

Survival Package Functions

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Contents

1	Introduction	1
2	residuals.survreg	1
3	Predicted survival from a Cox model	9
3.1	Individual survival	9

1 Introduction

Let us change our traditional attitude to the construction of programs. Instead of imagining that our main task is to instruct a *computer* what to do, let us concentrate rather on explaining to *humans* what we want the computer to do. (Donald E. Knuth, 1984).

This is the definition of a coding style called *literate programming*. I first made use of it in the *coxme* library and have become a full convert. For the survival library only selected objects are documented in this way; whenever I find need for a major revision I “convert” the source. An underlying motivation is to leave code that is well enough explained that someone else can take it over.

2 residuals.survreg

The residuals for a **survreg** model are one of several types

response residual y value on the scale of the original data

deviance an approximate deviance residual. A very bad idea statistically, retained for the sake of backwards compatibility.

dfbeta a matrix with one row per observation and one column per parameter showing the approximate influence of each observation on the final parameter value

dfbetas the dfbeta residuals scaled by the standard error of each coefficient

working residuals on the scale of the linear predictor

ldcase likelihood displacement wrt case weights

ldresp likelihood displacement wrt response changes

ldshape likelihood displacement wrt changes in shape

matrix matrix of derivatives of the log-likelihood wrt paramters

The other parameters are

rsigma whether the scale parameters should be included in the result for dfbeta results. I can think of no reason why one would not want them.

collapse optional vector of subject identifiers. This is for the case where a subject has multiple observations in a data set, and one wants to have residuals per subject rather than residuals per observation.

weighted whether the residuals should be multiplied by the case weights. The sum of weighted residuals will be zero.

The routine starts with standard stuff, checking arguments for validity and etc. The two cases of response or working residuals require a lot less computation. and are the most common calls, so they are taken care of first.

```
<residuals.survreg>≡
# $Id$
#
# Residuals for survreg objects
residuals.survreg <- function(object, type=c('response', 'deviance',
      'dfbeta', 'dfbetas', 'working', 'ldcase',
      'ldresp', 'ldshape', 'matrix'),
      rsigma =TRUE, collapse=FALSE, weighted=FALSE, ...) {
  type <-match.arg(type)
  n <- length(object$linear.predictors)
  Terms <- object$terms
  if(!inherits(Terms, "terms"))
    stop("invalid terms component of  object")

  # If there was a cluster directive in the model statment then remove
  # it. It does not correspond to a coefficient, and would just confuse
  # things later in the code.
  cluster <- untangle.specials(Terms,"cluster")$terms
  if (length(cluster) >0 )
    Terms <- Terms[-cluster]

  strata <- attr(Terms, 'specials')$strata
  coef <- object$coefficients
  intercept <- attr(Terms, "intercept")
```

```

response <- attr(Terms, "response")
weights <- object$weights
if (is.null(weights)) weighted <- FALSE

<rsr-dist>
<rsr-data>
<rsr-resid>
<rsr-finish>
}

```

First retrieve the distribution, which is used multiple times. The common case is a character string pointing to some element of `survreg.distributions`, but the other is a user supplied list of the form contained there. Some distributions are defined as the transform of another in which case we need to set `itrans` and `dtrans` and follow the link, otherwise the transformation and its inverse are the identity.

```

<rsr-dist>≡
  if (is.character(object$dist))
    dd <- survreg.distributions[[object$dist]]
  else dd <- object$dist
  if (is.null(dd$itrans)) {
    itrans <- dtrans <-function(x)x
  }
  else {
    itrans <- dd$itrans
    dtrans <- dd$dtrans
  }
  if (!is.null(dd$dist)) dd <- survreg.distributions[[dd$dist]]
  deviance <- dd$deviance
  dens <- dd$density

```

The next task is to decide what data we need. The response is always needed, but is normally saved as a part of the model. If it is a transformed distribution such as the Weibull (a transform of the extreme value) the saved object `y` is the transformed data, so we need to replicate that part of the `survreg()` code. (Why did I even allow for `y=F` in `survreg`? Because I was mimicing the `lm` function — oh the long, long consequences of a design decision.)

The covariate matrix `x` will be needed for all but response, deviance, and working residuals. If the model included a `strata()` term then there will be multiple scales, and the `strata` variable needs to be recovered. The variable `sigma` is set to a scalar if there are no strata, but otherwise to a vector with `n` elements containing the appropriate scale for each subject.

The leverage type residuals all need the second derivative matrix. If there was a `cluster` statement in the model this will be found in `naive.var`, otherwise in the `var` component.

```

<rsr-data>≡
  if (is.null(object$naive.var)) vv <- object$var
  else vv <- object$naive.var

need.x <- is.na(match(type, c('response', 'deviance', 'working')))
if (is.null(object$y) || !is.null(strata) || (need.x & is.null(object[['x']]]))

```

```

mf <- model.frame(object)

y <- object$y
if (is.null(y)) {
  y <- model.extract(mf, 'response')
  if (!is.null(dd$trans)) {
    tranfun <- dd$trans
    exactsurv <- y[,ncol(y)] ==1
    if (any(exactsurv)) logcorrect <-sum(log(dd$dtrans(y[exactsurv,1])))

    if (type=='interval') {
      if (any(y[,3]==3))
        y <- cbind(tranfun(y[,1:2]), y[,3])
      else y <- cbind(tranfun(y[,1]), y[,3])
    }
    else if (type=='left')
      y <- cbind(tranfun(y[,1]), 2-y[,2])
    else y <- cbind(tranfun(y[,1]), y[,2])
  }
  else {
    if (type=='left') y[,2] <- 2- y[,2]
    else if (type=='interval' && all(y[,3]<3)) y <- y[,c(1,3)]
  }
}

if (!is.null(strata)) {
  temp <- untangle.specials(Terms, 'strata', 1)
  Terms2 <- Terms[-temp$terms]
  if (length(temp$vars)==1) strata.keep <- mf[[temp$vars]]
  else strata.keep <- strata(mf[,temp$vars], shortlabel=TRUE)
  strata <- as.numeric(strata.keep)
  nstrata <- max(strata)
  sigma <- object$scale[strata]
}
else {
  Terms2 <- Terms
  nstrata <- 1
  sigma <- object$scale
}

if (need.x) {
  x <- object[['x']] #don't grab xlevels component
  if (is.null(x))
    x <- model.matrix(Terms2, mf, contrasts.arg=object$contrasts)
}

