

Examples of output from plotting functions

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Some minimal examples showing the output of plots from the examples.

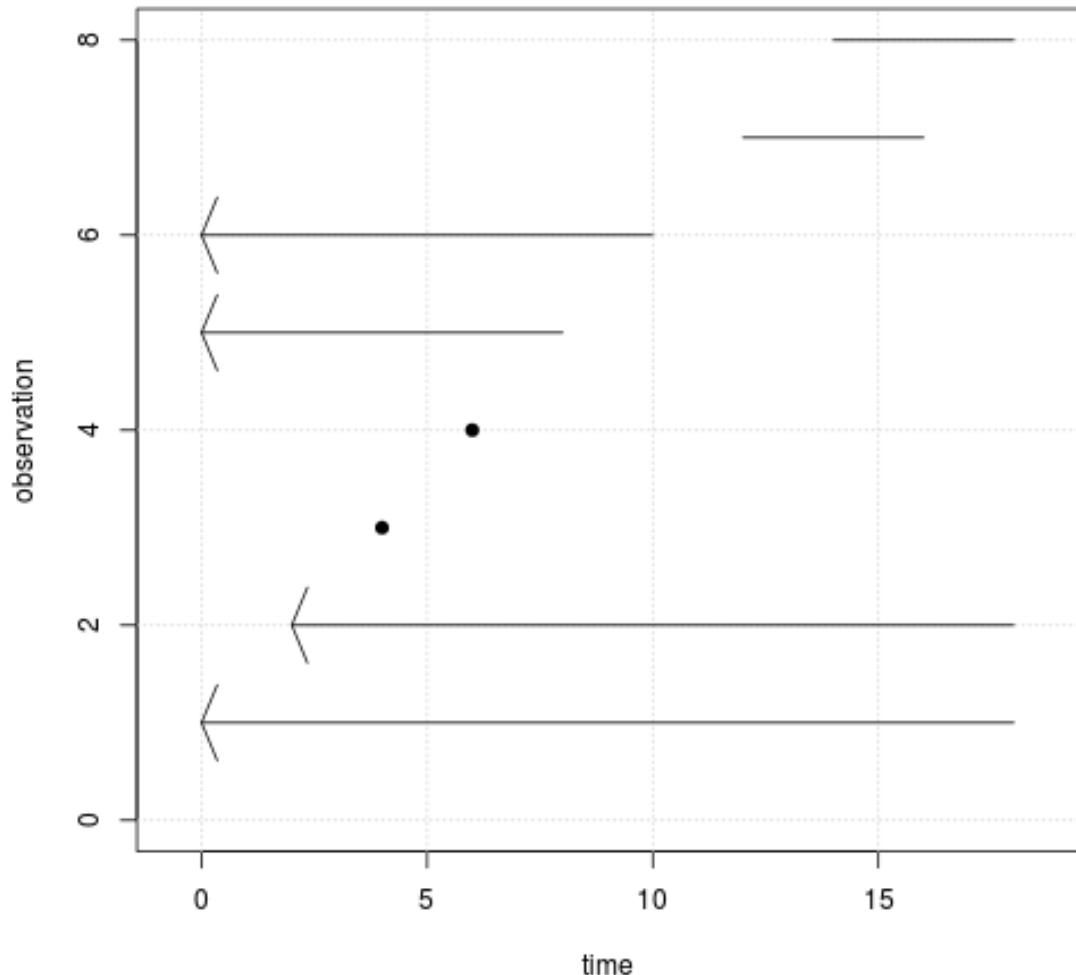
1 plotSurv

```
library("survMisc")

## Loading required package: survival
## Loading required package: splines

df0 <- data.frame(t1=c(0, 2, 4, 6, NA, NA, 12, 14),
                   t2=c(NA, NA, 4, 6, 8, 10, 16, 18))
s1 <- Surv(df0$t1, df0$t2, type="interval2")
plot(s1, l=2)
```

interval censored survival data
Arrow = censored observation



2 autoplot.Ten

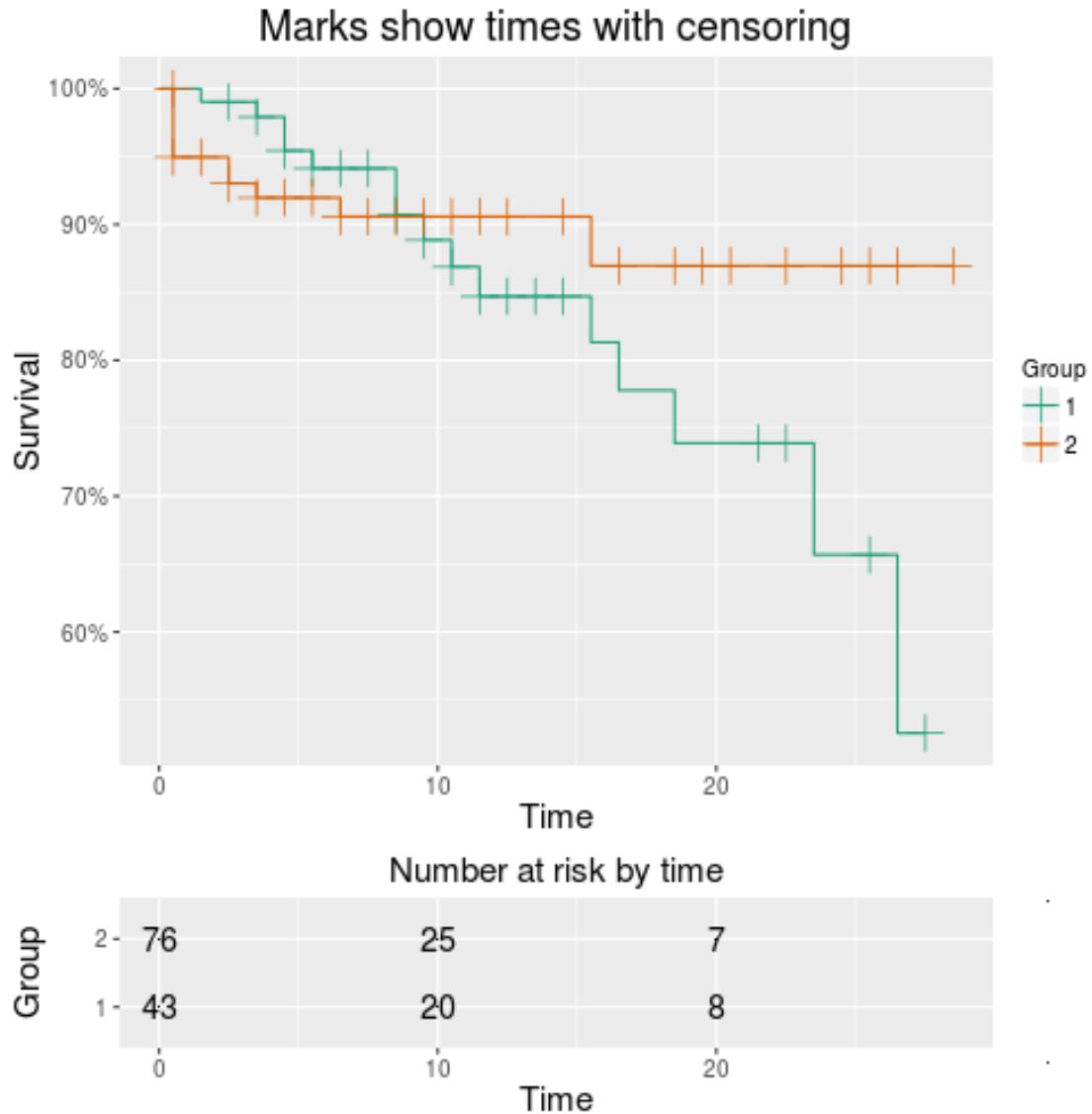
The 'autoplot' function is a generic S3 method used by 'ggplot2'.

2.1 Simple examples

```

data("kidney", package="KMsurv")
t1 <- ten(survfit(Surv(time, delta) ~ type, data=kidney))
autoplot(t1)

