent, the result will be reported for each unique value of the vector of times supplied in the response value of the formula.
- **method**: computational method for the creating the survival curves. The `individual` option does not create a curve, rather it retrieves the predicted survival `individual.s` or cumulative hazard `individual.h` for each subject. The default is to use `method='ederer'` if the formula has no response, and `method='hakulinen'` otherwise.
cohort logical value. This argument has been superseded by the method argument. To maintain backwards compatibility, if is present and FALSE, it implies method='individual.s'.

cohort conditional logical value. This argument has been superseded by the method argument. To maintain backwards compatibility, if it is present and TRUE it implies method='conditional'.

ratetable a table of event rates, such as survexp.mn, or a fitted Cox model. Note the survival:: prefix in the default argument is present to avoid the (rare) case of a user who expects the default table but just happens to have an object named "survexp.us" in their own directory.

scale numeric value to scale the results. If ratetable is in units/day, scale = 365.25 causes the output to be reported in years.

se.fit compute the standard error of the predicted survival. This argument is currently ignored. Standard errors are not a defined concept for population rate tables (they are treated as coming from a complete census), and for Cox models the calculation is hard. Despite good intentions standard errors for this latter case have not been coded and validated.

model,x,y flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.

Details

Individual expected survival is usually used in models or testing, to ‘correct’ for the age and sex composition of a group of subjects. For instance, assume that birth date, entry date into the study, sex and actual survival time are all known for a group of subjects. The survexp.us population tables contain expected death rates based on calendar year, sex and age. Then

```r
haz <- survexp(fu.time ~ 1, data=mydata,
               method='individual.s'))
```

gives for each subject the total hazard experienced up to their observed death time or last follow-up time (variable fu.time) This probability can be used as a rescaled time value in models:

```r
glm(status ~ 1 + offset(log(haz)), family=poisson)
glm(status ~ x + offset(log(haz)), family=poisson)
```

In the first model, a test for intercept=0 is the one sample log-rank test of whether the observed group of subjects has equivalent survival to the baseline population. The second model tests for an effect of variable x after adjustment for age and sex.

The ratetable being used may have different variable names than the user’s data set, this is dealt with by the rmap argument. The rate table for the above calculation was survexp.us, a call to summary(survexp.us) reveals that it expects to have variables age = age in days, sex, and year = the date of study entry, we create them in the rmap line. The sex variable was not mapped, therefore the function assumes that it exists in mydata in the correct format. (Note: for factors such as sex, the program will match on any unique abbreviation, ignoring case.)

Cohort survival is used to produce an overall survival curve. This is then added to the Kaplan-Meier plot of the study group for visual comparison between these subjects and the population at large.
There are three common methods of computing cohort survival. In the "exact method" of Ederer the cohort is not censored, for this case no response variable is required in the formula. Hakulinen recommends censoring the cohort at the anticipated censoring time of each patient, and Verheul recommends censoring the cohort at the actual observation time of each patient. The last of these is the conditional method. These are obtained by using the respective time values as the follow-up time or response in the formula.

Value

if cohort=TRUE an object of class survexp, otherwise a vector of per-subject expected survival values. The former contains the number of subjects at risk and the expected survival for the cohort at each requested time. The cohort survival is the hypothetical survival for a cohort of subjects enrolled from the population at large, but matching the data set on the factors found in the rate table.

References


See Also

survfit, pyears, survexp.us, ratetable, survexp.fit.

Examples

# Stanford heart transplant data
# We don't have sex in the data set, but know it to be nearly all males.
# Estimate of conditional survival
fit1 <- survexp(futime ~ 1, rmap=list(sex="male", year=accept.dt,
   age=(accept.dt-birth.dt)), method='conditional', data=jasa)
summary(fit1, times=1:10*182.5, scale=365) #expected survival by 1/2 years

# Estimate of expected survival stratified by prior surgery
survexp(~ surgery, rmap= list(sex="male", year=accept.dt,
   age=(accept.dt-birth.dt)), method='ederer', data=jasa,
   times=1:10 * 182.5)

## Compare the survival curves for the Mayo PBC data to Cox model fit
##
plfit <-coxph(Surv(time,status>0) ~ trt + log(bili) + log(protime) + age +
survexp.fit

Compute Expected Survival

Description

Compute expected survival times.

Usage

survexp.fit(group, x, y, times, death, ratetable)

Arguments

group  
if there are multiple survival curves this identifies the group, otherwise it is a constant. Must be an integer.

x  
A matrix whose columns match the dimensions of the ratetable, in the correct order.

y  the follow up time for each subject.

times  the vector of times at which a result will be computed.

death  a logical value, if TRUE the conditional survival is computed, if FALSE the cohort survival is computed. See survexp for more details.

ratetable  a rate table, such as survexp.uswhite.

Details

For conditional survival y must be the time of last follow-up or death for each subject. For cohort survival it must be the potential censoring time for each subject, ignoring death.

For an exact estimate times should be a superset of y, so that each subject at risk is at risk for the entire sub-interval of time. For a large data set, however, this can use an inordinate amount of storage and/or compute time. If the times spacing is more coarse than this, an actuarial approximation is used which should, however, be extremely accurate as long as all of the returned values are > .99.

For a subgroup of size 1 and times > y, the conditional method reduces to exp(-h) where h is the expected cumulative hazard for the subject over his/her observation time. This is used to compute individual expected survival.

Value

A list containing the number of subjects and the expected survival(s) at each time point. If there are multiple groups, these will be matrices with one column per group.
Warning

Most users will call the higher level routine `survexp`. Consequently, this function has very few error checks on its input arguments.

See Also

`survexp`, `survexp.us`.

---

**survexp.object**

**Expected Survival Curve Object**

**Description**

This class of objects is returned by the `survexp` class of functions to represent a fitted survival curve.

Objects of this class have methods for `summary`, and inherit the `print`, `plot`, `points` and `lines` methods from `survfit`.

**Arguments**

- `surv`: the estimate of survival at time t+0. This may be a vector or a matrix.
- `n.risk`: the number of subjects who contribute at this time.
- `time`: the time points at which the curve has a step.
- `std.err`: the standard error of the cumulative hazard or -log(survival).
- `strata`: if there are multiple curves, this component gives the number of elements of the `time` etc. vectors corresponding to the first curve, the second curve, and so on. The names of the elements are labels for the curves.
- `method`: the estimation method used. One of "Ederer", "Hakulinen", or "conditional".
- `na.action`: the returned value from the `na.action` function, if any. It will be used in the printout of the curve, e.g., the number of observations deleted due to missing values.
- `call`: an image of the call that produced the object.

**Structure**

The following components must be included in a legitimate `survfit` object.

**Subscripts**

Survexp objects that contain multiple survival curves can be subscripted. This is most often used to plot a subset of the curves.
Details

In expected survival each subject from the data set is matched to a hypothetical person from the parent population, matched on the characteristics of the parent population. The number at risk printed here is the number of those hypothetical subject who are still part of the calculation. In particular, for the Ederer method all hypotheticals are retained for all time, so \texttt{n.risk} will be a constant.

See Also

\texttt{plot.survfit}, \texttt{summary.survexp}, \texttt{print.survfit}, \texttt{survexp}.

survfit

Create survival curves

Description

This function creates survival curves from either a formula (e.g. the Kaplan-Meier), a previously fitted Cox model, or a previously fitted accelerated failure time model.

Usage

\texttt{survfit(formula, ...)}

Arguments

\texttt{formula} \hspace{1cm} either a formula or a previously fitted model
\texttt{...} \hspace{1cm} other arguments to the specific method

Details

A survival curve is based on a tabulation of the number at risk and number of events at each unique death time. When time is a floating point number the definition of "unique" is subject to interpretation. The code uses factor() to define the set. For further details see the documentation for the appropriate method, i.e., \texttt{?survfit.formula} or \texttt{?survfit.coxph}.