```

The most common residual is type response, which requires almost no more work, for the others we need to create the matrix of derivatives before proceeding. We use the **center** component from the deviance function for the distribution, which returns the data point **y** itself for an exact, left, or right censored observation, and an appropriate midpoint for interval censored ones.

```

<rsr-resid>≡
  if (type=='response') {
    yhat0 <- deviance(y, sigma, object$parms)
    rr <- itrans(yhat0$center) - itrans(object$linear.predictor)
  }
  else {
    <rtr-deriv>
    <rtr-resid2>
  }

```

The matrix of derviatives is used in all of the other cases. The starting point is the **density** function of the distribtion which return a matrix with columns of $F(x)$, $1-F(x)$, $f(x)$, $f'(x)/f(x)$ and $f''(x)/f(x)$. The matrix type residual contains columns for each of

$$L_i \quad \frac{\partial L_i}{\partial \eta_i} \quad \frac{\partial^2 L_i}{\partial \eta_i^2} \quad \frac{\partial L_i}{\partial \log(\sigma)} \quad \frac{\partial L_i}{\partial \log(\sigma)^2} \quad \frac{\partial^2 L_i}{\partial \eta \partial \log(\sigma)}$$

where L_i is the contribution to the log-likelihood from each individual. Note that if there are multiple scales, i.e. a `strata()` term in the model, then terms 3–6 are the derivatives for that subject with respect to their *particular* scale factor; derivatives with respect to all the other scales are zero for that subject.

The log-likelihood can be written as

$$\begin{aligned}
L &= \sum_{exact} [\log(f(z_i)) - \log(\sigma_i)] + \sum_{censored} \log \left(\int_{z_i^l}^{z_i^u} f(u) du \right) \\
&\equiv \sum_{exact} [g_1(z_i) - \log(\sigma_i)] + \sum_{censored} \log(g_2(z_i^l, z_i^u)) \\
z_i &= (y_i - \eta_i) / \sigma_i
\end{aligned}$$

For the interval censored observations we have a z defined at both the lower and upper endpoints. The linear predictor is $\eta = X\beta$.

The derivatives are shown below. Note that $f(-\infty) = f(\infty) = F(-\infty) = 0$, $F(\infty) = 1$, $z^u = \infty$ for a right censored observation and $z^l = -\infty$ for a left censored one.

$$\begin{aligned}
\frac{\partial g_1}{\partial \eta} &= -\frac{1}{\sigma} \left[\frac{f'(z)}{f(z)} \right] \\
\frac{\partial g_2}{\partial \eta} &= -\frac{1}{\sigma} \left[\frac{f(z^u) - f(z^l)}{F(z^u) - F(z^l)} \right] \\
\frac{\partial^2 g_1}{\partial \eta^2} &= \frac{1}{\sigma^2} \left[\frac{f''(z)}{f(z)} \right] - (\partial g_1 / \partial \eta)^2
\end{aligned}$$

$$\begin{aligned}
\frac{\partial^2 g_2}{\partial \eta^2} &= \frac{1}{\sigma^2} \left[\frac{f'(z^u) - f'(z^l)}{F(z^u) - F(z^l)} \right] - (\partial g_2 / \partial \eta)^2 \\
\frac{\partial g_1}{\partial \log \sigma} &= - \left[\frac{zf'(z)}{f(z)} \right] \\
\frac{\partial g_2}{\partial \log \sigma} &= - \left[\frac{z^u f(z^u) - z^l f(z^l)}{F(z^u) - F(z^l)} \right] \\
\frac{\partial^2 g_1}{\partial (\log \sigma)^2} &= \left[\frac{z^2 f''(z) + zf'(z)}{f(z)} \right] - (\partial g_1 / \partial \log \sigma)^2 \\
\frac{\partial^2 g_2}{\partial (\log \sigma)^2} &= \left[\frac{(z^u)^2 f'(z^u) - (z^l)^2 f'(z^l)}{F(z^u) - F(z^l)} \right] - \partial g_1 / \partial \log \sigma (1 + \partial g_1 / \partial \log \sigma) \\
\frac{\partial^2 g_1}{\partial \eta \partial \log \sigma} &= \frac{zf''(z)}{\sigma f(z)} - \partial g_1 / \partial \eta (1 + \partial g_1 / \partial \log \sigma) \\
\frac{\partial^2 g_2}{\partial \eta \partial \log \sigma} &= \frac{z^u f'(z^u) - z^l f'(z^l)}{\sigma [F(z^u) - F(z^l)]} - \partial g_2 / \partial \eta (1 + \partial g_2 / \partial \log \sigma)
\end{aligned}$$

In the code **z** is the relevant point for exact, left, or right censored data, and **z2** the upper endpoint for an interval censored one. The variable **tdenom** contains the denominator for each subject (which is the same for all derivatives for that subject). For an interval censored observation we try to avoid numeric cancellation by using the appropriate tail of the distribution. For instance with $(z^l, z^u) = (12, 15)$ the value of $F(x)$ will be very near 1 and it is better to subtract two upper tail values $(1 - F)$ than two lower tail ones F .

```

<rtr-deriv>≡
status <- y[,ncol(y)]
eta <- object$linear.predictors
z <- (y[,1] - eta)/sigma
dmat <- dens(z, object$parms)
dtemp<- dmat[,3] * dmat[,4]      #f'
if (any(status==3)) {
  z2 <- (y[,2] - eta)/sigma
  dmat2 <- dens(z2, object$parms)
}
else {
  dmat2 <- dmat      #dummy values
  z2 <- 0
}

tdenom <- ((status==0) * dmat[,2]) + #right censored
          ((status==1) * 1 )        + #exact
          ((status==2) * dmat[,1]) + #left
          ((status==3) * ifelse(z>0, dmat[,2]-dmat2[,2],
                                dmat2[,1] - dmat[,1])) #interval
g <- log(ifelse(status==1, dmat[,3]/sigma, tdenom)) #loglik
tdenom <- 1/tdenom