```

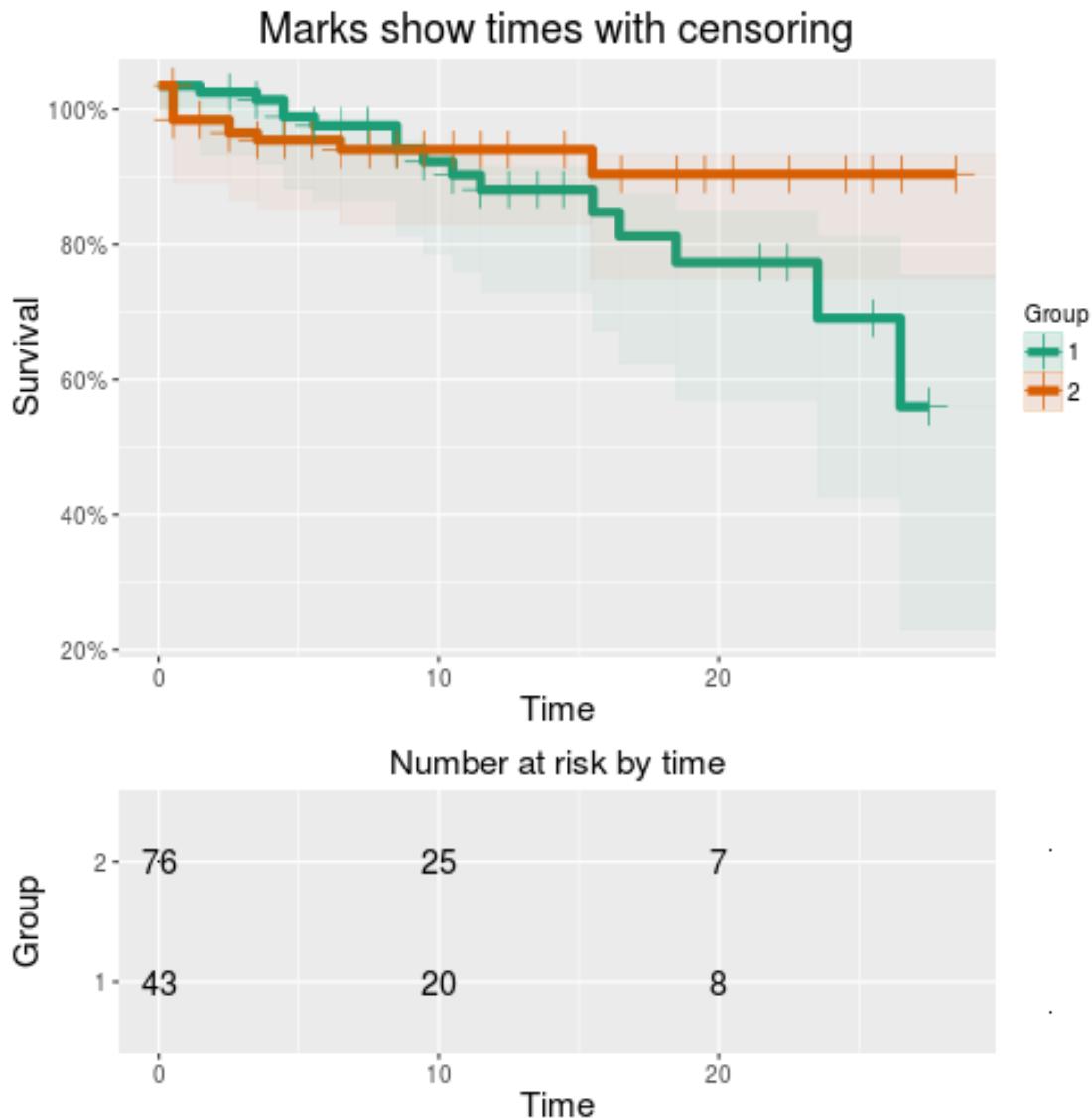


Now, we increase the line size and use jitter to prevent overlap; we also make the relative size of the table larger.

```

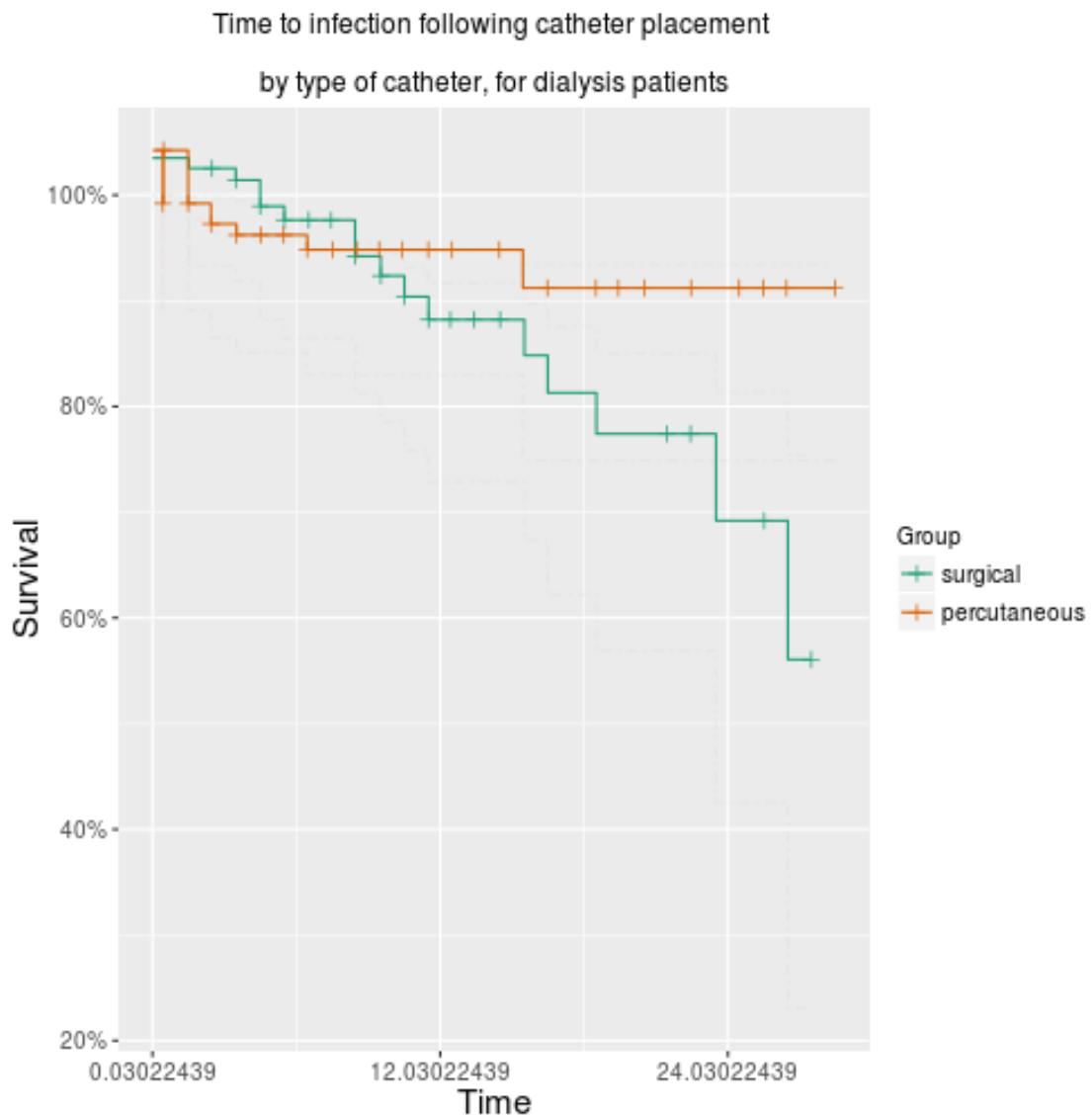
print(autoplot(t1, type="fill", survLineSize=2, jitter="all"), tabHeight=0.35)

```



A more customized example follows. Note that we return only the element marked 'plot' from the result (which is a list with two elements).

```
autoplots(t1, timeTicks="months",
          type="CI", jitter="all",
          legLabs=c("surgical", "percutaneous"),
          title="Time to infection following catheter placement \n
by type of catheter, for dialysis patients",
          titleSize=10, censSize=2)$plot
```



Here we assign the result in order to modify the *y* axis.

```
str(a1 <- autoplot(t1), max.level=1)

## List of 2
## $ table:List of 10
##   ..- attr(*, "class")= chr [1:2] "gg" "ggplot"
## $ plot :List of 9
##   ..- attr(*, "class")= chr [1:2] "gg" "ggplot"
##   - attr(*, "class")= chr [1:2] "tableAndPlot" "list"
```

```

## check the output is what we want
a1$plot + ggplot2::scale_y_continuous(limits=c(0.8, 1), name="Survival")

## Scale for 'y' is already present. Adding another scale
## for 'y', which will replace the existing scale.
## Warning: Removed 8 rows containing missing values (geom_path).
## Warning: Removed 4 rows containing missing values (geom_point).

## this is one simple way
a1 <- autoplot(t1)
suppressMessages(a1$plot <- a1$plot +
                 ggplot2::scale_y_continuous(limits=c(0.8, 1), name="Survival"))
a1

## Warning: Removed 8 rows containing missing values (geom_path).
## Warning: Removed 4 rows containing missing values (geom_point).

## or we can assign them as follows
a1 <- autoplot(t1)
ls(a1$plot$scales$scales[[3]]$super$super)

## [1] "aesthetics"    "breaks"        "call"
## [4] "expand"        "guide"         "labels"
## [7] "limits"         "minor_breaks"  "na.value"
## [10] "name"          "oob"           "palette"
## [13] "range"          "rescaler"      "scale_name"
## [16] "super"         "trans"

is.environment(a1$plot$scales$scales[[3]]$super$super$limits)

## [1] FALSE

is.null(a1$plot$scales$scales[[3]]$super$super$limits)

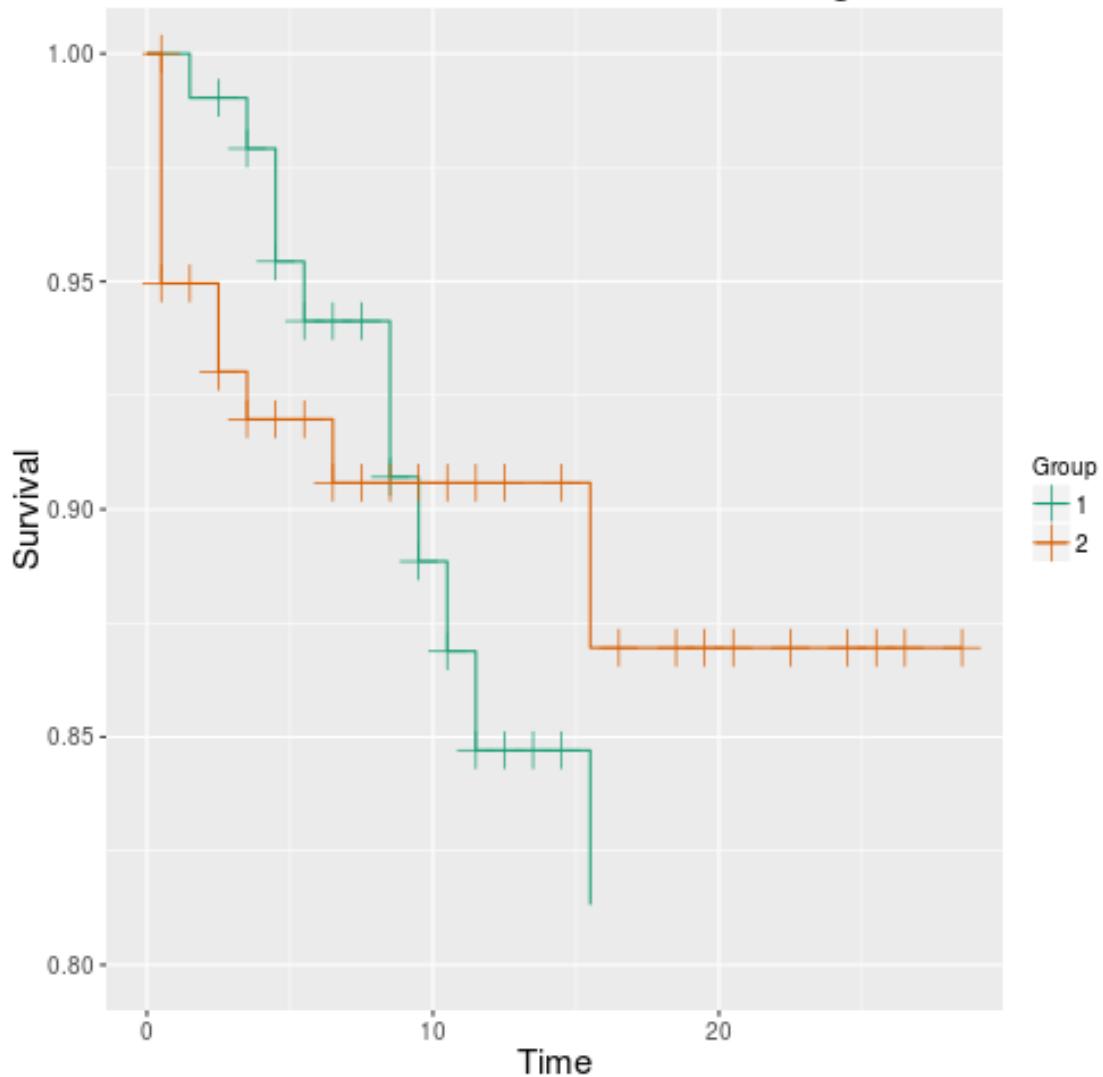
## [1] TRUE

a1$plot$scales$scales[[3]]$super$super$limits <- c(0.8, 1)
a1

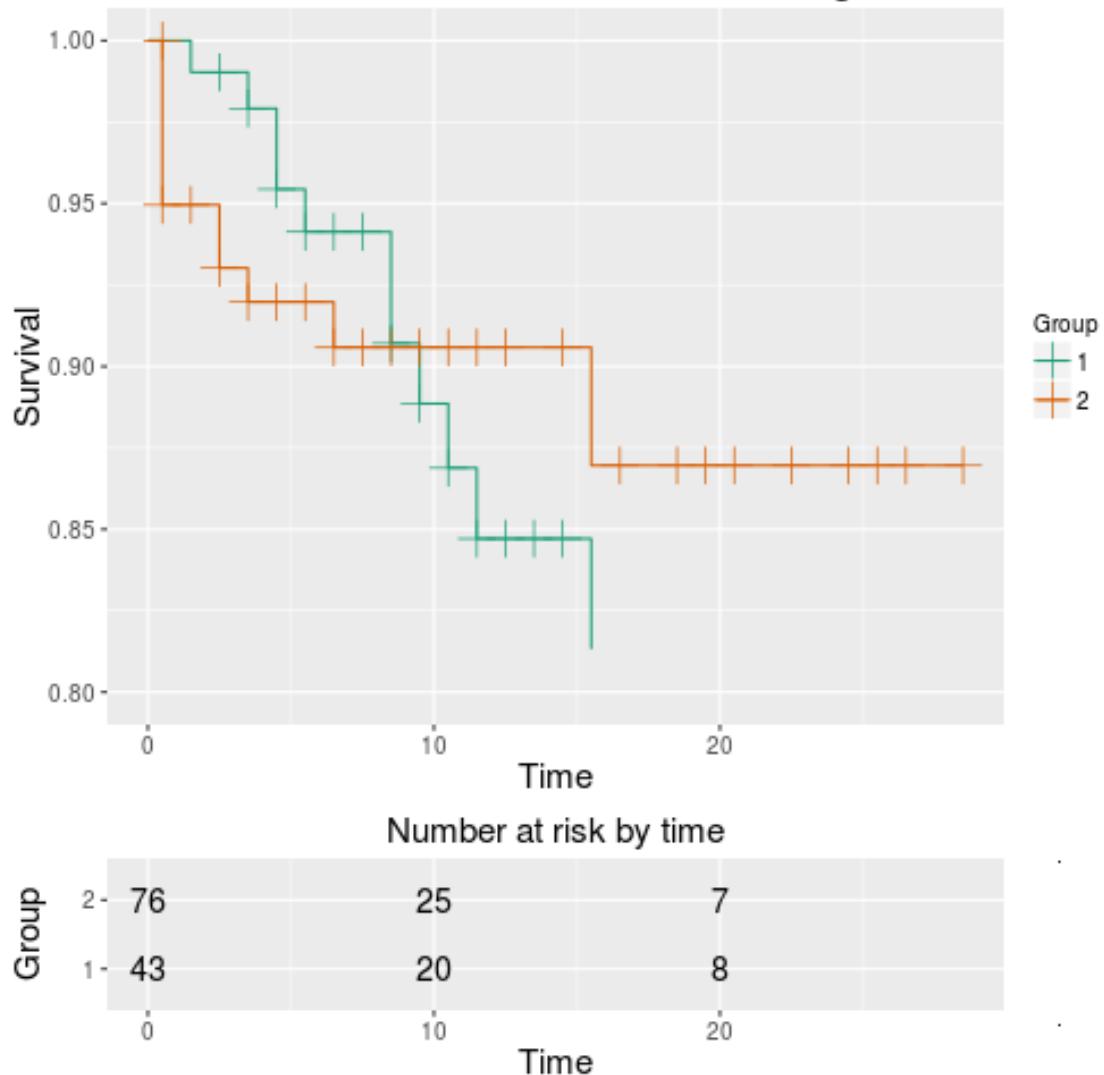
## Warning: Removed 8 rows containing missing values (geom_path).
## Warning: Removed 4 rows containing missing values (geom_point).

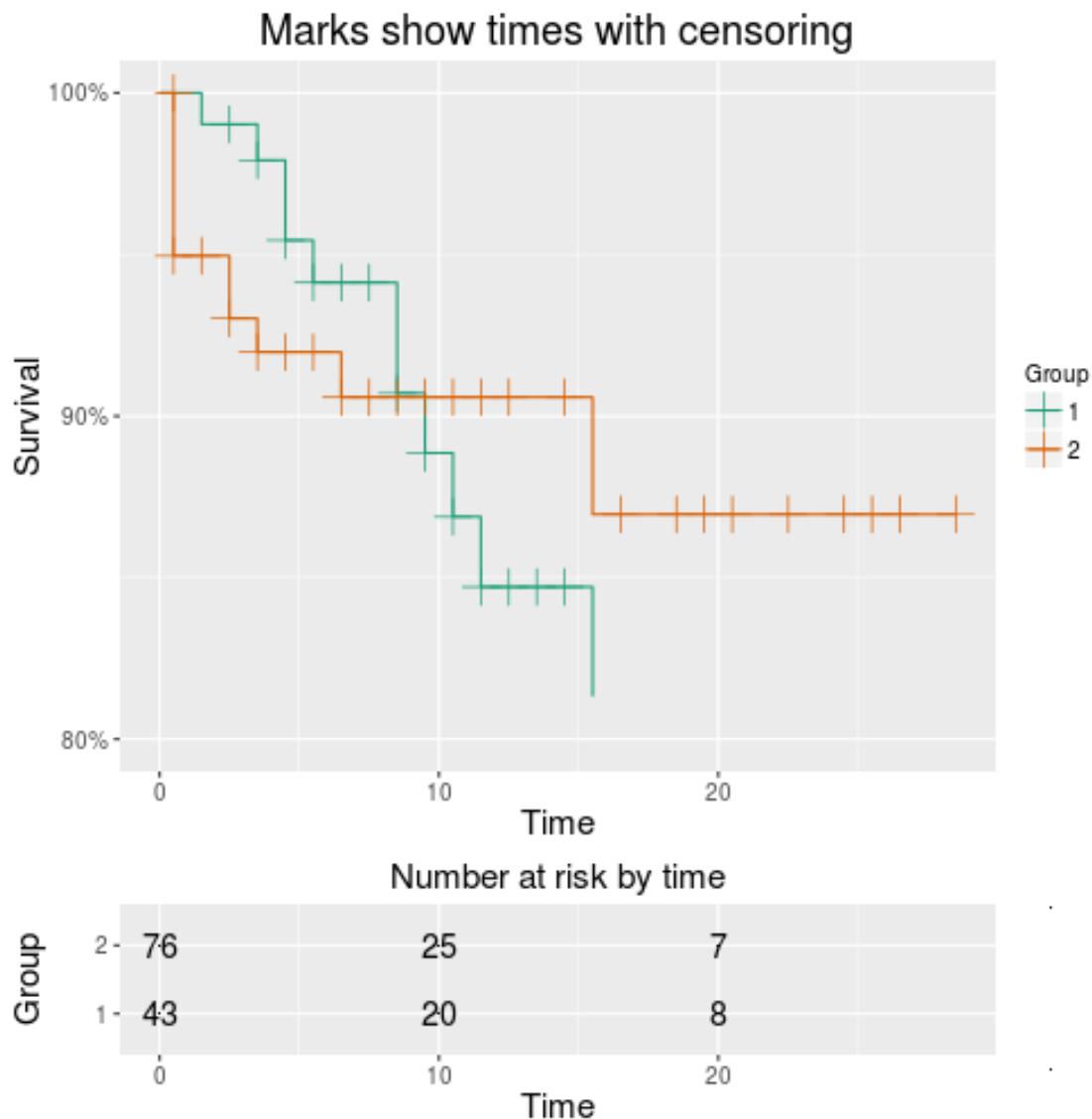
```