A survfit object may contain a single curve, a set of curves, or a matrix curves. Predicted curves from a coxph model have one row for each stratum in the Cox model fit and one column for each specified covariate set. Curves from a multi-state model have one row for each stratum and a column for each state, the strata correspond to predictors on the right hand side of the equation. The default printing and plotting order for curves is by column, as with other matrices.

Curves can be subscripted using either a single or double subscript. If the set of curves is a matrix, as in the above, and one of the dimensions is 1 then the code allows a single subscript to be used. (That is, it is not quite as general as using a single subscript for a numeric matrix.)

Value

An object of class \texttt{survfit} containing one or more survival curves.
Note

Older releases of the code also allowed the specification for a single curve to omit the right hand of the formula, i.e., `survfit(Surv(time, status))`, in which case the formula argument is not actually a formula. Handling this case required some non-standard and fairly fragile manipulations, and this case is no longer supported.

Author(s)

Terry Therneau

See Also

`survfit.formula`, `survfit.coxph`, `survfit.object`, `print.survfit`, `plot.survfit`, `quantile.survfit`, `summary.survfit`

---

**survfit.coxph**

**Compute a Survival Curve from a Cox model**

**Description**

Computes the predicted survivor function for a Cox proportional hazards model.

**Usage**

```r
## S3 method for class 'coxph'
survfit(formula, newdata,
       se.fit=TRUE, conf.int=.95,
       individual=FALSE,
       type,vartype,
       conf.type=c("log","log-log","plain","none","logit","arcsin"),
       censor=TRUE, id, start.time,
       na.action=na.pass, ...)
```

**Arguments**

- `formula`: A coxph object.
- `newdata`: A data frame with the same variable names as those that appear in the coxph formula. It is also valid to use a vector, if the data frame would consist of a single row.
  The curve(s) produced will be representative of a cohort whose covariates correspond to the values in newdata. Default is the mean of the covariates used in the coxph fit.
- `individual`: This argument has been superseded by the `id` argument and is present only for backwards compatibility. A logical value indicating whether each row of `newdata` represents a distinct individual (FALSE, the default), or if each row of the data frame represents different time epochs for only one individual (TRUE). In the former case the result will have one curve for each row in `newdata`, in the latter only a single curve will be produced.
conf.int  the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.

se.fit  a logical value indicating whether standard errors should be computed. Default is TRUE.

type,vartype  a character string specifying the type of survival curve. Possible values are "aalen", "efron", or "kalbfleisch-prentice" (only the first two characters are necessary). The default is to match the computation used in the Cox model. The Nelson-Aalen-Breslow estimate for ties='breslow', the Efron estimate for ties='efron' and the Kalbfleisch-Prentice estimate for a discrete time model ties='exact'. Variance estimates are the Aalen-Link-Tsiatis, Efron, and Greenwood. The default will be the Efron estimate for ties='efron' and the Aalen estimate otherwise.

cf.type One of "none", "plain", "log" (the default), "log-log" or "logit". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals curve ± k *se(curve), where k is determined from conf.int. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option uses the log hazard or log(-log(survival)), and the logit log(survival/(1-survival)).

censor  if FALSE time points at which there are no events (only censoring) are not included in the result.

id  optional variable name of subject identifiers. If this is present, then each group of rows with the same subject id represents the covariate path through time of a single subject, and the result will contain one curve per subject. If the coxph fit had strata then that must also be specified in newdata. If missing, then each individual row of newdata is presumed to represent a distinct subject and there will be nrow(newdata) times the number of strata curves in the result (one for each strata/subject combination). result.

start.time  optional starting time, a single numeric value. If present the returned curve contains survival after start.time conditional on surviving to start.time.

na.action  the na.action to be used on the newdata argument

Details

Serious thought has been given to removing the default value for newdata, which is to use a single "pseudo" subject with covariate values equal to the means of the data set, since the resulting curve(s) almost never make sense. It remains due to an unwarranted attachment to the option shown by some users and by other packages. Two particularly egregious examples are factor variables and interactions. Suppose one were studying interspecies transmission of a virus, and the data set has a factor variable with levels ("pig", "chicken") and about equal numbers of observations for each. The "mean" covariate level will be 1/2 – is this a flying pig? As to interactions assume data with sex coded as 0/1, ages ranging from 50 to 80, and a model with age*sex. The "mean" value for the age:sex interaction term will be about 30, a value that does not occur in the data. Users are strongly advised to use the newdata argument.

When the original model contains time-dependent covariates, then the path of that covariate through time needs to be specified in order to obtain a predicted curve. This requires newdata to contain
multiple lines for each hypothetical subject which gives the covariate values, time interval, and strata for each line (a subject can change strata), along with an id variable which demarks which rows belong to each subject. The time interval must have the same (start, stop, status) variables as the original model: although the status variable is not used and thus can be set to a dummy value of 0 or 1, it is necessary for the variables to be recognized as a Surv object. Last, although predictions with a time-dependent covariate path can be useful, it is very easy to create a prediction that is senseless. Users are encouraged to seek out a text that discusses the issue in detail.

When a model contains strata but no time-dependent covariates the user of this routine has a choice. If newdata argument does not contain strata variables then the returned object will be a matrix of survival curves with one row for each strata in the model and one column for each row in newdata. (This is the historical behavior of the routine.) If newdata does contain strata variables, then the result will contain one curve per row of newdata, based on the indicated stratum of the original model. In the rare case of a model with strata by covariate interactions the strata variable must be included in newdata, the routine does not allow it to be omitted (predictions become too confusing). (Note that the model Surv(time, status) ~ age*strata(sex) expands internally to strata(sex) + age:sex; the sex variable is needed for the second term of the model.)

When all the coefficients are zero, the Kalbfleisch-Prentice estimator reduces to the Kaplan-Meier, the Aalen estimate to the exponential of Nelson’s cumulative hazard estimate, and the Efron estimate to the Fleming-Harrington estimate of survival. The variances of the curves from a Cox model are larger than these non-parametric estimates, however, due to the variance of the coefficients.

See `survfit` for more details about the counts (number of events, number at risk, etc.)

The censor argument was fixed at FALSE in earlier versions of the code and not made available to the user. The default argument is sensible in most instances — and causes the familiar + sign to appear on plots — it is not sensible for time dependent covariates since it may lead to a large number of spurious marks.

**Value**

an object of class "survfit". See `survfit.object` for details. Methods defined for survfit objects are `print`, `plot`, `lines`, and `points`.

**Notes**

If the following pair of lines is used inside of another function then the model=TRUE argument must be added to the coxph call: `fit <- coxph(...); survfit(fit)`. This is a consequence of the non-standard evaluation process used by the model.frame function when a formula is involved.

**References**


**See Also**

`print.survfit`, `plot.survfit`, `lines.survfit`, `coxph`, `Surv`, `strata`.

**Examples**

```r
# fit a Kaplan-Meier and plot it
fit <- survfit(Surv(time, status) ~ x, data = aml)
plot(fit, lty = 2:3)
legend(100, .8, c("Maintained", "Nonmaintained"), lty = 2:3)

# fit a Cox proportional hazards model and plot the predicted survival for a 60 year old
fit <- coxph(Surv(futime, fustat) ~ age, data = ovarian)
plot(survfit(fit, newdata=data.frame(age=60)),
     xscale=365.25, xlab = "Years", ylab="Survival")

# Here is the data set from Turnbull
# There are no interval censored subjects, only left-censored (status=3),
# right-censored (status 0) and observed events (status 1)
#
# Time
# Type of observation
#  death  12  6  2  3
#  losses  3  2  0  3
#  late entry  2  4  2  5
#
tdata <- data.frame(time =c(1,1,2,2,3,3,3,4,4,4),
                     status=rep(1,0,2,4),
                     n =c(1,3,2,6,2,4,2,0,2,3,3,5))
fit <- survfit(Surv(time, time, status, type='interval') ~1,
               data=tdata, weight=n)

# Time to progression/death for patients with monoclonal gammapathy
# Competing risk curves (cumulative incidence)
fit1 <- survfit(Surv(stop, event=='pcm') ~1, data=mgus1,
                subset=(start==0))
fit2 <- survfit(Surv(stop, status) ~1, data=mgus1,
                subset=(start==0), etype=event) #competing risks
# CI curves are always plotted from 0 upwards, rather than 1 down
plot(fit2, fun='event', xscale=365.25, xmax=7300, mark.time=FALSE,
     conf.int=FALSE)
lines(fit1, fun='event', xscale=365.25, xmax=7300, mark.time=FALSE,
     conf.int=FALSE)

# "Competing Risk: death", col=3)
text(10, .4, "Competing Risk: progression", col=2)
text(15, .30,"KM:prog")
```
survfit.formula  
Compute a Survival Curve for Censored Data

Description
Computes an estimate of a survival curve for censored data. More multi-state data the Andersen-Johnsen estimate is use, for ordinary survival either the Kaplan-Meier or Fleming-Harrington estimate is produced.