```

```

dg <- -(tdenom/sigma) *(((status==0) * (0-dmat[,3])) +      #dg/ eta
  ((status==1) * dmat[,4]) +
  ((status==2) * dmat[,3]) +
  ((status==3) * (dmat2[,3]- dmat[,3])))

ddg <- (tdenom/sigma^2) *(((status==0) * (0- dtemp)) +      #ddg/eta^2
  ((status==1) * dmat[,5]) +
  ((status==2) * dtemp) +
  ((status==3) * (dmat2[,3]*dmat2[,4] - dtemp)))

ds <- ifelse(status<3, dg * sigma * z,
  tdenom*(z2*dmat2[,3] - z*dmat[,3]))
dds <- ifelse(status<3, ddg* (sigma*z)^2,
  tdenom*(z2*z2*dmat2[,3]*dmat2[,4] -
    z * z*dmat[,3] * dmat[,4]))
dsg <- ifelse(status<3, ddg* sigma*z,
  tdenom * (z2*dmat2[,3]*dmat2[,4] - z*dtemp))
deriv <- cbind(g, dg, ddg=ddg- dg^2,
  ds = ifelse(status==1, ds-1, ds),
  dds=dds - ds*(1+ds),
  dsg=dsg - dg*(1+ds))

```

Now, we can calculate the actual residuals case by case. For the dfbetas there will be one column per coefficient, so if there are strata column 4 of the deriv matrix needs to be *uncollapsed* into a matrix with nstrata columns. The same manipulation is needed for the ld residuals.

```

<rtr-resid2>≡
if (type=='deviance') {
  yhat0 <- deviance(y, sigma, object$parms)
  rr <- (-1)*deriv[,2]/deriv[,3] #working residuals
  rr <- sign(rr)* sqrt(2*(yhat0$loglik - deriv[,1]))
}

else if (type=='working') rr <- (-1)*deriv[,2]/deriv[,3]

else if (type=='dfbeta' || type== 'dfbetas' || type=='ldcase') {
  score <- deriv[,2] * x # score residuals
  if (rsigma) {
    if (nstrata > 1) {
      d4 <- matrix(0., nrow=n, ncol=nstrata)
      d4[cbind(1:n, strata)] <- deriv[,4]
      score <- cbind(score, d4)
    }
    else score <- cbind(score, deriv[,4])
  }
  rr <- score %*% vv
  if (type=='dfbetas') rr <- rr %*% diag(1/sqrt(diag(vv)))
}

```

```

    if (type=='ldcase') rr<- rowSums(rr*score)
  }

  else if (type=='ldresp') {
    rscore <- deriv[,3] * (x * sigma)
    if (rsigma) {
      if (nstrata >1) {
        d6 <- matrix(0., nrow=n, ncol=nstrata)
        d6[cbind(1:n, strata)] <- deriv[,6]*sigma
        rscore <- cbind(rscore, d6)
      }
      else rscore <- cbind(rscore, deriv[,6] * sigma)
    }
    temp <- rscore %*% vv
    rr <- rowSums(rscore * temp)
  }

  else if (type=='ldshape') {
    sscore <- deriv[,6] *x
    if (rsigma) {
      if (nstrata >1) {
        d5 <- matrix(0., nrow=n, ncol=nstrata)
        d5[cbind(1:n, strata)] <- deriv[,5]
        sscore <- cbind(sscore, d5)
      }
      else sscore <- cbind(sscore, deriv[,5])
    }
    temp <- sscore %*% vv
    rr <- rowSums(sscore * temp)
  }

  else { #type = matrix
    rr <- deriv
  }

```

Finally the two optional steps of adding case weights and collapsing over subject id.

<rsr-finish>≡

```

#case weights
if (weighted) rr <- rr * weights

#Expand out the missing values in the result
if (!is.null(object$na.action)) {
  rr <- naresid(object$na.action, rr)
  if (is.matrix(rr)) n <- nrow(rr)
  else n <- length(rr)
}

```



```

# Collapse if desired
if (!missing(collapse)) {
  if (length(collapse) != n) stop("Wrong length for 'collapse'")
  rr <- drop(rowsum(rr, collapse))
}

rr

```

3 Predicted survival from a Cox model

3.1 Individual survival

The `survfit` method for a Cox model produces individual survival curves. As might be expected these have much in common with ordinary survival curves, and share many of the same methods. The primary differences are first that a predicted curve always refers to a particular set of covariate values. It is often the case that a user wants multiple values at once, in which case the result will be a matrix of survival curves with a row for each time and a column for each covariate set. The second is that the computations are somewhat more difficult.

The input arguments are

formula a fitted object of class 'coxph'. The argument name of 'formula' is historic, from when the `survfit` function was not a generic and only did Kaplan-Meier type curves.

newdata contains the data values for which curves should be produced, one per row

se.fit TRUE/FALSE, should standard errors be computed.

individual a particular option for time-dependent covariates

type computation type for the survival curve

vartype computation type for the variance

All the other arguments are common to all the methods, refer to the help pages.