Marks show times with censoring



Marks show times with censoring



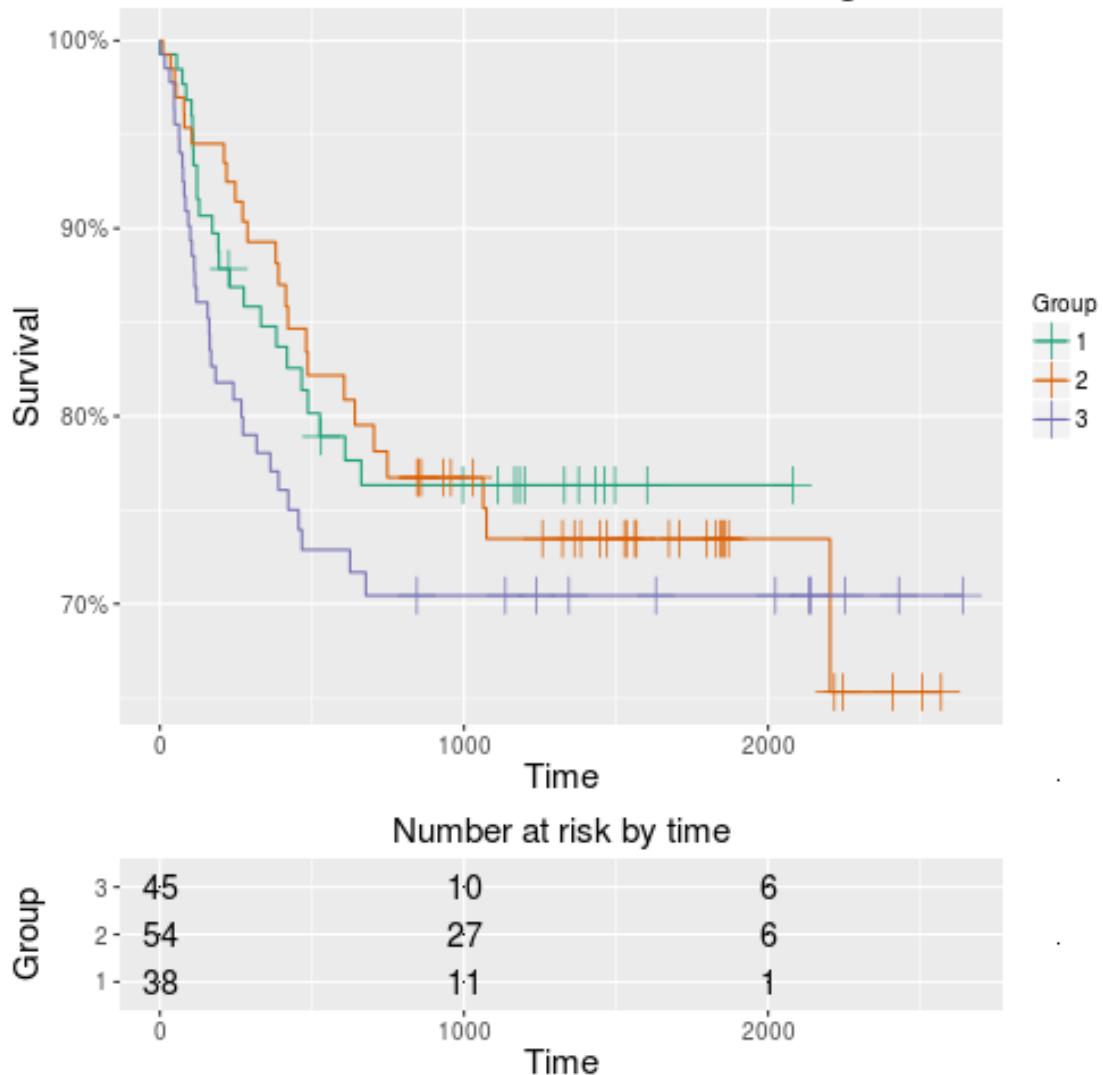


2.2 Modifying the legend

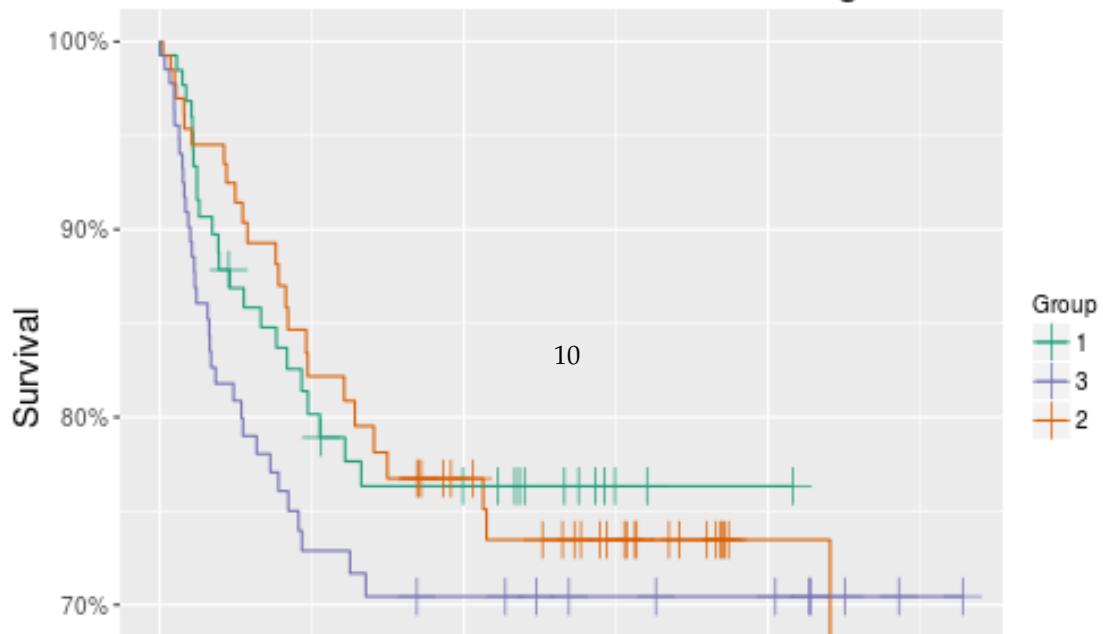
Reordering the legend labels (example with 3 groups).

```
data("bmt", package="KMsurv")
b1 <- ten(Surv(time=t2, event=d3) ~ group, data=bmt)
autoplot(b1)
autoplot(b1, legOrd=c(1, 3, 2))
```

