survival_package

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Fit a Kaplan-Meier and plot it

```
library(survival)
fit <- survfit(Surv(time,status)~x, data=aml)
aml
```

```
##      time status           x
## 1       9      1   Maintained
## 2      13      1   Maintained
## 3      13      0   Maintained
## 4      18      1   Maintained
## 5      23      1   Maintained
## 6      28      0   Maintained
## 7      31      1   Maintained
## 8      34      1   Maintained
## 9      45      0   Maintained
## 10     48      1   Maintained
## 11    161      0   Maintained
## 12      5      1 Nonmaintained
## 13      5      1 Nonmaintained
## 14      8      1 Nonmaintained
## 15      8      1 Nonmaintained
## 16     12      1 Nonmaintained
## 17     16      0 Nonmaintained
## 18     23      1 Nonmaintained
## 19     27      1 Nonmaintained
## 20     30      1 Nonmaintained
## 21     33      1 Nonmaintained
## 22     43      1 Nonmaintained
## 23     45      1 Nonmaintained
```

```
plot(fit, lty = 2:3)
legend(100, .8, c("Maintained","nonmaintained"), lty = 2:3)
```
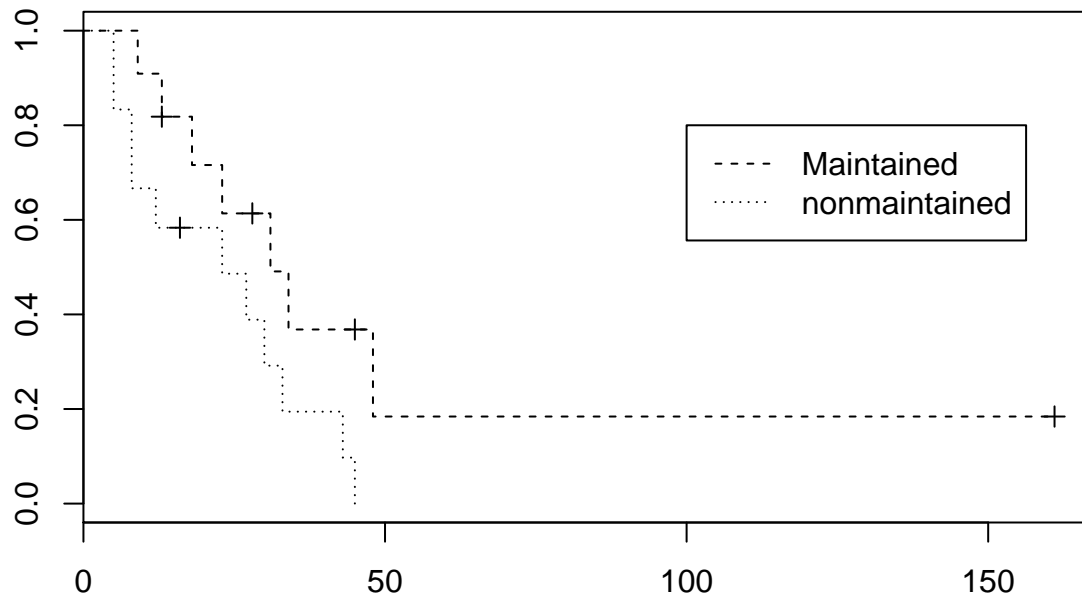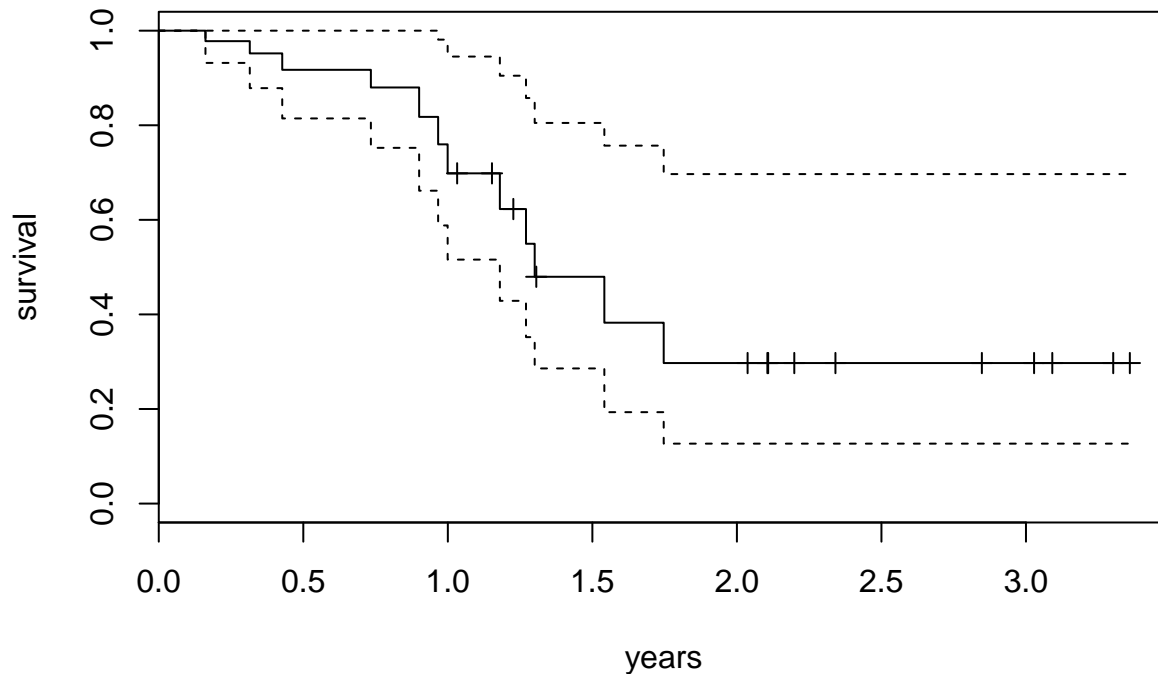
```
plot(fit, lty = 2:3, fun = "cumhaz")
```
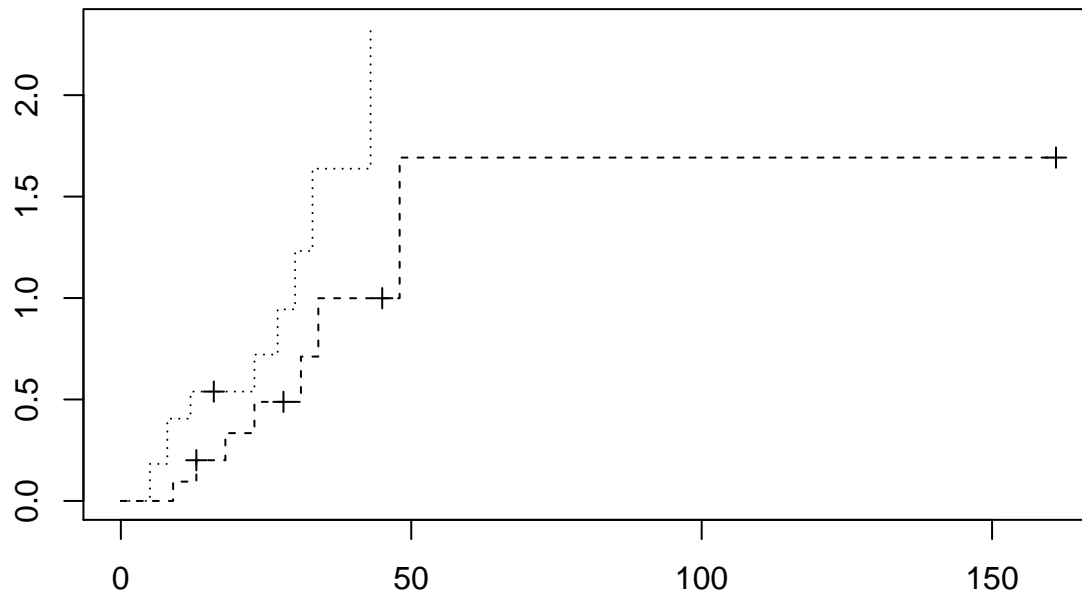

Fit a cox proportional hazards model and plot it

```
fit <- coxph(Surv(futime,fustat)~age, data = ovarian)
plot(survfit(fit,newdata = data.frame(age=60)),xscale = 365.25,xlab = "years", ylab = "survival")
```

use cgd data(counting process format) in coxph strata with sex

```r
library(survival)
head(cgd)
```

```
##   id              center       random    treat      sex age height weight
## 1  1 Scripps Institute 1989-06-07  rIFN-g female  12    147   62.0
## 2  1 Scripps Institute 1989-06-07  rIFN-g female  12    147   62.0
## 3  1 Scripps Institute 1989-06-07  rIFN-g female  12    147   