$\langle \text{survfit.coxph} \rangle \equiv$

```

survfit.coxph <-
  function(formula, newdata, se.fit=TRUE, conf.int=.95, individual=FALSE,
           type, vartype,
           conf.type=c("log", "log-log", "plain", "none"),
           censor=TRUE, ...) {

```

```

  Call <- match.call()
  Call[[1]] <- as.name("survfit") #nicer output for the user
  object <- formula #'formula' because it has to match survfit

```

$\langle \text{survfit.coxph-setup} \rangle$

```

  <survfit.coxph-compute>
  <survfit.coxph-finish>
}

```

The third line `as.name('survfit')` causes the printout to say ‘survfit’ instead of ‘survfit.coxph’.

The setup for the routine is fairly pedestrian. If the `newdata` argument is missing we used `object$means` as the default value. This choice has lots of statistical shortcomings, particularly in a stratified model, but is common in other packages and a historic option here. If the `type` or `vartype` are missing we use the appropriate one for the method in the Cox model. That is, the `coxph` computation used for `method='exact'` is the same approximation used in the Kalbfleish-Prentice estimate, that for the Breslow method matches the Aalen survival estimate, etc.

```

<survfit.coxph-setup>≡
  if (missing(type)) {
    # Use the appropriate one from the model
    temp1 <- c("exact", "breslow", "efron")
    survtype <- match(object$method, temp1)
  }
  else {
    temp1 <- c("kalbfleisch-prentice", "aalen", "efron")
    survtype <- match(match.arg(type, temp1), temp1)
  }
  if (missing(vartype)) {
    vartype <- survtype
  }
  else {
    temp2 <- c("greenwood", "tsiatis", "efron", "aalen")
    vartype <- match(match.arg(vartype, temp2), temp2)
    if (vartype=="tsiatis") vartype<- "aalen"
  }

  if (!se.fit) conf.type <- 'none'
  else conf.type <- match.arg(conf.type)

```

I need to retrieve a copy of the original data. This includes the survival times, model matrix, case weights and strata. The “failed to reconstruct” error messages are to avoid nonsense results when someone changes the data set under our feet. For instance

```

fit <- coxph(Surv(time,status) ~ age, data=lung)
lung <- lung[1:100,]
survfit(fit)

```

The check for `type` of the same flavor; since `coxph` can only deal with these two types, any other must signal a change in the data.

```

<survfit.coxph-setup>+≡
  mf <- model.frame(object)

```

```

y <- model.response(mf)
n <- nrow(y)
if (n != object$n[1]) stop("Failed to reconstruct the original data set")
if (!is.null(object$y) && !all.equal(y, object$y))
  stop("Failed to reconstruct the original data set")
type <- attr(y, 'type')
if (type != 'right' && type != 'counting')
  stop("Cannot handle \"", type, "\" type survival data")

x <- model.matrix.coxph(object, mf=mf)
wt <- model.weights(mf)
if (is.null(wt)) wt <- rep(1.0, n)
offset <- model.offset(mf)
if (is.null(offset)) offset <- 0

Terms <- object$terms
temp <- untangle.specials(Terms, 'strata')
if (length(temp$terms)==0) strata <- rep(OL,n)
else strata <- mf[[temp$vars]]

```

A key variable for the computation is the risk score $\exp(X\beta)$ for each original observation along with the risk score for the target subject(s). There are three choices for the new data

- For predictions with time-dependent covariates the user will have specified the option `individual=TRUE`, and the new data set contains the covariate trace over time of a single individual. We need to retrieve the covariates, strata, and response from the new data set.
- For ordinary predictions only the covariates are needed.
- If newdata is not present we assume that this is the ordinary case, and use the value of `object$means` as the default covariate set. (This is not a good idea statistically.)

Since the new data might not have all of the levels present for one of the factors, we need to ensure that levels match the original data. In all cases the computation depends only on the *difference* between the original covariates and the target set. We subtract the means from each column of the X matrices to avoid any problems with overflow in the exponential function.

If a variable is deemed redundant the `coxph` routine will have set its coefficient to NA as a marker. We want to ignore that coefficient: treating it as a zero has the desired effect. The other special case is a null model, having either 1 or only an offset on the right hand side. In that case we create a dummy covariate to allow the rest of the code to work without special if/else.

(survfit.coxph-setup) +=

```

if (is.null(x) || ncol(x)==0) { # a model with ~1 on the right hand side
  # Give it a dummy x so the rest of the code goes through
  # (This case is really rare)
  x <- matrix(0., nrow=n)
  coef <- 0.0
  varmat <- matrix(0.0,1,1)
}

```

```

else {
  varmat <- object$var
  x <- scale(x, center=object$means, scale=FALSE)
  coef <- ifelse(is.na(object$coefficients), 0, object$coefficients)
}
risk <- exp(x%*% coef + offset - mean(offset))

if (individual) {
  if (missing(newdata)) stop("The newdata argument must be present")
  if (!is.data.frame(newdata)) stop("Newdata must be a data frame")
  temp <- untangle.specials(Terms, 'cluster')
  if (length(temp$vars) > 0) Terms2 <- Terms[-temp$terms]
  else Terms2 <- Terms
  mf2 <- model.frame(Terms2, newdata, xlev=object$xlevels)

  temp <- untangle.specials(Terms2, 'strata')
  if (length(temp$vars) > 0) {
    strata2 <- strata(mf2[temp$vars], shortlabel=TRUE)
    strata2 <- factor(strata2, levels=levels(strata))
    if (any(is.na(strata2)))
      stop("New data set has strata levels not found in the original")
    Terms2 <- Terms2[-temp$terms]
  }
  else strata2 <- rep(0, nrow(mf2))

  x2 <- model.matrix(Terms2, mf2)[,-1, drop=FALSE] #no intercept
  if (length(x2)==0) x2 <- matrix(0.0, nrow=nrow(mf2), col=1)
  else x2 <- scale(x2, center=object$means, scale=FALSE)

  offset2 <- model.offset(mf2)
  if (length(offset2) > 0) offset2 <- offset2 - mean(offset)
  else offset2 <- 0

  y2 <- model.extract(mf2, 'response')
  if (attr(y2,'type') != type)
    stop("Survival type of newdata does not match the fitted model")
}
else {
  if (missing(newdata)) {
    x2 <- matrix(0.0, nrow=1, ncol=ncol(x))
    offset2 <- 0
  }
  else {