Marks show times with censoring

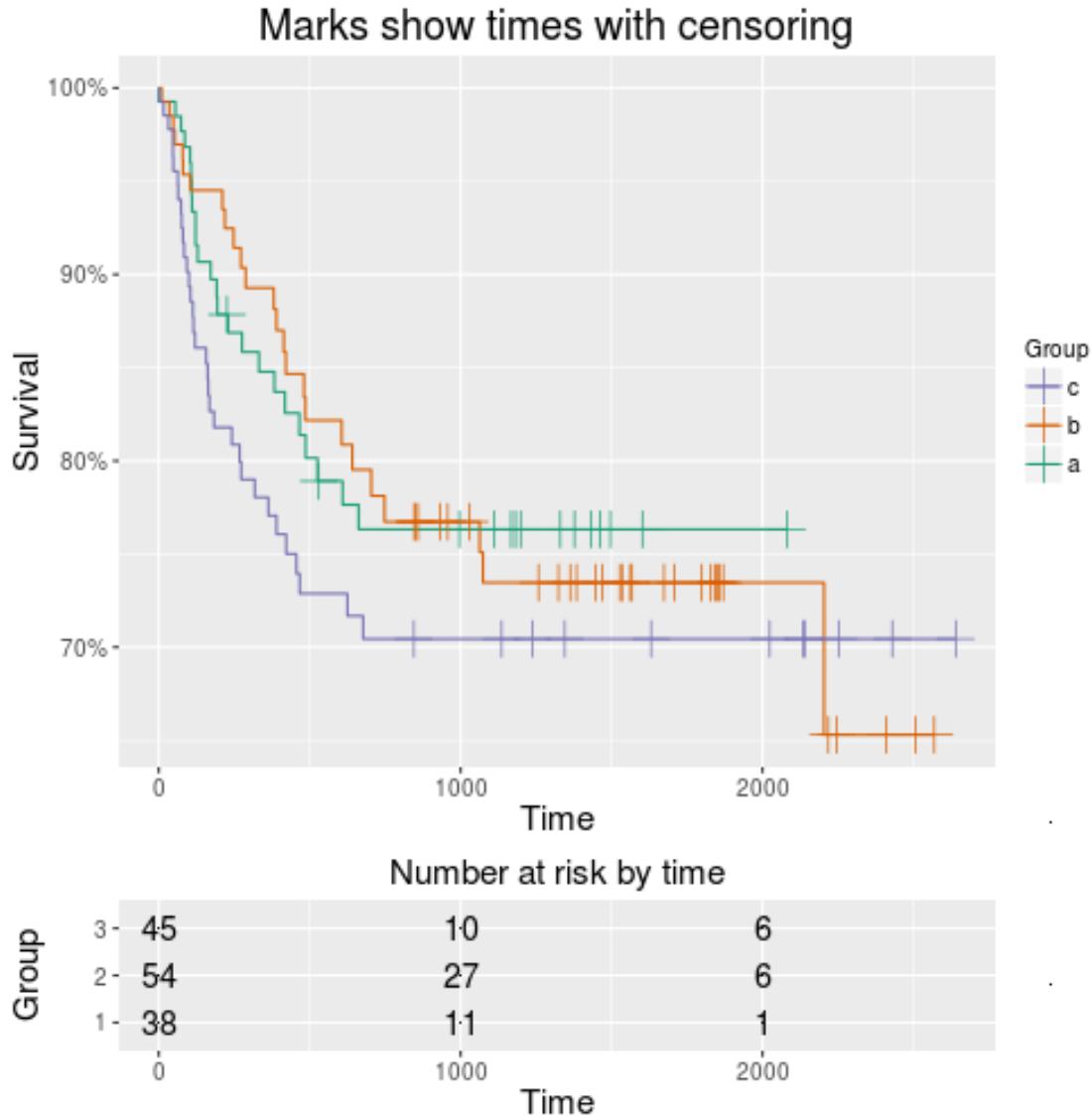


Marks show times with censoring



Here we also re-label the legend.

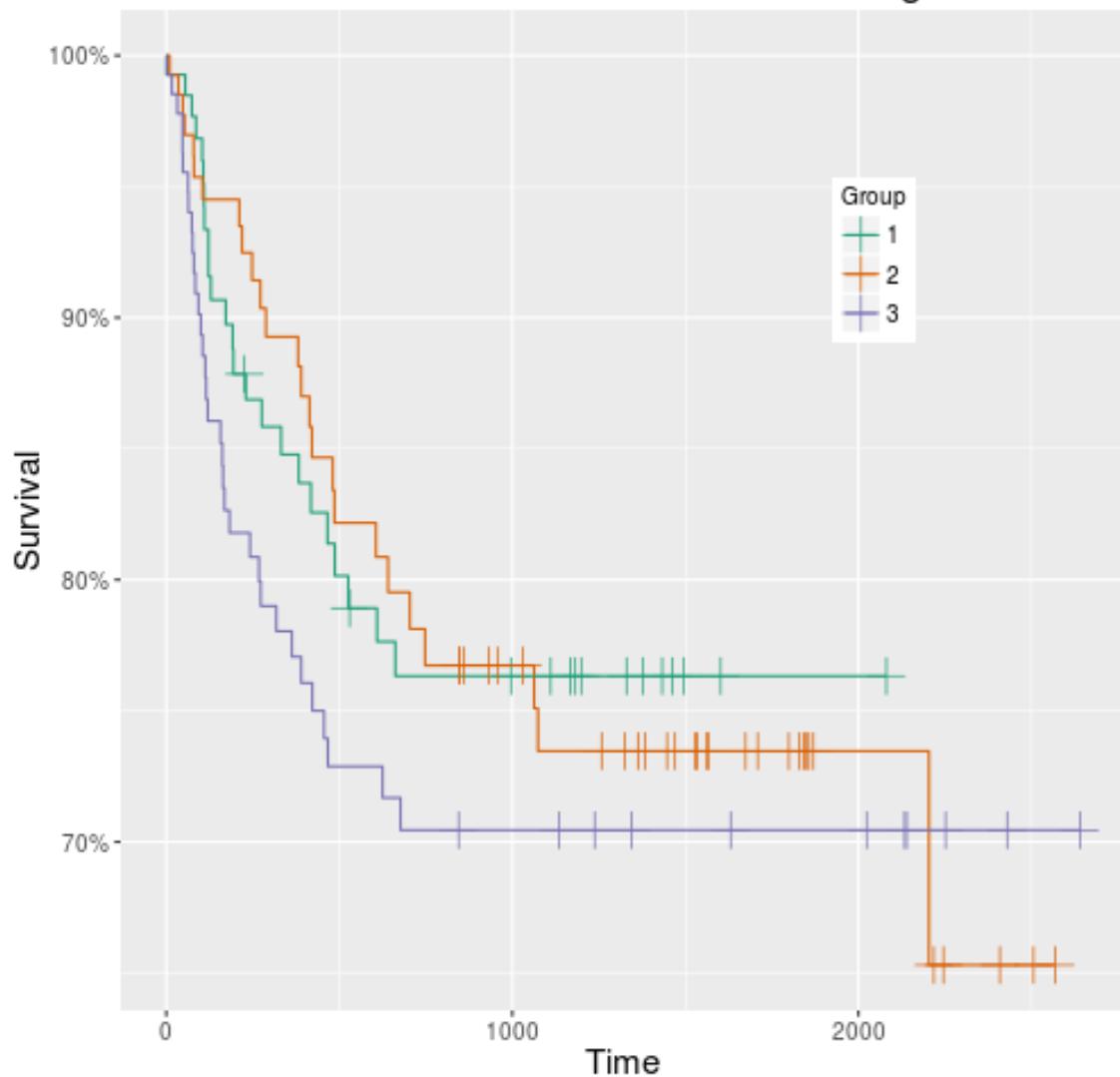
```
autoplot(b1, legOrd=c(3, 2, 1), legLabs=letters[1:3])
```



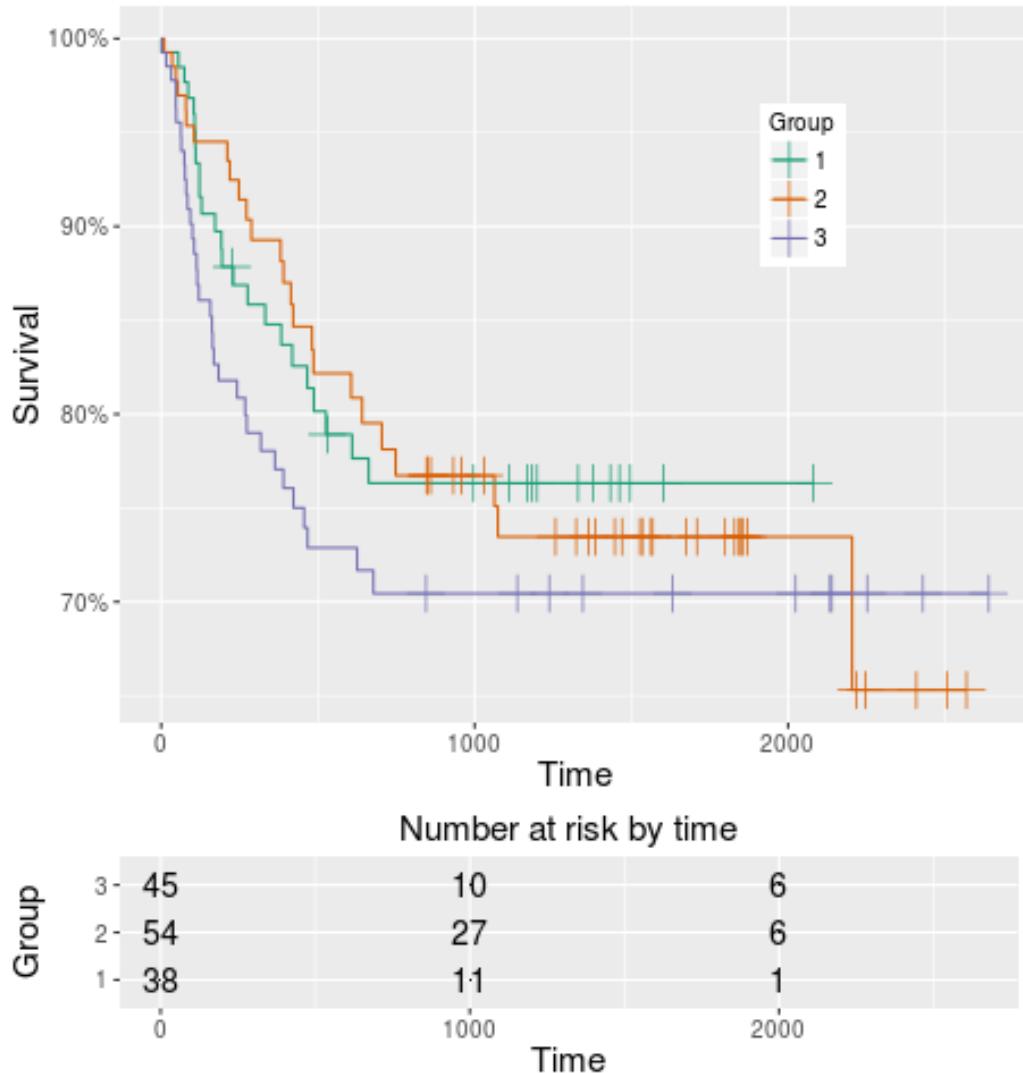
Now, let's put the legend inside the plot itself.

```
a2 <- autoplot(b1)
## ensure this is what we want
a2$plot + ggplot2::theme(legend.position=c(0.75, 0.75))
a2$plot <- a2$plot + ggplot2::theme(legend.position=c(0.75, 0.75))
a2
```