Usage
## S3 method for class 'formula'
survfit(formula, data, weights, subset, na.action, etype, id, istate, timefix=TRUE, ...)

Arguments

- **formula**  
a formula object, which must have a Surv object as the response on the left of the ~ operator and, if desired, terms separated by + operators on the right. One of the terms may be a strata object. For a single survival curve the right hand side should be ~ 1.

- **data**  
a data frame in which to interpret the variables named in the formula, subset and weights arguments.

- **weights**  
The weights must be nonnegative and it is strongly recommended that they be strictly positive, since zero weights are ambiguous, compared to use of the subset argument.

- **subset**  
expression saying that only a subset of the rows of the data should be used in the fit.

- **na.action**  
a missing-data filter function, applied to the model frame, after any subset argument has been used. Default is options()$na.action.

- **etype**  
a variable giving the type of event. This has been superseded by multi-state Surv objects; see example below.

- **id**  
identifies individual subjects, when a given person can have multiple lines of data.

- **istate**  
for multi-state models, identifies the initial state of each subject

- **timefix**  
process times through the aeqSurv function to eliminate potential roundoff issues.

- **...**  
The following additional arguments are passed to internal functions called by survfit.

  - **type**  
a character string specifying the type of survival curve. Possible values are "kaplan-meier", "fleming-harrington" or "fh2" if a formula is given. This is ignored for competing risks or when the Turnbull estimator is used.
error a character string specifying the error. Possible values are "greenwood" for the Greenwood formula or "tsiatis" or "aalen" for the Tsiatis/Aalen formula, or "robust" for a robust variance. The last of these is assumed if non-integer case weights are provided.

conf.type One of "none", "plain", "log" (the default), "log-log" or "logit". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals $\text{curve KM}$, where $k$ is determined from conf.int. The log option calculates intervals based on the cumulative hazard or log(survival). The log-log option bases the intervals on the log hazard or log(-log(survival)), and the logit option on log(survival/(1-survival)).

conf.lower a character string to specify modified lower limits to the curve, the upper limit remains unchanged. Possible values are "usual" (unmodified), "peto", and "modified". The modified lower limit is based on an "effective n" argument. The confidence bands will agree with the usual calculation at each death time, but unlike the usual bands the confidence interval becomes wider at each censored observation. The extra width is obtained by multiplying the usual variance by a factor $m/n$, where $n$ is the number currently at risk and $m$ is the number at risk at the last death time. (The bands thus agree with the un-modified bands at each death time.) This is especially useful for survival curves with a long flat tail.

The Peto lower limit is based on the same "effective n" argument as the modified limit, but also replaces the usual Greenwood variance term with a simple approximation. It is known to be conservative.

start.time numeric value specifying a time to start calculating survival information. The resulting curve is the survival conditional on surviving to start.time.

cnf.int the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.

se.fit a logical value indicating whether standard errors should be computed. Default is TRUE.

influence a logical value indicating whether to return the infinitesimal jackknife (influence) values for each subject. These contain the values of the derivative of each value with respect to the case weights of each subject $i$: $\partial p/\partial w_i$, evaluated at the vector of weights $w = 1$. The array will have dimensions (number of subjects, 1+ number of unique times, number of states); be forewarned that this can be huge. If the total number of elements is larger then the maximum integer the underlying C program can not create it.

istate this applies only to multi-state curves. An optional variable that gives the starting state for each subject. If missing then all subjects are assumed to start in an single un-named state. When a subject has multiple rows only the value from their first (minimal time) row is used.

p0 this applies only to multi-state curves. An optional vector giving the initial probability across the states. If this is missing, then p0 is estimated using the frequency of the starting states of all observations at risk at start.time, or if that is not specified, at the time of the first event.
Details

The estimates used are the Kalbfleisch-Prentice (Kalbfleisch and Prentice, 1980, p.86) and the Tsiatis/Link/Breslow, which reduce to the Kaplan-Meier and Fleming-Harrington estimates, respectively, when the weights are unity.

The Greenwood formula for the variance is a sum of terms $d/(n*(n-m))$, where $d$ is the number of deaths at a given time point, $n$ is the sum of weights for all individuals still at risk at that time, and $m$ is the sum of weights for the deaths at that time. The justification is based on a binomial argument when weights are all equal to one; extension to the weighted case is ad hoc. Tsiatis (1981) proposes a sum of terms $d/(n*n)$, based on a counting process argument which includes the weighted case.

The two variants of the F-H estimate have to do with how ties are handled. If there were 3 deaths out of 10 at risk, then the first increments the hazard by $3/10$ and the second by $1/10 + 1/9 + 1/8$. For the first method $S(t) = \exp(H)$, where $H$ is the Nelson-Aalen cumulative hazard estimate, whereas the $fh2$ method will give results $S(t)$ results closer to the Kaplan-Meier.

When the data set includes left censored or interval censored data (or both), then the EM approach of Turnbull is used to compute the overall curve. When the baseline method is the Kaplan-Meier, this is known to converge to the maximum likelihood estimate.

The cumulative incidence curve is an alternative to the Kaplan-Meier for competing risks data. For instance, in patients with MGUS, conversion to an overt plasma cell malignancy occurs at a nearly constant rate among those still alive. A Kaplan-Meier estimate, treating death due to other causes as censored, gives a 20 year cumulative rate of 33% for the 241 early patients of Kyle. This estimates the incidence of conversion if all other causes of death were removed, which is an unrealistic assumption given the mean starting age of 63 and a median follow up of over 21 years.

The CI estimate, on the other hand, estimates the total number of conversions that will actually occur. Because the population is older, this is much smaller than the KM, 22% at 20 years for Kyle’s data. If there were no censoring, then CI(t) could very simply be computed as total number of patients with progression by time t divided by the sample size n.

Value

an object of class "survfit". See survfit.object for details. Methods defined for survfit objects are print, plot, lines, and points.

References


See Also

`survfit.coxph` for survival curves from Cox models, `survfit.object` for a description of the components of a survfit object, `print.survfit`, `plot.survfit`, `lines.survfit`, `coxph`, `Surv`.

Examples

```r
# fit a Kaplan-Meier and plot it
fit <- survfit(Surv(time, status) ~ x, data = aml)
plot(fit, lty = 2:3)
legend(100, .8, c("Maintained", "Nonmaintained"), lty = 2:3)

# fit a Cox proportional hazards model and plot the
predicted survival for a 60 year old
fit <- coxph(Surv(futime, fustat) ~ age, data = ovarian)
plot(survfit(fit, newdata=data.frame(age=60)),
     xscale=365.25, xlab = "Years", ylab="Survival")

# Here is the data set from Turnbull
# There are no interval censored subjects, only left-censored (status=3),
# right-censored (status 0) and observed events (status 1)
#
# Time
#
# Type of observation
# death 12 6 2 3
# losses 3 2 0 3
# late entry 2 4 2 5
#
tdata <- data.frame(time =c(1,1,2,2,2,3,3,3,4,4,4),
                    status=rep(c(1,0,2),4),
                    n =c(12,3,2,6,2,4,2,8,2,3,3,5))
fit <- survfit(Surv(time, status, type='interval') ~1,
data=tdata, weight=n)

# Time to progression/death for patients with monoclonal gammopathy
# Competing risk curves (cumulative incidence)
fitKM <- survfit(Surv(stop, event=='pcm') ~1, data=mgus1,
                 subset=(start==0))
fitCI <- survfit(Surv(stop, status=as.numeric(event), type="mstate") ~1,
data=mgus1, subset=(start==0))

# CI curves are always plotted from 0 upwards, rather than 1 down
plot(fitCI, xscale=365.25, xmax=7300, mark.time=FALSE,
col=2:3, xlab="Years post diagnosis of MGUS")
lines(fitKM, fun='event', xmax=7300, mark.time=FALSE,
     conf.int=FALSE)
```
survfit.matrix

Create Aalen-Johansen estimates of multi-state survival from a matrix of hazards.