```

For backwards compatability: I allow someone to give an ordinary vector instead of a data frame, when only one curve is required. In this case I also need to verify that the element have a name. If not we attach the variable names from the model, and assume that it's the right order. (Documentation of this ability has been suppressed, however.)

```
<survfit.coxph-setup>+≡
  if (!is.data.frame(newdata)) {
    if (is.list(newdata)) newdata <- data.frame(newdata)
    else if (is.numeric(newdata) &&
              length(newdata)==length(object$coefficients)) {
      if (is.null(names(newdata)))
        names(newdata) <- names(object$coefficients)
      newdata <- data.frame(as.list(newdata))
    }
    else stop("Invalid newdata object")
  }
  Terms2 <- delete.response(Terms)
  temp <- untangle.specials(Terms2, 'cluster')
  if (length(temp$vars)) Terms2 <- Terms2[-temp$terms]
  temp <- untangle.specials(Terms2, 'strata')
  if (length(temp$vars)) Terms2 <- Terms2[-temp$terms]
  mf2 <- model.frame(Terms2, newdata, xlev=object$xlevels)
  x2 <- model.matrix(Terms2, mf2)[,-1, drop=FALSE] #no intercept
  x2 <- scale(x2, center=object$means, scale=FALSE)
  offset2 <- model.offset(mf2)
  if (length(offset2) >0) offset2 <- offset2 - mean(offset)
  else offset2 <- 0
}
}
newrisk <- exp(c(x2 %*% coef) + offset2)
```

Now, we're ready to do the main computation. Before this revision (the one documented here using noweb) there were three C routines used in calculating survival after a Cox model

1. agsurv1 creates a single curve, but for the most general case of a *covariate path*. It is used for time dependent covariates.
2. agsurv2 creates a set of curves. These curves are for a fixed covariate set, although (start, stop] data is supported. If there were 3 strata in the fit and 4 covariate sets are given, the result will be 12 curves.
3. agsurv3 is used to create population survival curves. The result is average survival curve (for 3 different definitions of 'average'). If there were 3 strata and 100 subjects, the first curve returned would be the average for those 100 individual curves in strata 1, the second for strata 2, and the third for strata 3.

In June 2010 the first two were re-written in (mostly) R, in the process of adding functionality and repairing some flaws in the computation of a weighted variance. In effect, the changes are similar to the rewrite of the survfitKM function a few years ago. Computations are separate for

each strata, but all have a different number of elements in their final result. So, for each strata we generate a list, and then unpack the results at the end. This is memory efficient, the number of curves is usually small enough that the "for" loop is no great cost, and it's easier to see what's going on than C code.

First, compute the baseline survival curves for each strata. If the strata was a factor we want to leave it in the same order, otherwise sort it.

```
<survfit.coxph-compute>≡
ustrata <- levels(as.factor(strata))
nstrata <- length(ustrata)
survlist <- vector('list', nstrata)
if (se.fit) varhaz <- vector('list', nstrata)

for (i in 1:nstrata) {
  indx <- which(strata== ustrata[i])
  survlist[[i]] <- agsurv(y[indx,,drop=F], x[indx,,drop=F],
                        wt[indx], risk[indx],
                        survtype, vartype)
}
```

In an ordinary survival curve object with multiple strata, as produced by `survfitKM`, the time, survival and etc components are each a single vector that contains the results for strata 1, followed by strata 2, The strata component is a vector of integers, one per strata, that gives the number of elements belonging to each stratum. The reason is that each strata will have a different number of observations, so that a matrix form was not viable, and the underlying C routines were not capable of handling lists (the code predates the `.Call` function by a decade). The lists above will be concatenated into vectors.

For `individual=FALSE` we have a second dimension, namely each of the target covariate sets (if there are multiples). Each of these generates a unique set of survival and variance(survival) values, but all of the same size since each uses all the strata. The final output structure in this case has single vectors for the time, number of events, number censored, and number at risk values since they are common to all the curves, and a matrix of survival and variance estimates, one column for each of the distinct target values. If Λ_0 is the baseline cumulative hazard from the above calculation, then $r_i\Lambda_0$ is the cumulative hazard for the i th new risk score r_i . The variance has two parts, the first of which is $r_i^2 H_1$ where H_1 is returned from the `agsurv` routine, and the second is

$$H_2(t) = d'(t)Vd(t)$$

$$d(t) = \int_0^t [\bar{x}(t) - z]dN(t)$$

V is the variance matrix for β from the fitted Cox model, and $d(t)$ is the distance between the target covariate z and the mean of the original data, summed up over the interval from 0 to t . Essentially the variance in $\hat{\beta}$ has a larger influence when prediction is far from the mean.

```
<survfit.coxph-compute>+=
  if (!individual) {
    cumhaz <- unlist(lapply(survlist, function(x) x$cumhaz))
```

```

varhaz <- unlist(lapply(survlist, function(x) cumsum(x$varhaz)))
nevent <- unlist(lapply(survlist, function(x) x$n.event)) #weighted
ndeath <- unlist(lapply(survlist, function(x) x$ndeath)) #unweighted
xbar <- t(matrix(unlist(lapply(survlist, function(x) t(x$xbar))),
               nrow=ncol(x)))
hazard <- unlist(lapply(survlist, function(x) x$hazard))

if (survtype==1)
  surv <-unlist(lapply(survlist, function(x) cumprod(x$surv)))
else surv <- exp(-cumhaz)

if (is.matrix(x2) && nrow(x2) >1) { #more than 1 row in newdata
  surv <- outer(surv, newrisk, '^')
  varh <- matrix(0., nrow=length(varhaz), ncol=nrow(x2))
  for (i in 1:nrow(x2)) {
    dt <- outer(cumhaz, x2[i,], '*') - xbar
    varh[,i] <- (varhaz + rowSums((dt %*% varmat)* dt)) *
      newrisk[i]^2
  }
}
else {
  surv <- surv^newrisk
  dt <- outer(cumhaz, c(x2)) - xbar
  varh <- (varhaz + rowSums((dt %*% varmat)* dt)) *
    newrisk^2
}

```

In the lines just above: I have a matrix dt with one row per death time and one column per variable. For each row d_i separately we want the quadratic form $d_i V d_i'$. The first matrix product can be done for all rows at once: found in the inner parenthesis. Ordinary (not matrix) multiplication followed by rowsums does the rest in one fell swoop.