Marks show times with censoring



Marks show times with censoring

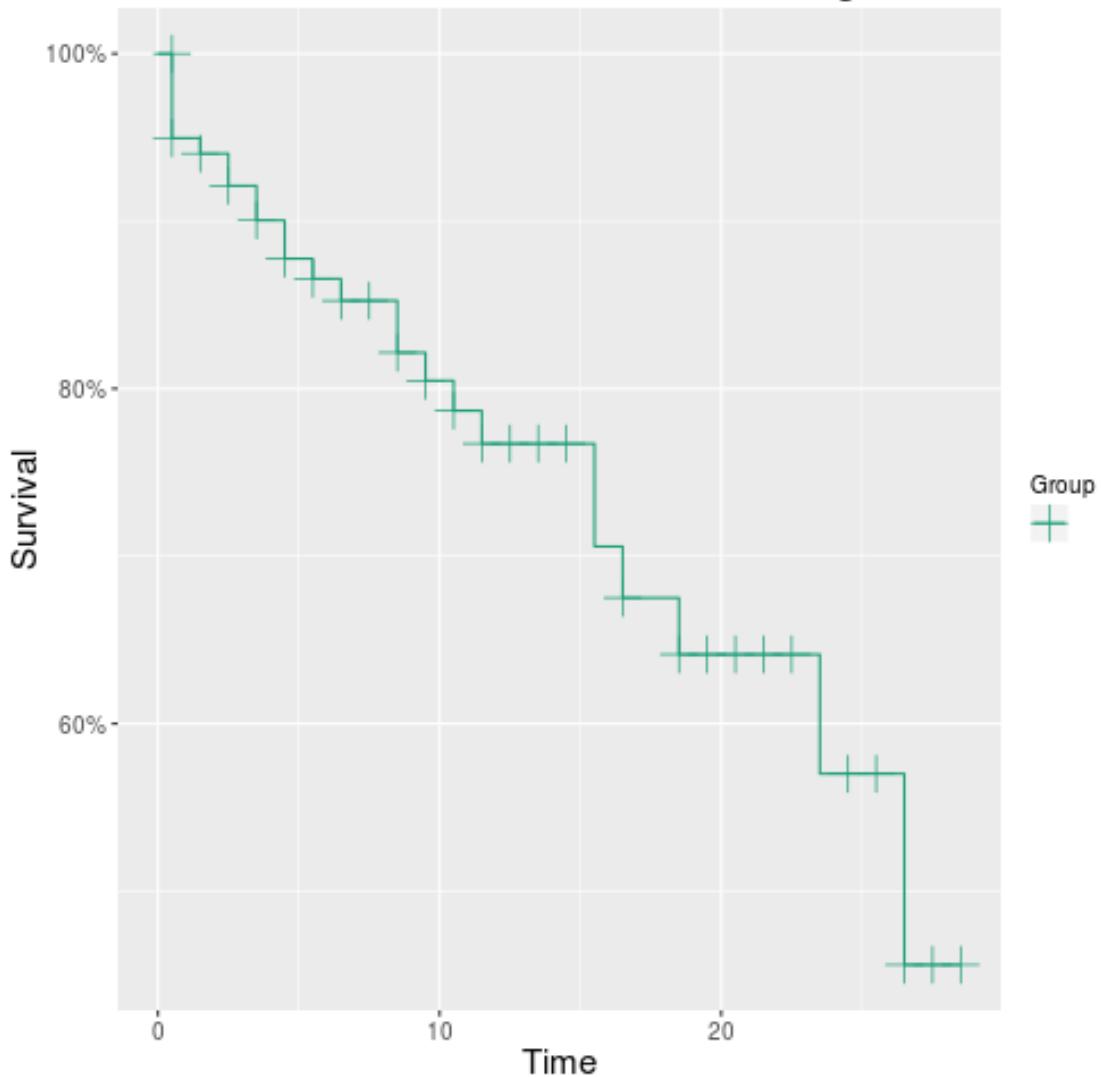


2.3 One group only

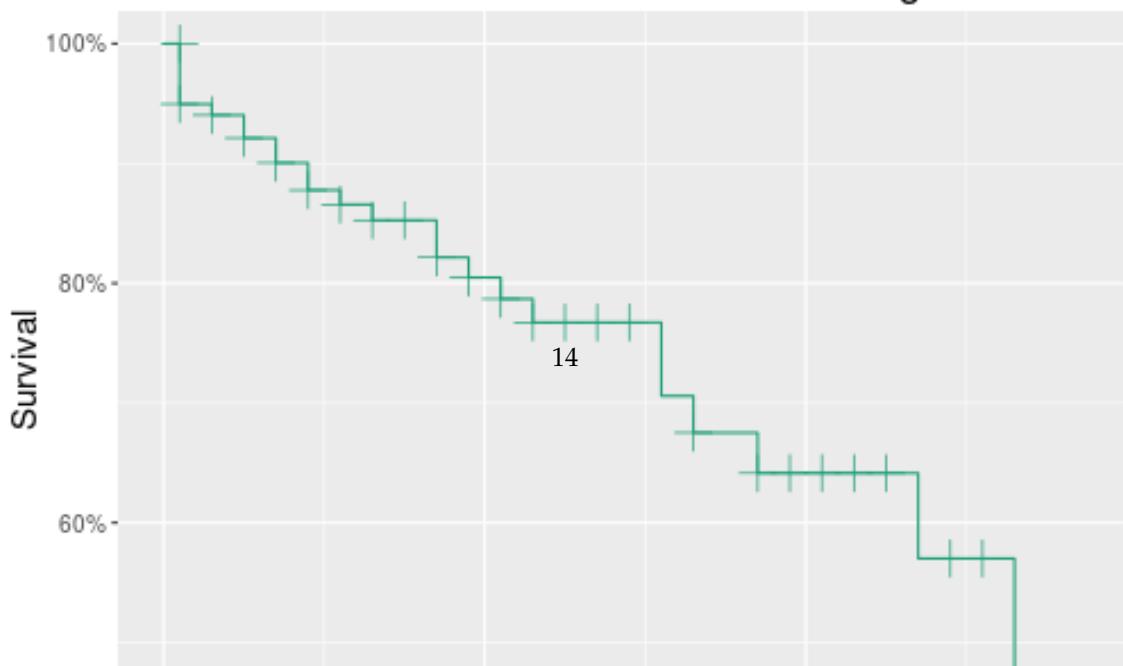
A number of options for plotting a line with just one group.

```
t2 <- ten(survfit(Surv(time=delta) ~ 1, data=kidney))  
autoplot(t2, legLabs="")$plot  
autoplot(t2, legend=FALSE)
```

Marks show times with censoring



Marks show times with censoring



2.4 Using confidence bands

Here we change the default pointwise confidence intervals to bands.

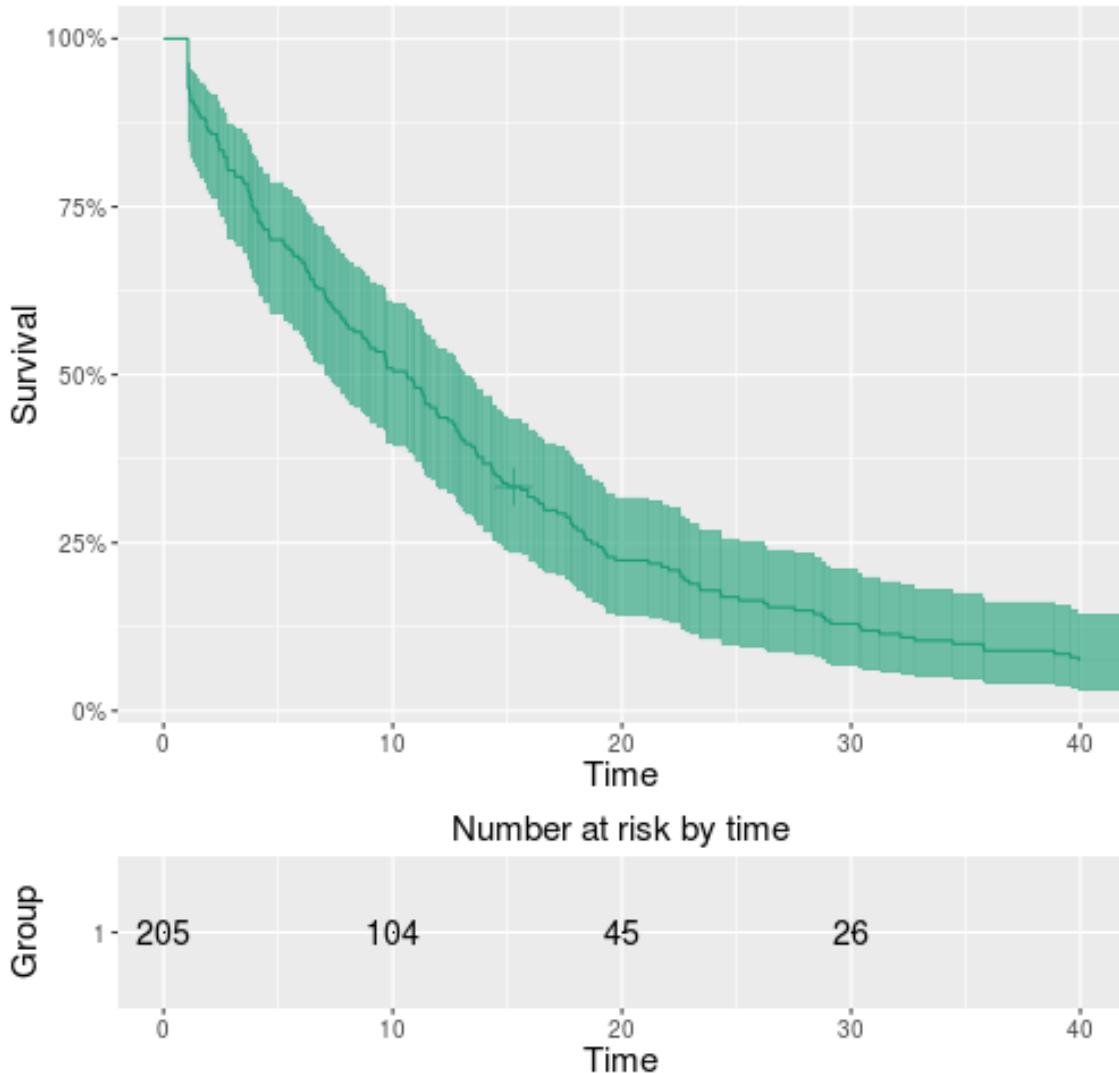
```
data("rectum.dat", package="km.ci")
t3 <- ten(survfit(Surv(time, status) ~ 1, data=rectum.dat))
## change confidence intervals to confidence bands
ci(t3, how="nair", tL=1, tU=40)

##      cg     t      S      Sv      SCV lower upper
## 1:  1 1.1  0.93 0.00033 0.00039  0.85  0.97
## 2:  1 1.1  0.92 0.00037 0.00044  0.83  0.96
## 3:  1 1.2  0.91 0.00041  5e-04  0.82  0.95
## 4:  1 1.3   0.9 0.00043 0.00053  0.82  0.95
## 5:  1 1.4   0.9 0.00045 0.00056  0.81  0.95
## ---
## 155: 1 36 0.095 0.00042   0.048 0.044  0.17
## 156: 1 36 0.09  4e-04    0.05 0.041  0.16
## 157: 1 39 0.085 0.00038   0.054 0.037  0.16
## 158: 1 40 0.08  0.00036   0.057 0.034  0.15
## 159: 1 40 0.075 0.00034   0.062 0.031  0.14

autoplot(t3, type="fill", alpha=0.6, legend=FALSE)

## Warning: Removed 1 rows containing missing values (geom_point).
## Warning: Removed 1 rows containing missing values (geom_text).
```