Description

This allows one to create the Aalen-Johansen estimate of P, a matrix with one column per state and one row per time, starting with the individual hazard estimates. Each row of P will sum to 1.

Usage

```r
## S3 method for class 'matrix'
survfit(formula, p0, method = c("discrete", "matexp"),
        start.time, ...)
```

Arguments

- `formula`: a matrix of lists, each element of which is either NULL or a survival curve object.
- `p0`: the initial state vector. The names of this vector are used as the names of the states in the output object. If there are multiple curves then `p0` can be a matrix with one row per curve.
- `method`: use a product of discrete hazards, or a product of matrix exponentials. See details below.
- `start.time`: optional; start the calculations at a given starting point
- `...`: further arguments used by other survfit methods

Details

On input the matrix should contain a set of predicted curves for each possible transition, and NULL in other positions. Each of the predictions will have been obtained from the relevant Cox model. This approach for multistate curves is easy to use but has some caveats. First, the input curves must be consistent. The routine checks as best it can, but can easily be fooled. For instance, if one were to fit two Cox models, obtain predictions for males and females from one, and for treatment A and B from the other, this routine will create two curves but they are not meaningful. A second issue is that standard errors are not produced.

The names of the resulting states are taken from the names of the vector of initial state probabilities. If they are missing, then the dimnames of the input matrix are used, and lacking that the labels '1', '2', etc. are used.

For the usual Aalen-Johansen estimator the multiplier at each event time is the matrix of hazards H (also written as I + dA). When using predicted survival curves from a Cox model, however, it is possible to get predicted hazards that are greater than 1, which leads to probabilities less than 0. If
the method argument is not supplied and the input curves are derived from a Cox model this routine instead uses the approximation expm(H-I) as the multiplier, which always gives valid probabilities. (This is also the standard approach for ordinary survival curves from a Cox model.)

**Value**

a `survfitms` object

**Note**

The R syntax for creating a matrix of lists is very fussy.

**Author(s)**

Terry Therneau

**See Also**

`survfit`

**Examples**

```r
etime <- with(mgus2, ifelse(pstat==0, ftime, ptime))
event <- with(mgus2, ifelse(pstat==0, 2*death, 1))
event <- factor(event, 0:2, labels=c("censor", "pcm", "death"))

cfit1 <- coxph(Surv(etime, event="pcm") ~ age + sex, mgus2)
cfit2 <- coxph(Surv(etime, event="death") ~ age + sex, mgus2)

# predicted competing risk curves for a 72 year old with mspike of 1.2
# (median values), male and female.
# The survfit call is a bit faster without standard errors.
newdata <- expand.grid(sex=c("F", "M"), age=72, mspike=1.2)

AJmat <- matrix(list(), 3,3)
AJmat[1,2] <- list(survfit(cfit1, newdata, std.err=FALSE))
AJmat[1,3] <- list(survfit(cfit2, newdata, std.err=FALSE))
csurv <- survfit(AJmat, p= c(entry=1, PCM=0, death=0))
```

---

**Description**

This class of objects is returned by the `survfit` class of functions to represent a fitted survival curve. For a multi-state model the object has class `c('survfitms', 'survfit').` Objects of this class have methods for the functions `print`, `summary`, `plot`, `points` and `lines`. The `print.survfit` method does more computation than is typical for a print method and is documented on a separate page.
Arguments

- **n**: total number of subjects in each curve.
- **time**: the time points at which the curve has a step.
- **n.risk**: the number of subjects at risk at time t.
- **n.event**: the number of events that occur at time t.
- **n.enter**: for counting process data only, the number of subjects that enter at time t.
- **n.censor**: for counting process data only, the number of subjects who exit the risk set, without an event, at time t. (For right censored data, this number can be computed from the successive values of the number at risk).
- **surv**: the estimate of survival at time t+0. This may be a vector or a matrix. The latter occurs when a set of survival curves is created from a single Cox model, in which case there is one column for each covariate set.
- **prev, p0**: a multi-state survival will have the `prev` component instead of `surv`. It will be a matrix containing the estimated probability of each state at each time, one column per state. The `p0` matrix contains the initial distribution of states. (On further reflection `pstate = "probability in state"` would have been a much better label than "prevalence", but by that point too many other packages were dependent on the form of the result.)
- **std.err**: for a survival curve this contains standard error of the cumulative hazard or `-log(survival)`, for a multi-state curve it contains the standard error of `prev`. This difference is a reflection of the fact that each is the natural calculation for that case.
- **cumhaz, hazard**: optional. For a multi-state curve this is an k by k array for each time point, where k is the number of states.
- **upper**: upper confidence limit for the survival curve or probability
- **lower**: lower confidence limit for the survival curve or probability
- **strata**: if there are multiple curves, this component gives the number of elements of the `time` etc. vectors corresponding to the first curve, the second curve, and so on. The names of the elements are labels for the curves.
- **start.time**: the value specified for the `start.time` argument, if it was used in the call.
- **n.all**: for counting process data, and any time that the `start.time` argument was used, this contains the total number of observations that were available. Not all may have been used in creating the curve, in which case this value will be larger than `n` above.
- **conf.type**: the approximation used to compute the confidence limits.
- **conf.int**: the level of the confidence limits, e.g. 90 or 95%.
- **transitions**: for multi-state data, the total number of transitions of each type.
- **na.action**: the returned value from the `na.action` function, if any. It will be used in the printout of the curve, e.g., the number of observations deleted due to missing values.
- **call**: an image of the call that produced the object.
- **type**: type of survival censoring.
influence

optional, for survfitms objects only. A list with one element per stratum, each element of the list is an array indexed by subject, time, state. The time dimension will have one more element than the prev matrix, the first row is the subject’s influence on the initial prevalence (just before the first time point). If there is only one curve a list is not needed.

Structure

The following components must be included in a legitimate survfit or survfitms object.

Subscripts

Survfit objects that contain multiple survival curves can be subscripted. This is often used to plot a subset of the curves. If the surv or prev component is a matrix then the survfit object will be treated as a matrix, otherwise only a single subscript is used.

See Also

plot.survfit, summary.survfit, print.survfit, survfit.

survfitcoxph.fit

A direct interface to the ‘computational engine’ of survfit.coxph

Description

This program is mainly supplied to allow other packages to invoke the survfit.coxph function at a ‘data’ level rather than a ‘user’ level. It does no checks on the input data that is provided, which can lead to unexpected errors if that data is wrong.

Usage

survfitcoxph.fit(y, x, wt, x2, risk, newrisk, strata, se.fit, survtype, vartype, varmat, id, y2, strata2, unlist=TRUE)

Arguments

y

d the response variable used in the Cox model. (Missing values removed of course.)

x
covariate matrix used in the Cox model

wt
weight vector for the Cox model. If the model was unweighted use a vector of 1s.

x2
matrix describing the hypothetical subjects for which a curve is desired. Must have the same number of columns as x.

risk
the risk score exp(X beta) from the fitted Cox model. If the model had an offset, include it in the argument to exp.

newrisk
risk scores for the hypothetical subjects
strata variable used in the Cox model. This will be a factor.

se.fit if TRUE the standard errors of the curve(s) are returned

survtype 1=Kalbfleisch-Prentice, 2=Nelson-Aalen, 3=Efron. It is usual to match this to the approximation for ties used in the coxph model: KP for ‘exact’, N-A for ‘breslow’ and Efron for ‘efron’.

vartype 1=Greenwood, 2=Aalen, 3=Efron

varmat the variance matrix of the coefficients

id optional; if present and not NULL this should be a vector of identifiers of length nrow(x2). A non-null value signifies that x2 contains time dependent covariates, in which case this identifies which rows of x2 go with each subject.

y2 survival times, for time dependent prediction. It gives the time range [time1,time2] for each row of x2. Note: this must be a Surv object and thus contains a status indicator, which is never used in the routine, however.

strata2 vector of strata indicators for x2. This must be a factor.

unlist if FALSE the result will be a list with one element for each strata. Otherwise the strata are “unpacked” into the form found in a survfit object.