(survfit.coxph-compute)+≡

```

result <- list(n=as.vector(table(strata)),
              time=unlist(lapply(survlist, function(x) x$time)),
              n.risk= unlist(lapply(survlist, function(x) x$n.risk)),
              n.event=nevent,
              n.censor=unlist(lapply(survlist, function(x) x$n.censor)),
              surv=surv,
              type=type)
if (nstrata >1) {
  result$strata <- unlist(lapply(survlist, function(x) length(x$n.risk)))
  names(result$strata) <- ustrata
}
}

```

For the case with `individual=TRUE` we always produce a single survival curve. A subject will spend blocks of time with different covariate sets, sometimes even jumping between strata. Retrieve each one and save it into a list, and then sew them together end to end. The `n` component is the number of observations in the strata — but this subject might visit several. We report the first one they were in for printout. The `time` component will be cumulative on this subject's scale. Counting this is a bit trickier than I first thought. Say that the subject's first interval goes from 1 to 10, with observed time points in that interval at 2, 5, and 7, and a second interval from 10 to 20 with observed time points in the data of 15 and 18. On the subject's time scale things happen at days 1, 4, 6, 14 and 17. The deltas saved below are 2-1, 5-2, 7-5, 3+ 14-10, 17-14. Note the 3+ part, kept in the `timeforward` variable. Why all this “adding up” nuisance? If the subject spent time in two strata, the second one might be on an internal time scale of ‘time since entering the strata’. The two intervals in `newdata` could be 0–10 followed by 0–20. Time for the subject can't go backwards though: the change between internal/external time scales is a bit like following someone who was stepping back and forth over the international date line.

In the code the `indx` variable points to the set of times that the subject was present, for this row of the new data. Note the $>$ on one end and \leq on the other. If someone's interval 1 was 0–10 and interval 2 was 10–20, and there happened to be a jump in the baseline survival curve at exactly time 10, we can't let them count the jump twice.

```
<survfit.coxph-compute>)+≡
else {
  ntarget <- nrow(x2) #number of different time intervals
  surv <- vector('list', ntarget)
  n.event <- n.risk <- n.censor <- varh1 <- varh2 <- time <- surv
  stemp <- match(strata2, ustrata)
  timeforward <- 0
  for (i in 1:ntarget) {
    slist <- survlist[[stemp[i]]]
    indx <- which(slist$time > y2[i,1] & slist$time <= y2[i,2])
    time[[i]] <- diff(c(y2[i,1], slist$time[indx])) #time increments
    time[[i]][1] <- time[[i]][1] + timeforward
    timeforward <- y2[i,2] - max(slist$time[indx])

    if (survtype==1) surv[[i]] <- slist$surv[indx]^newrisk[i]
    else surv[[i]] <- slist$hazard[indx]*newrisk[i]
    n.event[[i]] <- slist$n.event[indx]
    n.risk[[i]] <- slist$n.risk[indx]
    n.censor[[i]] <- slist$n.censor[indx]
    dt <- outer(slist$cumhaz[indx], x2[i,]) - slist$xbar[indx,,drop=F]
    varh1[[i]] <- slist$varhaz[indx] *newrisk[i]^2
    varh2[[i]] <- rowSums((dt %*% varmat)* dt) * newrisk[i]^2
  }
  varh <- cumsum(unlist(varh1)) + unlist(varh2)

  if (survtype==1) surv <- cumprod(unlist(surv)) #increments
```



```

else surv <- exp(-cumsum(unlist(surv)))          #hazards

result <- list(n=as.vector(table(strata)[stemp[1]]),
              time=cumsum(unlist(time)),
              n.risk = unlist(n.risk),
              n.event= unlist(n.event),
              n.censor= unlist(n.censor),
              surv = surv, type=type)
}

```

Next is the code for the `agsurv` function, which actually does the work. The estimates of survival are the Kalbfleisch-Prentice (KP), Breslow, and Efron. Each has an increment at each unique death time. First a bit of notation: $Y_i(t)$ is 1 if bservation i is “at risk” at time t and 0 otherwise. For a simple survival (`ncol(y)==2`) a subject is at risk until the time of censoring or death (first column of `y`). For (start, stop] data (`ncol(y)==3`) a subject becomes a part of the risk set at start+0 and stays through stop. $dN_i(t)$ will be 1 if subject i had an event at time t . The risk score for each subject is $r_i = \exp(X_i\beta)$.

The Breslow increment at time t is $\sum w_i dN_i(t) / \sum w_i r_i Y_i(t)$, the number of events at time t over the number at risk at time t . The final survival is `exp(-cumsum(increment))`.

The Kalbfleisch-Prentice increment is a multiplicative term z which is the solution to the equation

$$\sum w_i r_i Y_i(t) = \sum dN_i(t) w_i \frac{r_i}{1 - z(t)^{r_i}}$$

The left hand side is the weighted number at risk at time t , the right hand side is a sum over the tied events at that time. If there is only one event the equation has a closed form solution. If not, and knowing the solution must lie between 0 and 1, we do 35 steps of bisection to get a solution within 1e-8. An alternative is to use the -log of the Breslow estimate as a starting estimate, which is faster but requires a more sophisticated iteration logic. The final curve is $\prod_t z(t)^{r_c}$ where r_c is the risk score for the target subject.