Marks show times with censoring



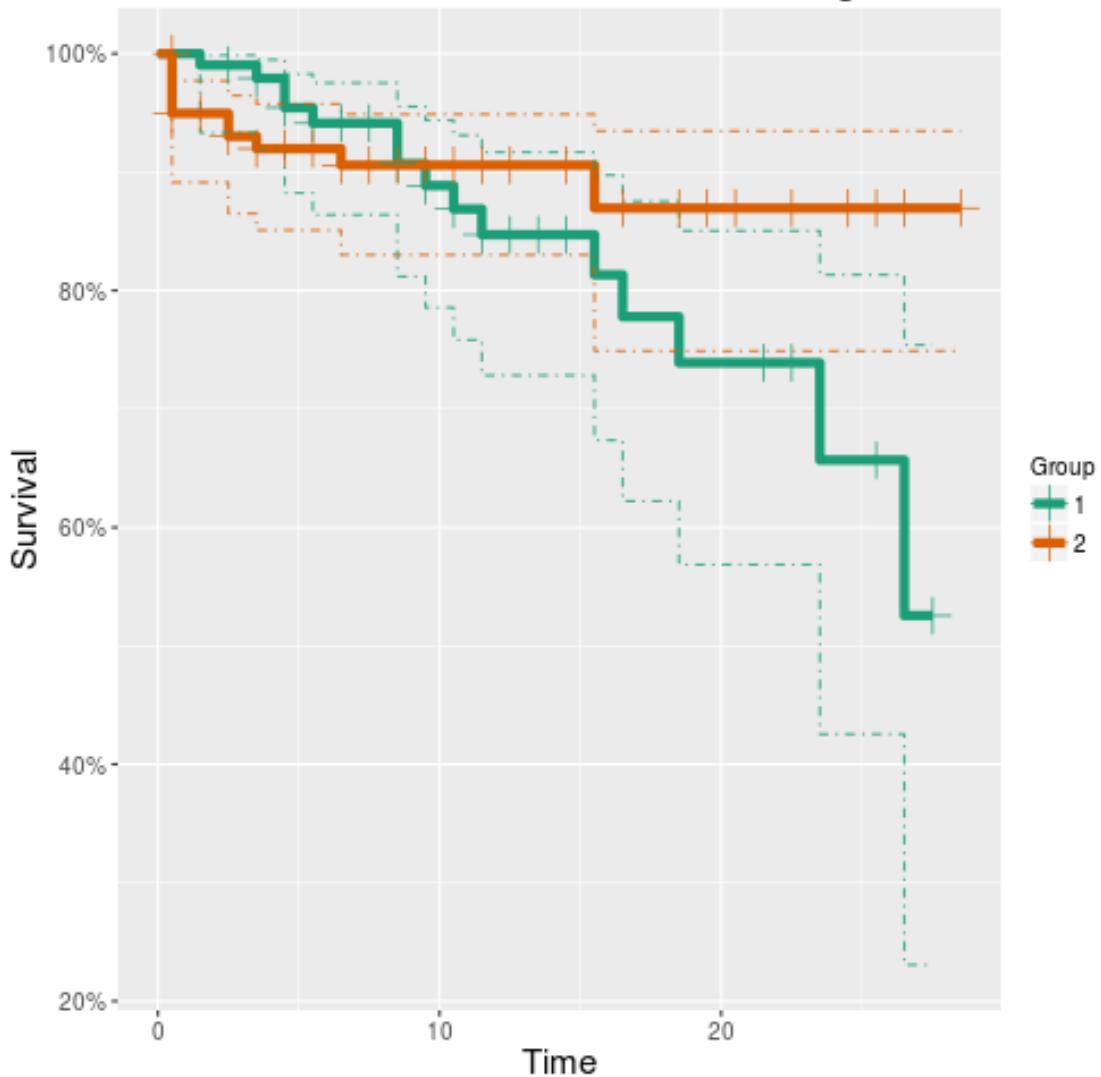
2.5 More customization

If the output of 'autplot.ten' is assigned, it can be modified in place. The list elements are ggplot2 objects which can be altered as usual.

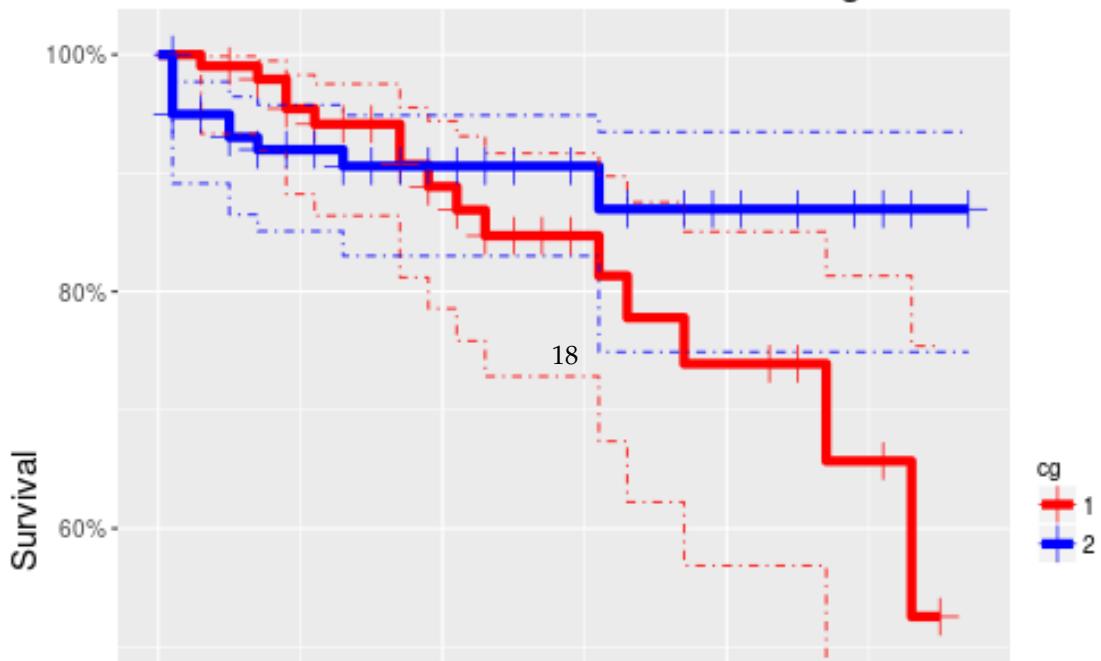
```
## manually changing the output
t4 <- ten(survfit(Surv(time, delta) ~ type, data=kidney))
(a4 <- autplot(t4, type="CI", alpha=0.8, survLineSize=2)$plot)
## change default colors
```

```
suppressMessages(a4 + list(
  ggplot2::scale_color_manual(values=c("red", "blue")),
  ggplot2::scale_fill_manual(values=c("red", "blue"))))
## change limits of y-axis
suppressMessages(a4 + ggplot2::scale_y_continuous(limits=c(0, 1)))
```