Value

a list containing nearly all the components of a survfit object. All that is missing is to add the confidence intervals, the type of the original model’s response (as in a coxph object), and the class.

Note

The source code for for both this function and survfit.coxph is written using noweb. For complete documentation see the inst/sourcecode.pdf file.

Author(s)

Terry Therneau

See Also

survfit.coxph

survobrien O’Brien’s Test for Association of a Single Variable with Survival

Description

Peter O’Brien’s test for association of a single variable with survival This test is proposed in Biometrics, June 1978.

Usage

survobrien(formula, data, subset, na.action, transform)
Arguments

**formula**
- a valid formula for a cox model.

**data**
- a data.frame in which to interpret the variables named in the formula, or in the subset and the weights argument.

**subset**
- expression indicating which subset of the rows of data should be used in the fit. All observations are included by default.

**na.action**
- a missing-data filter function. This is applied to the model.frame after any subset argument has been used. Default is \texttt{options(\$na.action)}.

**transform**
- the transformation function to be applied at each time point. The default is O’Brien’s suggestion \texttt{logit(tr) where tr = (rank(x)- 1/2)/ length(x) is the rank shifted to the range 0-1 and logit(x) = log(x/(1-x)) is the logit transform.}

Value

A new data frame. The response variables will be column names returned by the Surv function, i.e., "time" and "status" for simple survival data, or "start", "stop", "status" for counting process data. Each individual event time is identified by the value of the variable \texttt{strata}. Other variables retain their original names. If a predictor variable is a factor or is protected with \texttt{I()}, it is retained as is. Other predictor variables have been replaced with time-dependent logit scores.

The new data frame will have many more rows that the original data, approximately the original number of rows * number of deaths/2.

Method

A time-dependent cox model can now be fit to the new data. The univariate statistic, as originally proposed, is equivalent to single variable score tests from the time-dependent model. This equivalence is the rationale for using the time dependent model as a multivariate extension of the original paper.

In O’Brien’s method, the x variables are re-ranked at each death time. A simpler method, proposed by Prentice, ranks the data only once at the start. The results are usually similar.

Note

A prior version of the routine returned new time variables rather than a strata. Unfortunately, that strategy does not work if the original formula has a strata statement. This new data set will be the same size, but the coxph routine will process it slightly faster.

References


See Also

\texttt{survdiff}
Examples

xx <- survbrien(Surv(futime, fustat) ~ age + factor(rx) + I(ecog.ps),
               data=ovarian)
coxph(Surv(time, status) ~ age + strata(strata.), data=xx)

survreg
Regression for a Parametric Survival Model

Description

Fit a parametric survival regression model. These are location-scale models for an arbitrary transform of the time variable; the most common cases use a log transformation, leading to accelerated failure time models.

Usage

survreg(formula, data, weights, subset,
        na.action, dist="weibull", init=NULL, scale=0,
        control,parms=NULL,model=FALSE, x=FALSE,
        y=TRUE, robust=FALSE, score=FALSE, ...)

Arguments

formula a formula expression as for other regression models. The response is usually
         a survival object as returned by the Surv function. See the documentation for
         Surv, lm and formula for details.
data a data frame in which to interpret the variables named in the formula, weights
         or the subset arguments.
weights optional vector of case weights
subset subset of the observations to be used in the fit
na.action a missing-data filter function, applied to the model.frame, after any subset argument has been used. Default is options()$na.action.
dist assumed distribution for y variable. If the argument is a character string, then
       it is assumed to name an element from survreg.distributions. These include
       "weibull","exponential","gaussian","logistic","lognormal" and "loglogistic". 
       Otherwise, it is assumed to be a user defined list conforming to the format de-
       scribed in survreg.distributions.
parms a list of fixed parameters. For the t-distribution for instance this is the degrees
of freedom; most of the distributions have no parameters.
init optional vector of initial values for the parameters.
scale optional fixed value for the scale. If set to <=0 then the scale is estimated.
control a list of control values, in the format produced by survreg.control. The de-
         fault value is survreg.control()
model, x, y  flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.

score  return the score vector. (This is expected to be zero upon successful convergence.)

robust  Use robust ‘sandwich’ standard errors, based on independence of individuals if there is no cluster() term in the formula, based on independence of clusters if there is.

...  other arguments which will be passed to survreg.control.

Details

All the distributions are cast into a location-scale framework, based on chapter 2.2 of Kalbfleisch and Prentice. The resulting parameterization of the distributions is sometimes (e.g. gaussian) identical to the usual form found in statistics textbooks, but other times (e.g. Weibull) it is not. See the book for detailed formulas.

Value

an object of class survreg is returned.

References


See Also

survreg.object, survreg.distributions, pspline, frailty, ridge

Examples

# Fit an exponential model: the two fits are the same
survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='weibull', 
  scale=1)

survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, 
  dist='exponential')

# A model with different baseline survival shapes for two groups, i.e.,
# two different scale parameters
survreg(Surv(time, status) ~ ph.ecog + age + strata(sex), lung)

# There are multiple ways to parameterize a Weibull distribution. The survreg
# function embeds it in a general location-scale family, which is a
# different parameterization than the rweibull function, and often leads
# to confusion.
# survreg's scale = 1/(rweibull shape)
# survreg's intercept = log(rweibull scale)
# For the log-likelihood all parameterizations lead to the same value.
y <- rweibull(1000, shape=2, scale=5)
survreg(Surv(y)-1, dist="weibull")

# Economists fit a model called 'tobit regression', which is a standard
# linear regression with Gaussian errors, and left censored data.
tobinfit <- survreg(Surv(durable, durable>0, type='left') ~ age + quant,
                   data=tobin, dist='gaussian')

survreg.control

Package options for survreg and coxph

Description

This function checks and packages the fitting options for survreg

Usage

survreg.control(maxiter=30, rel.tolerance=1e-09, 
                toler.chol=1e-10, iter.max, debug=0, outer.max=10)

Arguments

maxiter maximum number of iterations
rel.tolerance relative tolerance to declare convergence
toler.chol Tolerance to declare Cholesky decomposition singular
iter.max same as maxiter
debuge debug print debugging information
outer.max maximum number of outer iterations for choosing penalty parameters

Value

A list with the same elements as the input

See Also

survreg
Description
List of distributions for accelerated failure models. These are location-scale families for some transformation of time. The entry describes the cdf $F$ and density $f$ of a canonical member of the family.

Usage
survreg.distributions

Format
There are two basic formats, the first defines a distribution de novo, the second defines a new distribution in terms of an old one.

name: name of distribution
variance: function(parms) returning the variance (currently unused)
init(x,weights,...): Function returning an initial estimate of the mean and variance (used for initial values in the iteration)
density(x,parms): Function returning a matrix with columns $F$, $1 - F$, $f$, $f'/f$, and $f''/f$
quantile(p,parms): Quantile function
scale: Optional fixed value for the scale parameter
parms: Vector of default values and names for any additional parameters
deviance(y,scale,parms): Function returning the deviance for a saturated model; used only for deviance residuals.

and to define one distribution in terms of another

name: name of distribution
dist: name of parent distribution
trans: transformation (eg log)
dtrans: derivative of transformation
itrans: inverse of transformation
scale: Optional fixed value for scale parameter

details
There are four basic distributions: extreme, gaussian, logistic and t. The last three are parametrised in the same way as the distributions already present in R. The extreme value cdf is

$$F = 1 - e^{-e^t}.$$
When the logarithm of survival time has one of the first three distributions we obtain respectively weibull, lognormal, and loglogistic. The location-scale parameterization of a Weibull distribution found in \texttt{survreg} is not the same as the parameterization of \texttt{rweibull}.