The Efron estimate can be viewed as a modified Breslow estimate under the assumption that tied deaths are not really tied – we just don’t know the order. So if there are 3 subjects who die at some time t we will have three psuedo-terms for t , $t + \epsilon$, and $t + 2\epsilon$. All 3 subjects are present for the denominator of the first term, 2/3 of each for the second, and 1/3 for the third terms denominator. All contribute 1/3 of the weight to each numerator (1/3 chance they were the one to die there). The formulas will require $\sum w_i dN_i(t)$, $\sum w_i r_i dN_i(t)$, and $\sum w_i X_i dN_i(t)$, i.e., the sums only over the deaths.

For simple survival data the risk sum $\sum w_i r_i Y_i(t)$ for all the unique death times t is fast to compute as a cumulative sum, starting at the longest followup time an summing towards the shortest. There are two algorithms for (start, stop] data.

- Do a separate sum at each death time. The problem is for very large data sets. For each death time the selection `who <- (start<t & stop>=t)` is $O(n)$ and can take more time then all the remaining calculations together.
- Use the difference of two cumulative sums, one ordered by start time and one ordered by stop time. This is $O(2n)$ for the intial sums. The problem here is potential round off error if the sums get large, which can happen if the time scale were very, very finely divided. This issue is mostly precluded by subtracting means first.

We compute the extended number still at risk — all whose stop time is \geq each unique death time — in the vector `xin`. From this we have to subtract all those who haven't actually entered yet found in `xout`. Remember that $(3,20]$ enters at time 3+. The total at risk at any time is the difference between them. Output is only for the stop times; a call to `approx` is used to reconcile the two time sets. The `irisk` vector is for the printout, it is a sum of weighted counts rather than weighted risk scores.

```
<agsurv>≡
agsurv <- function(y, x, wt, risk, survtype, vartype) {
  nvar <- ncol(as.matrix(x))
  status <- y[,ncol(y)]
  dtime <- y[,ncol(y) -1]
  death <- (status==1)

  time <- sort(unique(dtime))
  nevent <- as.vector(rowsum(wt*death, dtime))
  ncens <- as.vector(rowsum(wt*(!death), dtime))
  wrisk <- wt*risk
  rcumsum <- function(x) rev(cumsum(rev(x))) # sum from last to first
  nrisk <- rcumsum(rowsum(wrisk, dtime))
  irisk <- rcumsum(rowsum(wt, dtime))
  if (ncol(y) ==2) {
    temp2 <- rowsum(wrisk*x, dtime)
    xsum <- apply(temp2, 2, rcumsum)
  }
  else {
    delta <- min(diff(time))/2
    etime <- c(sort(unique(y[,1])), max(y[,1])+delta) #unique entry times
    indx <- approx(etime, 1:length(etime), time, method='constant',
                  rule=2, f=1)$y
    esum <- rcumsum(rowsum(wrisk, y[,1])) #not yet entered
    nrisk <- nrisk - c(esum,0)[indx]
    irisk <- irisk - c(rcumsum(rowsum(wt, y[,1])),0)[indx]
    xout <- apply(rowsum(wrisk*x, y[,1]), 2, rcumsum) #not yet entered
    xin <- apply(rowsum(wrisk*x, dtime), 2, rcumsum) # dtime or alive
    xsum <- xin - (rbind(xout,0))[indx,,drop=F]
  }

  ndeath <- rowsum(status, dtime) #unweighted death count
```

The KP estimate requires a short C routine to do the iteration efficiently, and the Efron estimate a different C routine to efficiently compute the partial sums.

```
<agsurv>+≡
dtimes <- which(nevent >0)
ntime <- length(time)
if (survtype ==1) {
  indx <- (which(status==1))[order(dtime[status==1])] #deaths
```

```

km <- .C('agsurv4',
        as.integer(ndeath),
        as.double(risk[indx]),
        as.double(wt[indx]),
        as.integer(ntime),
        as.double(nrisk),
        inc = double(ntime))
}

if (survtype==3 || vartype==3) {
  xsum2 <- rowsum((wrisk*death) *x, dtime)
  erisk <- rowsum(wrisk*death, dtime) #risk score sums at each death
  tsum <- .C('agsurv5',
            as.integer(length(nevent)),
            as.integer(nvar),
            as.integer(ndeath),
            as.double(nrisk),
            as.double(erisk),
            as.double(xsum),
            as.double(xsum2),
            sum1 = double(length(nevent)),
            sum2 = double(length(nevent)),
            xbar = matrix(0., length(nevent), nvar))
}
haz <- switch(survtype,
             nevent/nrisk,
             nevent/nrisk,
             nevent* tsum$sum1)
varhaz <- switch(vartype,
                nevent/(nrisk *
                      ifelse(nevent>=nrisk, nrisk, nrisk-nevent)),
                nevent/nrisk^2,
                nevent* tsum$sum2)
xbar <- switch(vartype,
              (xsum/nrisk)*haz,
              (xsum/nrisk)*haz,
              nevent * tsum$xbar)

result <- list(time=time, n.event=nevent, n.risk=nrisk, n.censor=ncens,
              hazard=haz,
              cumhaz=cumsum(haz), varhaz=varhaz, ndeath=ndeath,
              xbar=apply(matrix(xbar, ncol=nvar),2, cumsum))
if (survtype==1) result$surv <- km$inc
result
}