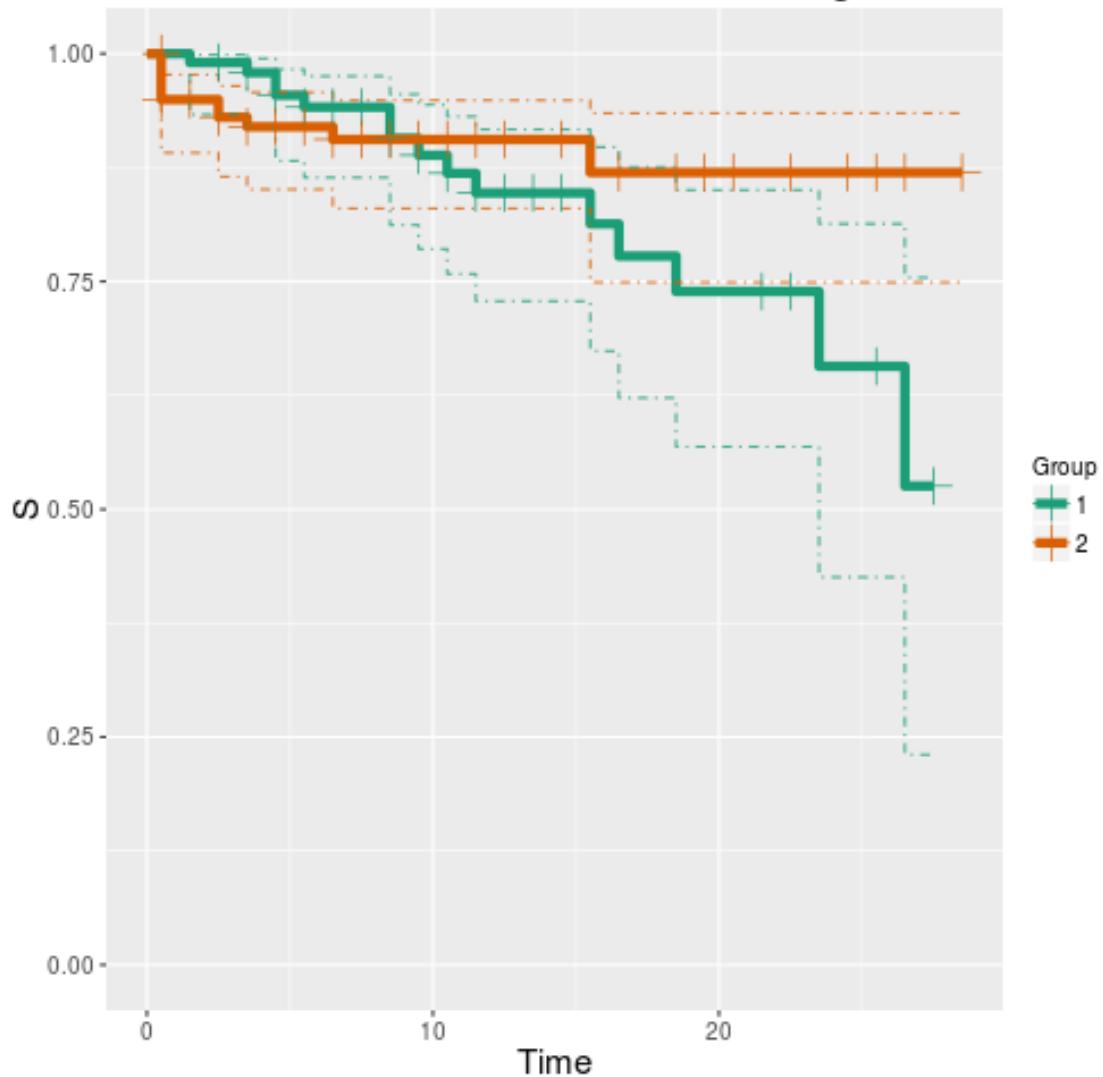
Marks show times with censoring



Marks show times with censoring



Marks show times with censoring



3 autoplot.StratTen

An example of the plots from a stratified model:

```
data("pbc", package="survival")
t1 <- ten(Surv(time, status==2) ~ trt + strata(edema), data=pbc, abbNames=FALSE)
suppressWarnings(str(a1 <- autoplot(t1), max.level=1))

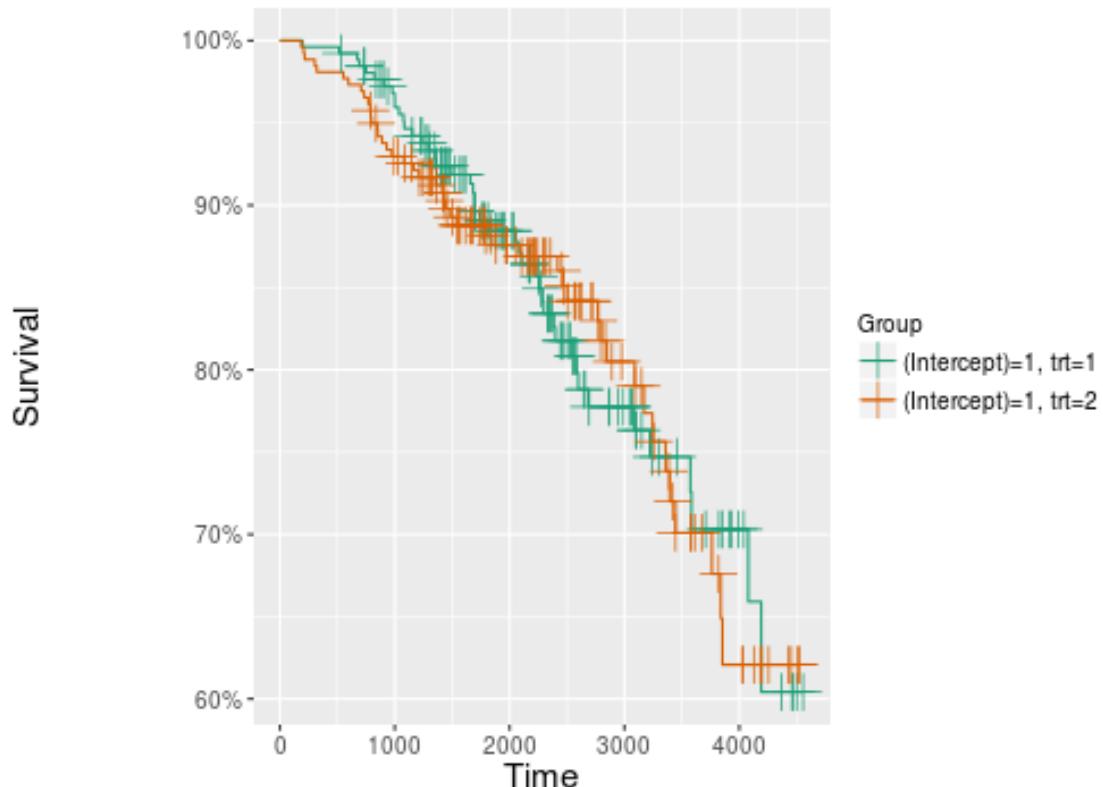
## List of 3
```

```
## $ edema=0.5=FALSE, edema=1=FALSE:List of 2
##   ..- attr(*, "class")= chr [1:2] "tableAndPlot" "list"
## $ edema=0.5=FALSE, edema=1=TRUE :List of 2
##   ..- attr(*, "class")= chr [1:2] "tableAndPlot" "list"
## $ edema=0.5=TRUE, edema=1=FALSE :List of 2
##   ..- attr(*, "class")= chr [1:2] "tableAndPlot" "list"
## - attr(*, "class")= chr [1:2] "stratTableAndPlot" "list"

a1

## Warning: Removed 2 rows containing missing values (geom_text).
## Warning: Removed 2 rows containing missing values (geom_text).
```

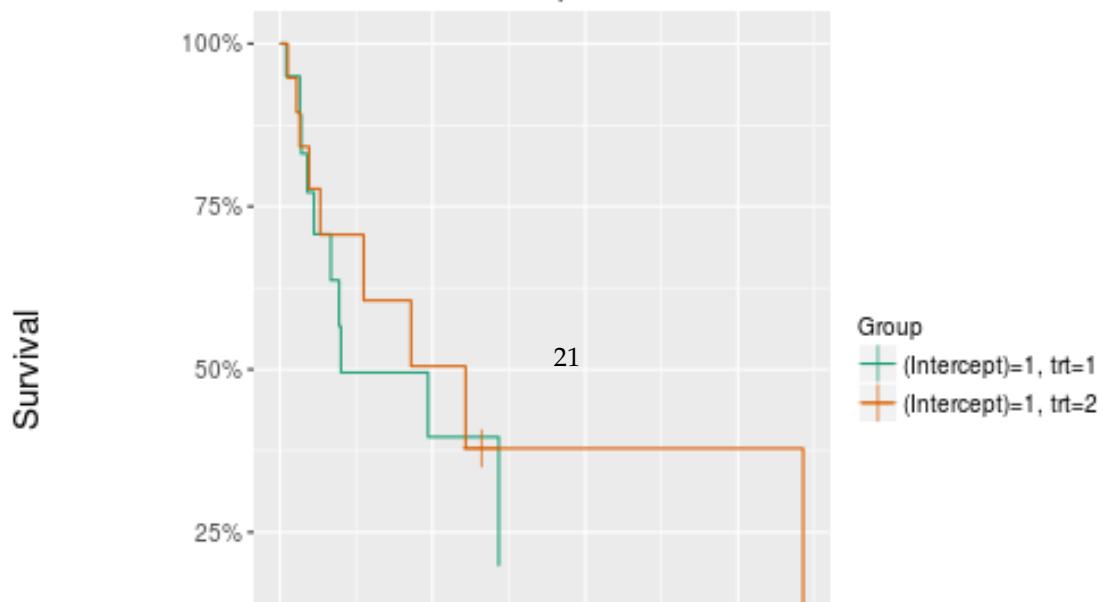
$\text{edema}=0.5=\text{FALSE}$, $\text{edema}=1=\text{FALSE}$

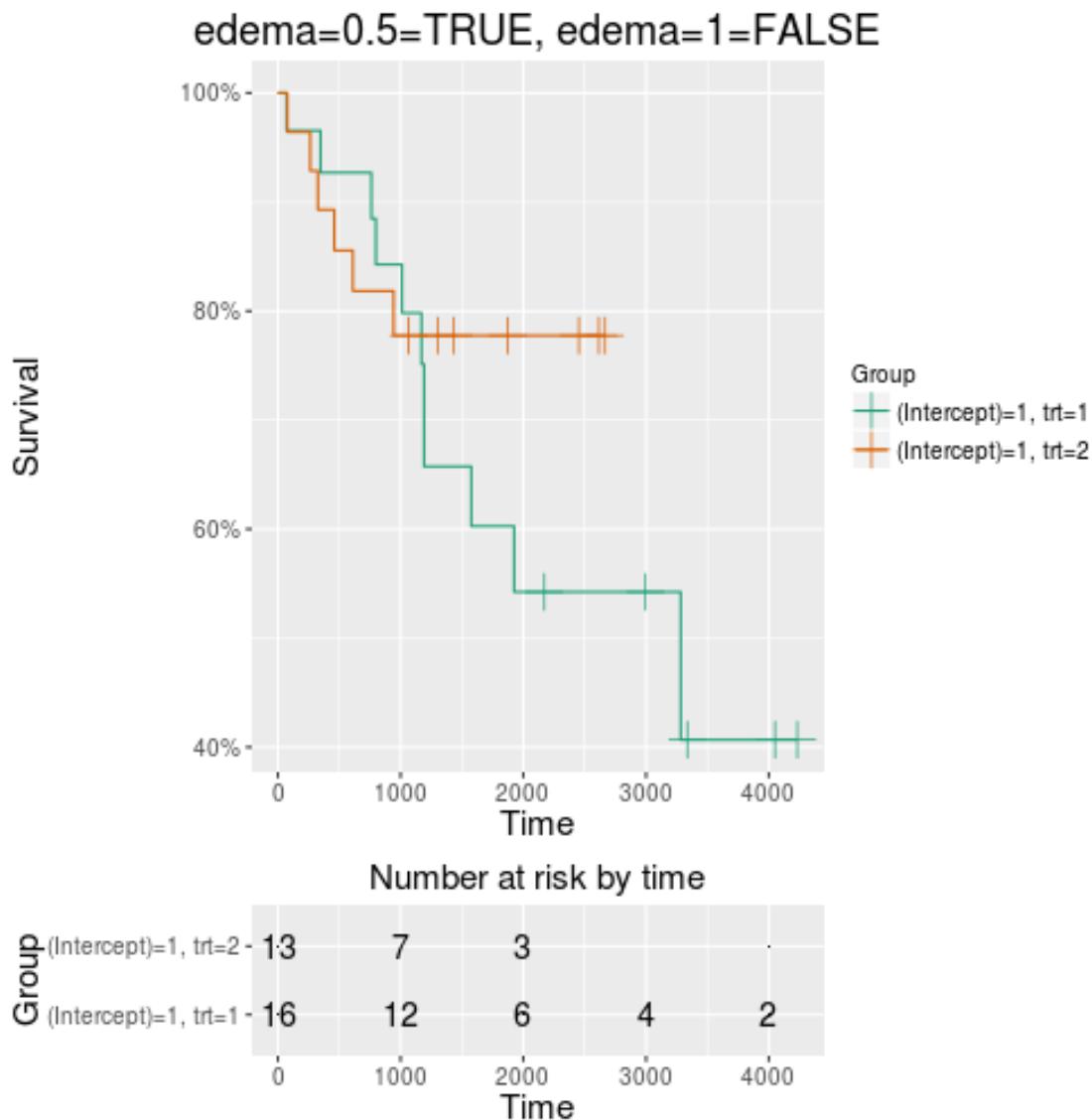


Number at risk by time

Group	(Intercept)=1, trt=2	(Intercept)=1, trt=1
0	131	132
1000	110	116
2000	66	68
3000	31	27
4000	11	8