The other predefined distributions are defined in terms of these. The exponential and rayleigh distributions are Weibull distributions with fixed scale of 1 and 0.5 respectively, and loggaussian is a synonym for lognormal.

For speed parts of the three most commonly used distributions are hardcoded in C; for this reason the elements of \texttt{survreg.distributions} with names of "Extreme value", "Logistic" and "Gaussian" should not be modified. (The order of these in the list is not important, recognition is by name.) As an alternative to modifying \texttt{survreg.distributions} a new distribution can be specified as a separate list. This is the preferred method of addition and is illustrated below.

**See Also**

\texttt{survreg}, \texttt{pweibull}, \texttt{pnorm}, \texttt{plogis}, \texttt{pt}, \texttt{survregDtest}

**Examples**

```r
# time transformation
survreg(Surv(time, status) ~ ph.ecog + sex, dist='weibull', data=lung)
# change the transformation to work in years
# intercept changes by log(365), everything else stays the same
my.weibull <- survreg.distributions$weibull
my.weibull$trans <- function(y) log(y/365)
my.weibull$itrans <- function(y) 365*exp(y)
survreg(Surv(time, status) ~ ph.ecog + sex, lung, dist=my.weibull)

# Weibull parametrisation
y <- rweibull(1000, shape=2, scale=5)
survreg(Surv(y)-1, dist="weibull")
# survreg scale parameter maps to 1/shape, linear predictor to log(scale)

# Cauchy fit
mycauchy <- list(name='Cauchy',
                 init = function(x, weights, ...)
                   c(median(x), mad(x)),
                 density = function(x, parms) {
                   temp <- 1/(1 + x^2)
                   cbind(.5 + atan(x)/pi, .5+ atan(-x)/pi,
                         temp/pi, -2*x*temp, 2*temp*(4*x^2*temp -1))
                 },
                 quantile = function(p, parms) tan((p-.5)*pi),
                 deviance = function(...) stop('deviance residuals not defined'))
survreg(Surv(log(time), status) ~ ph.ecog + sex, lung, dist=mycauchy)
```
**survreg.object**

---

### Description

This class of objects is returned by the `survreg` function to represent a fitted parametric survival model. Objects of this class have methods for the functions `print`, `summary`, `predict`, and `residuals`.

### COMPONENTS

The following components must be included in a legitimate `survreg` object.

- **coefficients** the coefficients of the `linear.predictors`, which multiply the columns of the model matrix. It does not include the estimate of error (sigma). The names of the coefficients are the names of the single-degree-of-freedom effects (the columns of the model matrix). If the model is over-determined there will be missing values in the coefficients corresponding to non-estimable coefficients.

- **icoef** coefficients of the baseline model, which will contain the intercept and log(scale), or multiple scale factors for a stratified model.

- **var** the variance-covariance matrix for the parameters, including the log(scale) parameter(s).

- **loglik** a vector of length 2, containing the log-likelihood for the baseline and full models.

- **iter** the number of iterations required

- **linear.predictors** the linear predictor for each subject.

- **df** the degrees of freedom for the final model. For a penalized model this will be a vector with one element per term.

- **scale** the scale factor(s), with length equal to the number of strata.

- **idf** degrees of freedom for the initial model.

- **means** a vector of the column means of the coefficient matrix.

- **dist** the distribution used in the fit.

- **weights** included for a weighted fit.

The object will also have the following components found in other model results (some are optional): `linear.predictors, weights, x, y, model, call, terms` and `formula`. See `lm`.

### See Also

- `survreg`, `lm`
survregDtest  
Verify a survreg distribution

Description

This routine is called by survreg to verify that a distribution object is valid.

Usage

survregDtest(dlist, verbose = F)

Arguments

dlist  
the list describing a survival distribution

verbose  
return a simple TRUE/FALSE from the test for validity (the default), or a verbose description of any flaws.

Details

If the survreg function rejects your user-supplied distribution as invalid, this routine will tell you why it did so.

Value

TRUE if the distribution object passes the tests, and either FALSE or a vector of character strings if not.

Author(s)

Terry Therneau

See Also

survreg.distributions, survreg

Examples

# An invalid distribution (it should have "init =" on line 2)
# survreg would give an error message
mycauchy <- list(name='Cauchy',
  init<- function(x, weights, ...)
    c(median(x), mad(x)),
  density= function(x, parms) {
    temp <- 1/(1 + x^2)
    cbind(.5 + atan(temp)/pi, .5+ atan(-temp)/pi,
      temp/pi, -2 *x*temp, 2*temp^2*(4*x^2*temp -1))
  },
  quantile= function(p, parms) tan((p-.5)*pi),
  deviance= function(...) stop('deviance residuals not defined')
survSplit

Survival data set at specified times

Description
Given a survival data set and a set of specified cut times, split each record into multiple subrecords at each cut time. The new data set will be in ‘counting process’ format, with a start time, stop time, and event status for each record.

Usage
survSplit(formula, data, subset, na.action=na.pass,
cut, start="tstart", id, zero=0, episode,
end="tstop", event="event")

Arguments
formula a model formula
data a data frame
subset, na.action rows of the data to be retained
cut the vector of timepoints to cut at
start character string with the name of a start time variable (will be created if needed)
id character string with the name of new id variable to create (optional). This can be useful if the data set does not already contain an identifier.
zero If start doesn’t already exist, this is the time that the original records start.
episode character string with the name of new episode variable (optional)
end character string with the name of event time variable
event character string with the name of censoring indicator

Details
Each interval in the original data is cut at the given points; if an original row were (15, 60] with a cut vector of (10,30, 40) the resulting data set would have intervals of (15,30], (30,40] and (40, 60].

Each row in the final data set will lie completely within one of the cut intervals. Which interval for each row of the output is shown by the episode variable, where 1= less than the first cutpoint, 2= between the first and the second, etc. For the example above the values would be 2, 3, and 4.

The routine is called with a formula as the first argument. The right hand side of the formula can be used to delimit variables that should be retained; normally one will use ~. as a shorthand to retain them all. The routine will try to retain variable names, e.g. Survadam, joe, fred~. will
result in a data set with those same variable names for tstart, end, and event options rather than the defaults. Any user specified values for these options will be used if they are present, of course. However, the routine is not sophisticated; it only does this substitution for simple names. A call of Surv(time, stat=-2) for instance will not retain "stat" as the name of the event variable.

Rows of data with a missing time or status are copied across unchanged, unless the na.action argument is changed from its default value of na.pass. But in the latter case any row that is missing for any variable will be removed, which is rarely what is desired.

Value

New, longer, data frame.

See Also

Surv, cut, reshape

Examples

```r
fit1 <- coxph(Surv(time, status) ~ karno + age + trt, veteran)
plot(cox.zph(fit1)[1])
# a cox.zph plot of the data suggests that the effect of Karnofsky score
# begins to diminish by 60 days and has faded away by 120 days.
# Fit a model with separate coefficients for the three intervals.
#
vet2 <- survSplit(Surv(time, status) ~., veteran,
                   cut=c(60, 120), episode ="timegroup")
fit2 <- coxph(Surv(tstart, time, status) ~ karno* strata(timegroup) +
               age + trt, data= vet2)
c(overall= coef(fit1)[1],
   t0_60  = coef(fit2)[1],
   t60_120= sum(coef(fit2)[c(1,4)]),
   t120   = sum(coef(fit2)[c(1,5)]))
```

---

tcut  
Factors for person-year calculations

Description

Attaches categories for person-year calculations to a variable without losing the underlying continuous representation

Usage

```r
tcut(x, breaks, labels, scale=1)
## S3 method for class 'tcut'
levels(x)
```
Arguments

- **x**: numeric/date variable
- **breaks**: breaks between categories, which are right-continuous
- **labels**: labels for categories
- **scale**: Multiply x and breaks by this.