```

The arguments to this function are the number of unique times n , which is the length of the vectors `ndeath` (number at each time), `denom`, and the returned vector `km`. The `risk` and `wt` vectors contain individual values for the subjects with an event. Their length will be equal to `sum(ndeath)`.

```

<agsurv4>≡
#include "survS.h"
#include "survproto.h"

void agsurv4(Sint    *ndeath,    double *risk,    double *wt,
             Sint    *sn,        double *denom,    double *km)
{
    int i,j,k, l;
    int n; /* number of unique death times */
    double sumt, guess, inc;

    n = *sn;
    j =0;
    for (i=0; i<n; i++) {
        if (ndeath[i] ==0) km[i] =1;
        else if (ndeath[i] ==1) { /* not a tied death */
            km[i] = pow(1- wt[j]*risk[j]/denom[i], 1/risk[j]);
        }
        else { /* bisection solution */
            guess = .5;
            inc = .25;
            for (l=0; l<35; l++) { /* bisect it to death */
                sumt =0;
                for (k=j; k<(j+ndeath[i]); k++) {
                    sumt += wt[k]*risk[k]/(1-pow(guess, risk[k]));
                }
                if (sumt < denom[i]) guess += inc;
                else guess -= inc;
                inc = inc/2;
            }
            km[i] = guess;
        }
        j += ndeath[i];
    }
}

```

Do a computation which is slow in R, needed for the Efron approximation. Input arguments are

n number of observations (unique death times)

d number of deaths at that time

nvar number of covariates

x1 weighted number at risk at the time

x2 sum of weights for the deaths

xsum matrix containing the cumulative sum of x values

xsum2 matrix of sums, only for the deaths

On output the values are

- $d=0$: the outputs are unchanged (they initialize at 0)
- $d=1$
 $\text{sum1 } 1/x1$
 $\text{sum2 } 1/x1^2$
 $\text{xbar } xsum/x1^2$
- $d=2$
 $\text{sum1 } (1/2) (1/x1 + 1/(x1 - x2/2))$
 $\text{sum2 } (1/2) (\text{ same terms, squared})$
 $\text{xbar } (1/2) (xsum/x1^2 + (xsum - 1/2 x3)/(x1- x2/2)^2)$
- $d=3$
 $\text{sum1 } (1/3) (1/x1 + 1/(x1 - x2/3 + 1/(x1 - 2*x2/3))$
 $\text{sum2 } (1/3) (\text{ same terms, squared})$
 $\text{xbar } (1/3) (xsum/x1^2 + (xsum - 1/3 xsum2)/(x1- x2/3)^2 +$
 $(xsum - 2/3 xsum2)/(x1- 2/3 x3)^2)$
- etc

Sum1 will be the increment to the hazard, sum2 the increment to the first term of the variance, and xbar the increment in the hazard times the mean of x at this point.

```
<agsurv5>≡
#include "survS.h"
void agsurv5(Sint *n,      Sint *nvar,  Sint *dd, double *x1,
             double *x2,   double *xsum, double *xsum2,
             double *sum1, double *sum2, double *xbar) {
    double temp;
    int i,j, k, kk;
    double d;

    for (i=0; i< *n; i++) {
        d = dd[i];
        if (d==1){
            temp = 1/x1[i];
```

```

        sum1[i] = temp;
        sum2[i] = temp*temp;
        for (k=0; k< *nvar; k++)
            xbar[i+ *n*k] = xsum[i + *n*k] * temp*temp;
    }
    else {
        temp = 1/x1[i];
        for (j=0; j<d; j++) {
            temp = 1/(x1[i] - x2[i]*j/d);
            sum1[i] += temp/d;
            sum2[i] += temp*temp/d;
            for (k=0; k< *nvar; k++){
                kk = i + *n*k;
                xbar[kk] += ((xsum[kk] - xsum2[kk]*j/d) * temp*temp)/d;
            }
        }
    }
}

```

Finally, the last (somewhat boring) part of the code. First, if given the argument `censor=FALSE` we need to remove all the time points from the output at which there was only censoring activity. This action is mostly for backwards compatability with older releases that never returned censoring times. Second, add in the variance and the confidence intervals to the result. The code is nearly identical to that in `survfitKM`.

```

<survfit.coxph-finish>≡
if (!censor) {
    kfun <- function(x, keep){ if (is.matrix(x)) x[keep,,drop=F]
                                else if (length(x)==length(keep)) x[keep]
                                else x}

    keep <- (result$n.event > 0)
    if (nstrata >1) {
        temp <- rep(ustrata, each=result$strata)
        result$strata <- c(table(temp[keep]))
    }
    result <- lapply(result, kfun, keep)
    if (se.fit) varh <- kfun(varh, keep)
}

if (se.fit) {
    result$std.err <- sqrt(varh)

    zval <- qnorm(1- (1-conf.int)/2, 0,1)
    if (conf.type=='plain') {
        temp1 <- result$surv + zval* result$std.err * result$surv
        temp2 <- result$surv - zval* result$std.err * result$surv
    }
}

```

```

    result <- c(result, list(upper=pmin(temp1,1), lower=pmax(temp2,0),
                           conf.type='plain', conf.int=conf.int))
  }
  if (conf.type=='log') {
    xx <- ifelse(result$surv==0,1,result$surv) #avoid some "log(0)" messages
    temp1 <- ifelse(result$surv==0, 0*result$std.err,
                   exp(log(xx) + zval* result$std.err))
    temp2 <- ifelse(result$surv==0, 0*result$std.err,
                   exp(log(xx) - zval* result$std.err))
    result <- c(result, list(upper=pmin(temp1,1), lower=temp2,
                              conf.type='log', conf.int=conf.int))
  }
  if (conf.type=='log-log') {
    who <- (result$surv==0 | result$surv==1) #special cases
    xx <- ifelse(who, .1,result$surv) #avoid some "log(0)" messages
    temp1 <- exp(-exp(log(-log(xx)) + zval*result$std.err/log(xx)))
    temp1 <- ifelse(who, result$surv + 0*result$std.err, temp1)
    temp2 <- exp(-exp(log(-log(xx)) - zval*result$std.err/log(xx)))
    temp2 <- ifelse(who, result$surv + 0*result$std.err, temp2)
    result <- c(result, list(upper=temp1, lower=temp2,
                              conf.type='log-log', conf.int=conf.int))
  }

  result$call <- Call
  if (is.R()) class(result) <- c('survfit.cox', 'survfit')
  else      oldClass(result) <- 'survfit.cox'
  result
}

```