$\text{edema}=0.5=\text{FALSE}$, $\text{edema}=1=\text{TRUE}$



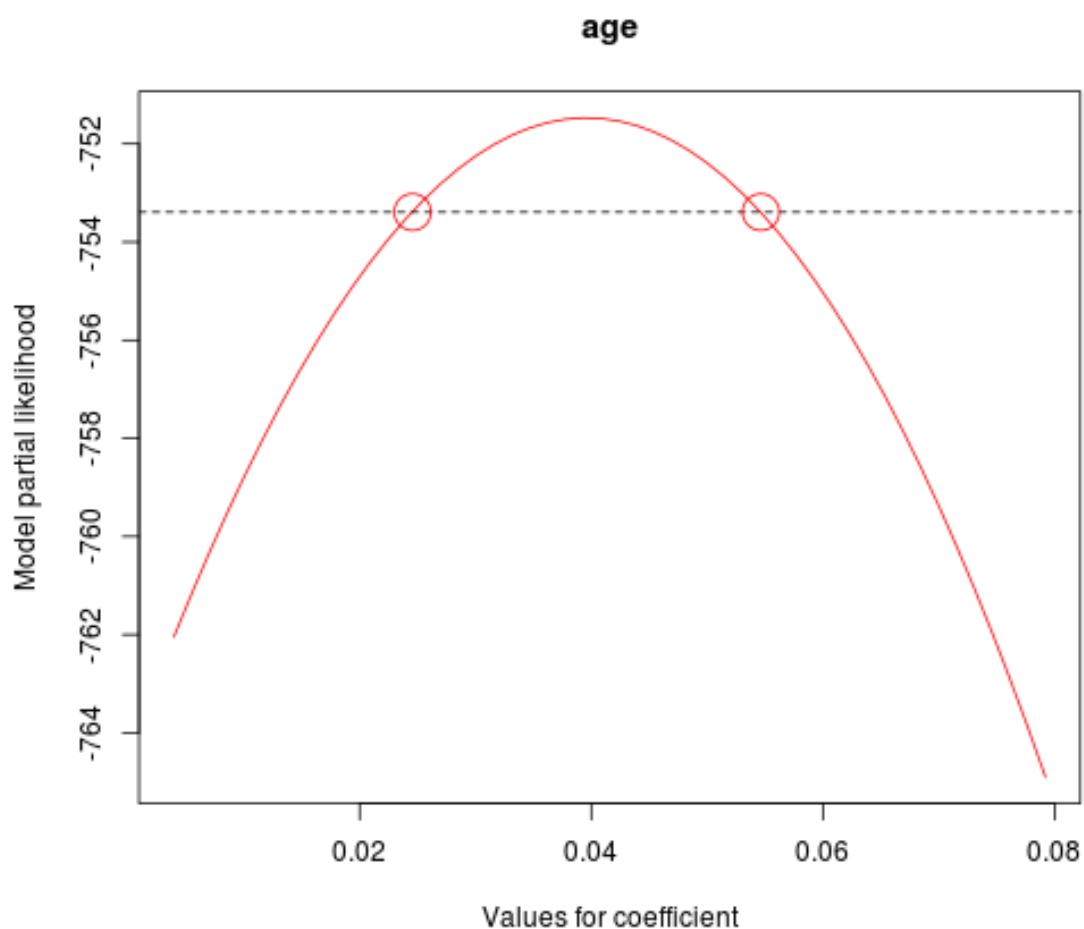


4 profLik

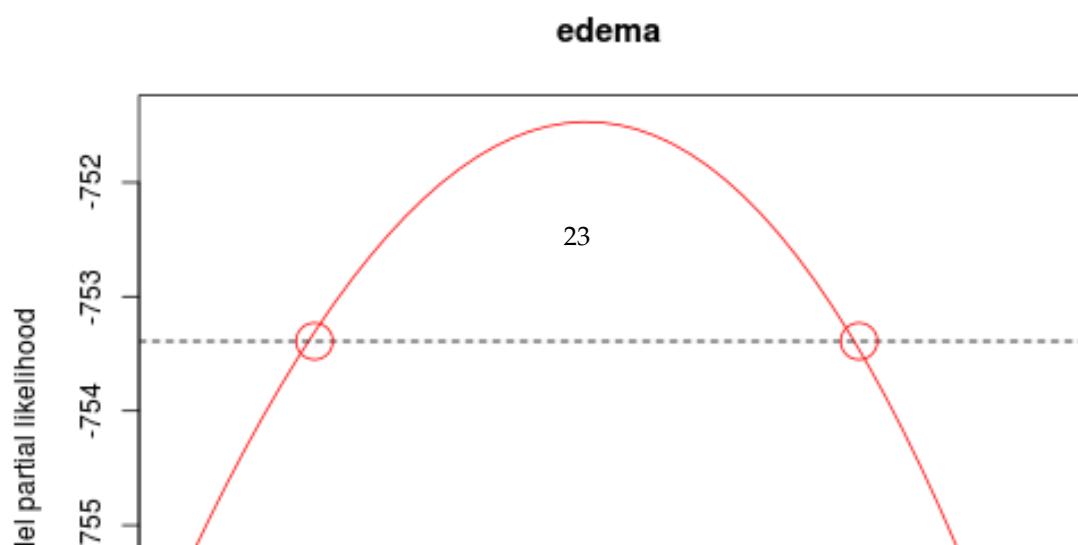
Plotting profile likelihood.

```
data("pbct", package="survival")
c1 <- survival::coxph(formula = Surv(time, status == 2) ~ age + edema + log(bili) +
  log(albumin) + log(prottime), data = pbct)
profLik(c1, col="red", devNew=FALSE)
```

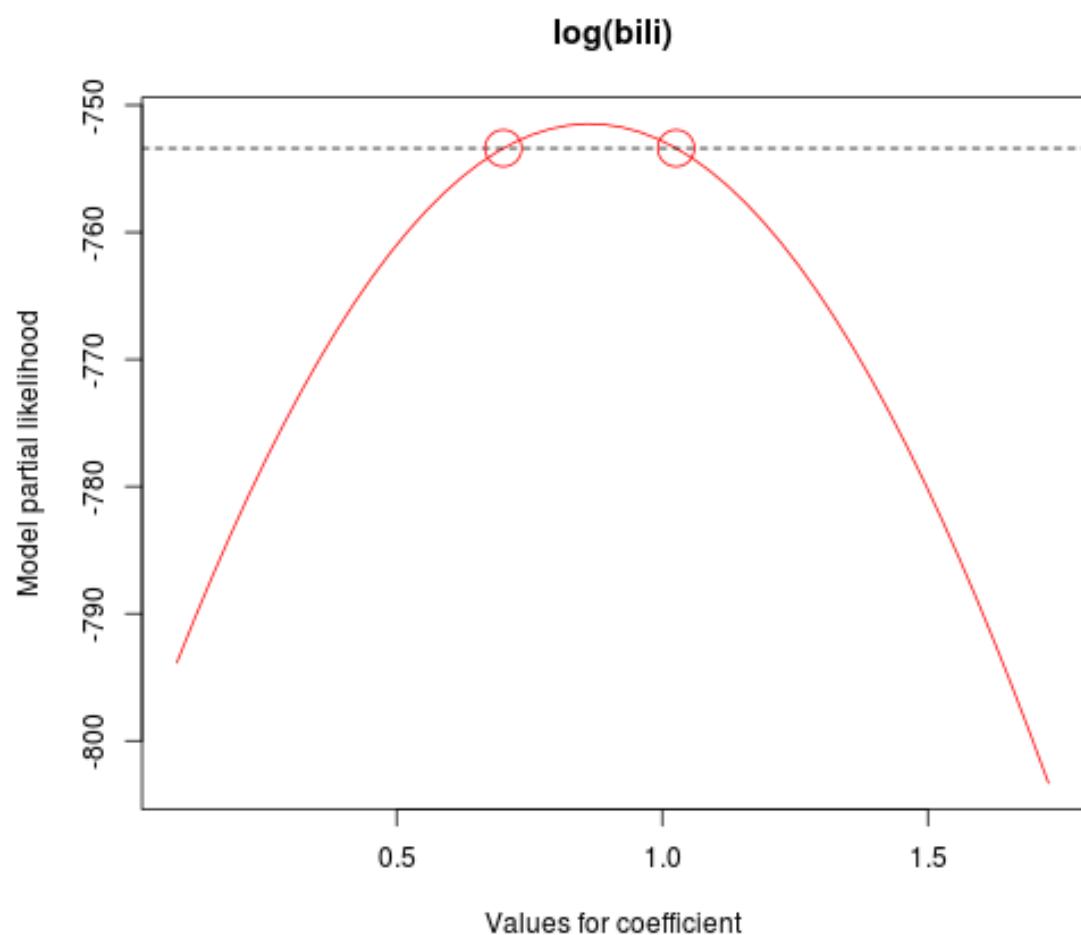
Partial likelihood profiles and 95% CI cutoff for model:
Surv(time, status == 2) ~ age + edema + log(bili) + log(albumin) + log(protime)
Circles show 95% CI limits for Wald interval



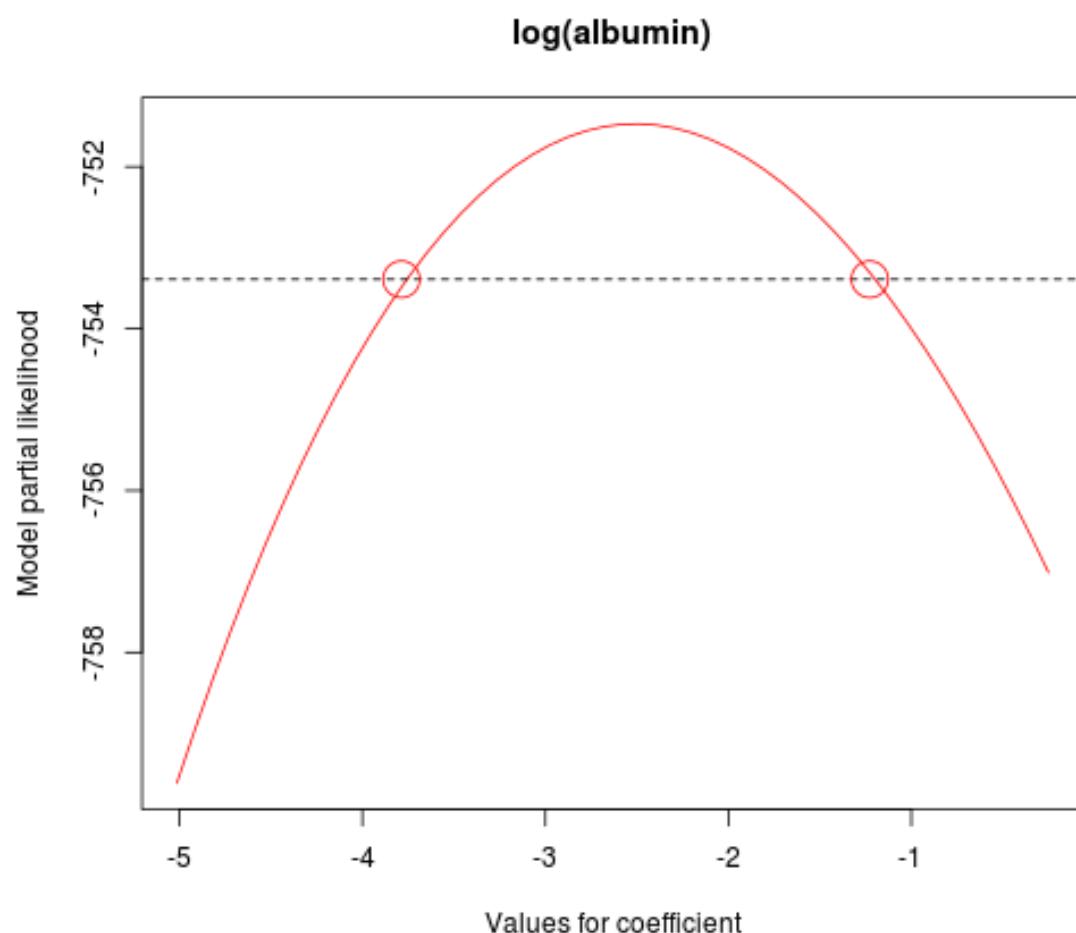
Partial likelihood profiles and 95% CI cutoff for model:
Surv(time, status == 2) ~ age + edema + log(bili) + log(albumin) + log(protime)
Circles show 95% CI limits for Wald interval



Partial likelihood profiles and 95% CI cutoff for model:
Surv(time, status == 2) ~ age + edema + log(bili) + log(albumin) + log(protime)
Circles show 95% CI limits for Wald interval



Partial likelihood profiles and 95% CI cutoff for model:
Surv(time, status == 2) ~ age + edema + log(bili) + log(albumin) + log(protime)
Circles show 95% CI limits for Wald interval



Partial likelihood profiles and 95% CI cutoff for model:
Surv(time, status == 2) ~ age + edema + log(bili) + log(albumin) + log(prottime)
Circles show 95% CI limits for Wald interval