Value

An object of class `tcut`

See Also

cut, pyears

Examples

```r
mdy.date <- function(m,d,y)
  as.Date(paste(ifelse(y<1900, y+1900, y), m, d, sep='/'))
temp1 <- mdy.date(6,6,36)
temp2 <- mdy.date(6,6,55)# Now compare the results from person-years
  #
temp.age <- tcut(temp2-temp1, floor(c(-1, (18:31 * 365.24))),
  labels=c('0-18', paste(18:30, 19:31, sep='-' )))
temp.yr <- tcut(temp2, mdy.date(1,1,1954:1965), labels=1954:1964)
temp.time <- 3700 #total days of fu
py1 <- pyears(temp.time - temp.age + temp.yr, scale=1) #output in days
py1
```
Arguments

data1 the primary data set, to which new variables and/or observation will be added
data2 second data set in which all the other arguments will be found
id subject identifier
... operations that add new variables or intervals, see below
tstart optional variable to define the valid time range for each subject, only used on an initial call
tstop optional variable to define the valid time range for each subject, only used on an initial call
options a list of options. Valid ones are idname, tstartname, tstopname, delay, na.rm, and tdcstart. See the explanation below.

Details

The program is often run in multiple passes, the first of which defines the basic structure, and subsequent ones that add new variables to that structure. For a more complete explanation of how this routine works refer to the vignette on time-dependent variables.

There are 4 types of operational arguments: a time dependent covariate (tdc), cumulative count (cumtdc), event (event) or cumulative event (cumevent). Time dependent covariates change their values before an event, events are outcomes.

• newname = tdc(y, x) A new time dependent covariate variable will created. The argument y is assumed to be on the scale of the start and end time, and each instance describes the occurrence of a "condition" at that time. The second argument x is optional. In the case where x is missing the count variable starts at 0 for each subject and becomes 1 at the time of the event. If x is present the value of the time dependent covariate is initialized to the tdcstart option and is reset to the value of x at each observation. If the option na.rm=TRUE missing values of x are first removed, i.e., the update will not create missing values.

newname = cumtdc(y,x) Similar to tdc, except that the event count is accumulated over time for each subject.

newname = event(y,x) Mark an event at time y. In the usual case that x is missing the new 0/1 variable will be similar to the 0/1 status variable of a survival time.

newname = cumevent(y,x) Cumulative events.

The function adds three new variables to the output data set: tstart, tstop, and id. The options argument can be used to change these names. If data1 contains the tstart variable then that is used as the starting point for the created time intervals, otherwise the initial interval for each id will begin at 0 by default. This will lead to an invalid interval and subsequent error if say a death time were <= 0.

The na.rm option affects creation of time-dependent covariates. Should a data row in data2 that has a missing value for the variable be ignored (na.rm=FALSE, default) or should it generate an observation with a value of NA? The default value leads to "last value carried forward" behavior.

The delay option causes a time-dependent covariate’s new value to be delayed, see the vignette for an example.
Value

A data frame with two extra attributes: \texttt{tname} and \texttt{tcount}. The first contains the names of the key variables; its persistence from call to call allows the user to avoid constantly reentering the options argument. The \texttt{tcount} variable contains counts of the match types. New time values that occur before the first interval for a subject are "early", those after the last interval for a subject are "late", and those that fall into a gap are of type "gap". All these are considered to be outside the specified time frame for the given subject. An event of this type will be discarded. A time-dependent covariate value will be applied to later intervals but will not generate a new time point in the output.

The most common type will usually be "within", for those new times that fall inside an existing interval and cause it to be split into two. Observations that fall exactly on the edge of an interval but within the \((\text{min}, \text{max}]\) time for a subject are counted as being on a "leading" edge, "trailing" edge or "boundary". The first corresponds for instance to an occurrence at 17 for someone with an intervals of \((0,15]\) and \((17, 35]\). A \texttt{tdc} at time 17 will affect this interval but an event at 17 would be ignored. An event occurrence at 15 would count in the \((0,15]\) interval. The last case is where the main data set has touching intervals for a subject, e.g. \((17, 28]\) and \((28,35]\) and a new occurrence lands at the join. Events will go to the earlier interval and counts to the latter one. A last column shows the number of additions where the id and time point were identical. When this occurs, the \texttt{tdc} and \texttt{event} operators will use the final value in the data (last edit wins), but ignoring missing, while \texttt{cumtdc} and \texttt{cumevent} operators add up the values.

These extra attributes are ephemeral and will be discarded if the dataframe is modified. This is intentional, since they will become invalid if for instance a subset were selected.

Author(s)

Terry Therneau

See Also

\texttt{neardate}

Examples

\begin{verbatim}
# The pbc data set contains baseline data and follow-up status
# for a set of subjects with primary biliary cirrhosis, while the
# pbcseq data set contains repeated laboratory values for those
# subjects.
# The first data set contains data on 312 subjects in a clinical trial plus
# 186 that agreed to be followed off protocol, the second data set has data
# only on the trial subjects.
temp <- subset(pbc, id <= 312, select=c(id,sex, stage)) # baseline data
pbc2 <- tmerge(temp, temp, id=id, endpt = event(time, status))
pbc2 <- tmerge(pbc2, pbcseq, id=id, ascites = tdc(day, ascites),
               bili = tdc(day, bili), albumin = tdc(day, albumin),
               protime = tdc(day, protime), alk.phos = tdc(day, alk.phos))

fit <- coxph(Surv(tstart, tstop, endpt==2) ~ protime + log(bili), data=pbc2)
\end{verbatim}
tobin  

*Tobin’s Tobit data*

**Description**

Economists fit a parametric censored data model called the ‘tobit’. These data are from Tobin’s original paper.

**Usage**

tobin

**Format**

A data frame with 20 observations on the following 3 variables.

- **durable**  Durable goods purchase
- **age**  Age in years
- **quant**  Liquidity ratio (x 1000)

**Source**


**Examples**

```r
  tfit <- survreg(Surv(durable, durable>0, type='left') ~age + quant, 
                  data=tobin, dist='gaussian')
  predict(tfit,type="response")
```

transplant  

*Liver transplant waiting list*

**Description**

Subjects on a liver transplant waiting list from 1990-1999, and their disposition: received a transplant, died while waiting, withdrew from the list, or censored.

**Usage**

data("transplant")
Format

A data frame with 815 observations on the following 6 variables.

age  age at addition to the waiting list
sex  m or f
abo  blood type: A, B, AB or O
year  year in which they entered the waiting list
futime  time from entry to final disposition
event  final disposition: censored, death, ltx or withdraw

Details

This represents the transplant experience in a particular region, over a time period in which liver transplant became much more widely recognized as a viable treatment modality. The number of liver transplants rises over the period, but the number of subjects added to the liver transplant waiting list grew much faster. Important questions addressed by the data are the change in waiting time, who waits, and whether there was an consequent increase in deaths while on the list.

Blood type is an important consideration. Donor livers from subjects with blood type O can be used by patients with A, B, AB or 0 blood types, whereas an Ab liver can only be used by an AB recipient. Thus type O subjects on the waiting list are at a disadvantage, since the pool of competitors is larger for type O donor livers.

This data is of historical interest and provides a useful example of competing risks, but it has little relevance to current practice. Liver allocation policies have evolved and now depend directly on each individual patient’s risk and need, assessments of which are regularly updated while a patient is on the waiting list. The overall organ shortage remains acute, however.

References


Examples

# since event is a factor, survfit creates competing risk curves
pfit <- survfit(Surv(futime, event) ~ abo, transplant)
pfit[,2]  # time to liver transplant, by period
plot(pfit[,2], mark.time=FALSE, col=1:4, lwd=2, xaxs=235,
     xlab="Months", ylab="Fraction transplanted",
     xaxt = 'n')
temp <- c(0, 6, 12, 18, 24)
axis(1, temp, temp)
legend(450, .35, levels(transplant$abo), lty=1, col=1:4, lwd=2, bty='n')

# competing risks for type O
plot(pfit[4,], xlab="Months", ylab="Fraction transplanted", c=1:3, lwd=2)
legend(450, .4, c("Death", "Transplant", "Withdrawal"), col=1:3, lwd=2)
udca

Data from a trial of ursodeoxycholic acid

Description

Data from a trial of ursodeoxycholic acid (UDCA) in patients with primary biliary cirrhosis (PBC).

Usage

data("udca")

Format

A data frame with 170 observations on the following 15 variables.

- id: subject identifier
- trt: treatment of 0=placebo, 1=UDCA
- entry.dt: date of entry into the study
- last.dt: date of last on-study visit
- stage: stage of disease
- bili: bilirubin value at entry
- riskscore: the Mayo PBC risk score at entry
- death.dt: date of death
- tx.dt: date of liver transplant
- hprogress.dt: date of histologic progression
- varices.dt: appearance of esophageal varices
- ascites.dt: appearance of ascites
- enceph.dt: appearance of encephalopathy
- double.dt: doubling of initial bilirubin
- worsen.dt: worsening of symptoms by two stages

Details

This data set is used in the Therneau and Grambsh. The udca1 data set contains the baseline variables along with the time until the first endpoint (any of death, transplant, . . . , worsening). The udca2 data set treats all of the endpoints as parallel events and has a stratum for each.

References


untangle.specials  Help Process the 'specials' Argument of the 'terms' Function.

Description

Given a terms structure and a desired special name, this returns an index appropriate for subscripting the terms structure and another appropriate for the data frame.

Usage

untangle.specials(tt, special, order=1)

Arguments

- `tt` a terms object.
- `special` the name of a special function, presumably used in the terms object.
- `order` the order of the desired terms. If set to 2, interactions with the special function will be included.

Value

a list with two components:

- `vars` a vector of variable names, as would be found in the data frame, of the specials.
- `terms` a numeric vector, suitable for subscripting the terms structure, that indexes the terms in the expanded model formula which involve the special.

Examples

```r
formula<-Surv(tt,ss)-x+z*strata(id)
tms<-terms(formula, specials="strata")
## the specials attribute
attr(tms,"specials")
## main effects
untangle.specials(tms,"strata")
## and interactions
untangle.specials(tms,"strata",order=1:2)
```
Description

US population by age and sex, for 2000 through 2020

Usage

data(uspop2)

Format

The data is a matrix with dimensions age, sex, and calendar year. Age goes from 0 through 100, where the value for age 100 is the total for all ages of 100 or greater.

Details

This data is often used as a "standardized" population for epidemiology studies.

Source


See Also

uspop

Examples

us50 <- uspop2[51:101, , "2000"] # US 2000 population, 50 and over
age <- as.integer(dimnames(us50)[[1]])
smat <- model.matrix(~ factor(floor(age/5)) -1)
ustot <- t(smat) %*% us50 # totals by 5 year age groups
temp <- c(50, 55, 60, 65, 70, 75, 80, 85, 90, 95)
dimnames(ustot) <- list(c(paste(temp, temp+4, sep=""), "100+"),
c("male", "female"))
Description

Extract and return the variance-covariance matrix.

Usage

```r
## S3 method for class 'coxph'
vcov(object, complete=TRUE, ...)
## S3 method for class 'survreg'
vcov(object, complete=TRUE, ...)
```

Arguments

- `object` a fitted model object
- `complete` logical indicating if the full variance-covariance matrix should be returned. This has an effect only for an over-determined fit where some of the coefficients are undefined, and `coef(object)` contains corresponding NA values. If `complete=TRUE` the returned matrix will have row/column for each coefficient, if FALSE it will contain rows/columns corresponding to the non-missing coefficients. The `coef()` function has a similar `complete` argument.
- `...` additional arguments for method functions

Details

For the coxph and survreg functions the returned matrix is a particular generalized inverse: the row and column corresponding to any NA coefficients will be zero. This is a side effect of the generalized cholesky decompositon used in the underlying computation.

Value

- a matrix

---

**veteran**

*Veterans' Administration Lung Cancer study*

Description

Randomised trial of two treatment regimens for lung cancer. This is a standard survival analysis data set.

Usage

```r
veteran
```
xtfrm.Surv

Format

trt:  1=standard 2=test
celltype:  1=squamous, 2=smallcell, 3=adenoc, 4=large
time:  survival time
status:  censoring status
karno:  Karnofsky performance score (100=good)
diagtime: months from diagnosis to randomisation
age:  in years
prior:  prior therapy 0=no, 10=yes

Source


xtfrm.Surv  Sorting order for Surv objects

Description

Sort survival objects into a partial order, which is the same one used internally for many of the calculations.

Usage

```r
## S3 method for class 'Surv'
xxtfrm(x)
```

Arguments

- `x` a Surv object

Details

This creates a partial ordering of survival objects. The result is sorted in time order, for tied pairs of times right censored events come after observed events (censor after death), and left censored events are sorted before observed events. For counting process data (tstart, tstop, status) the ordering is by stop time, status, and start time, again with censoring last. Interval censored data is sorted using the midpoint of each interval.

The `xtfrm` routine is used internally by `order` and `sort`, so these results carry over to those routines.

Value

a vector of integers which will have the same sort order as `x`. 
Author(s)
Terry Therneau

See Also
sort, order

Examples

test <- c(Surv(c(10, 9, 9, 8, 8, 7, 5, 5, 4), rep(1:0, 5)), Surv(6.2, NA))
test
sort(test)

yates Population prediction

Description
Compute population marginal means (PMM) from a model fit, for a chosen population and statistic.

Usage
yates(fit, term, population = c("data", "factorial", "sas"),
levels, test = c("global", "trend", "pairwise"), predict = "linear",
options, nsim = 200, method = c("direct", "sgtt"))

Arguments
fit a model fit. Examples using lm, glm, and coxph objects are given in the vignette.
term the term from the model which is to be evaluated. This can be written as a character string or as a formula.
population the population to be used for the adjusting variables. User can supply their own data frame or select one of the built in choices. The argument also allows "empirical" and "yates" as aliases for data and factorial, respectively, and ignores case.
levels optional, what values for term should be used.
test the test for comparing the population predictions.
predict what to predict. For a glm model this might be the 'link' or 'response'. For a coxph model it can be linear, risk, or survival. User written functions are allowed.
options optional arguments for the prediction method.
nsim number of simulations used to compute a variance for the predictions. This is not needed for the linear predictor.
method the computational approach for testing equality of the population predictions. Either the direct approach or the algorithm used by the SAS glim procedure for "type 3" tests.
Details

The many options and details of this function are best described in a vignette on population prediction.

Value

an object of class yates with components of

- **estimate**: a data frame with one row for each level of the term, and columns containing the level, the mean population predicted value (mppv) and its standard deviation.
- **tests**: a matrix giving the test statistics
- **mvar**: the full variance-covariance matrix of the mppv values
- **summary**: optional: any further summary if the values provided by the prediction method.

Author(s)

Terry Therneau

Examples

```r
fit1 <- lm(skips ~ Solder*Opening + Mask, data = solder)
yates(fit1, ~Opening, population = "factorial")

fit2 <- coxph(Surv(time, status) ~ factor(ph.ecog)*sex + age, lung)
yates(fit2, ~ ph.ecog, predict="risk") # hazard ratio
```

---

**yates_setup**

*Method for adding new models to the yates function.*

Description

This is a method which is called by the yates function, in order to setup the code to handle a particular model type. Methods for glm, coxph, and default are part of the survival package.

Usage

```r
yates_setup(fit, ...)
```

Arguments

- **fit**: a fitted model object
- **...**: optional arguments for some methods
Details
If the predicted value should be the linear predictor, the function should return NULL. The yates routine has particularly efficient code for this case. Otherwise it should return a prediction function or a list of two elements containing the prediction function and a summary function. The prediction function will be passed the linear predictor as a single argument and should return a vector of predicted values.

Note
See the vignette on population prediction for more details.

Author(s)
Terry Therneau

See Also
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