62.0
## 4  2 Scripps Institute 1989-06-07 placebo   male  15    159   47.5
## 5  2 Scripps Institute 1989-06-07 placebo   male  15    159   47.5
## 6  2 Scripps Institute 1989-06-07 placebo   male  15    159   47.5
##      inherit steroids propylac  hos.cat tstart enum tstop status
## 1 autosomal        0        0 US:other      0    1   219      1
## 2 autosomal        0        0 US:other    219    2   373      1
## 3 autosomal        0        0 US:other    373    3   414      0
## 4 autosomal        0        1 US:other      0    1     8      1
## 5 autosomal        0        1 US:other      8    2    26      1
## 6 autosomal        0        1 US:other     26    3   152      1
```

```r
fit <- coxph(Surv(tstart,tstop,status)~1+strata(sex), data = cgd)
plot(survfit(fit), lty = 2:3, xlab = "time", ylab = "Survival")
legend("topright",legend=c("female","male"), lty = 2:3)
```
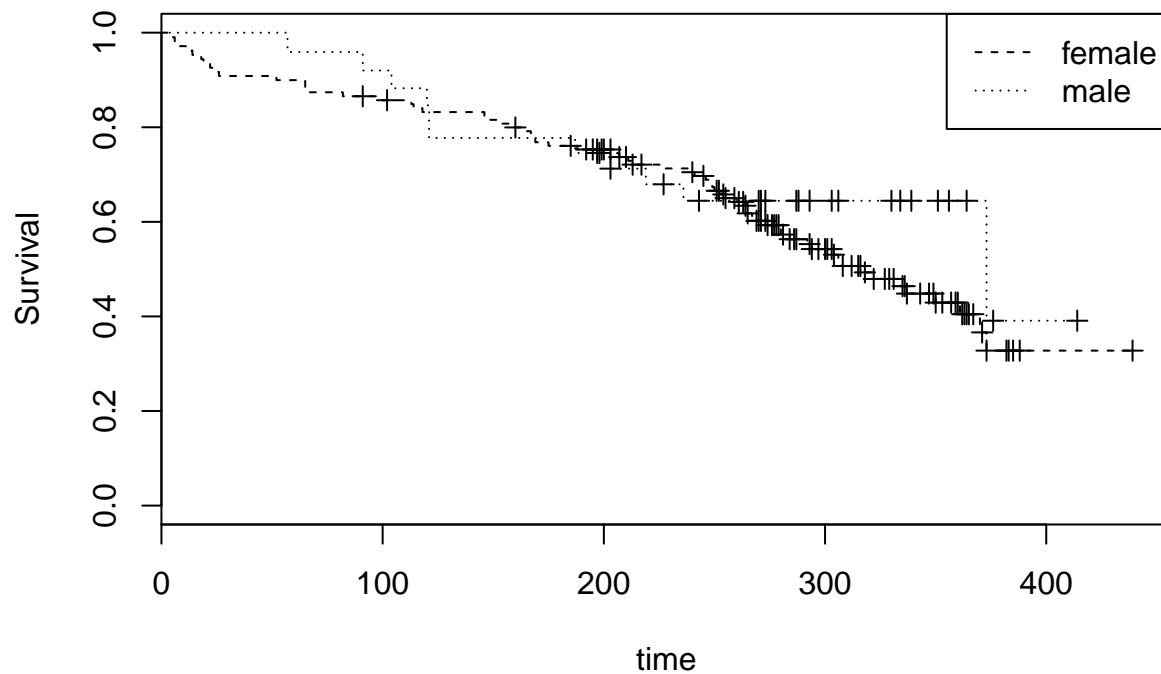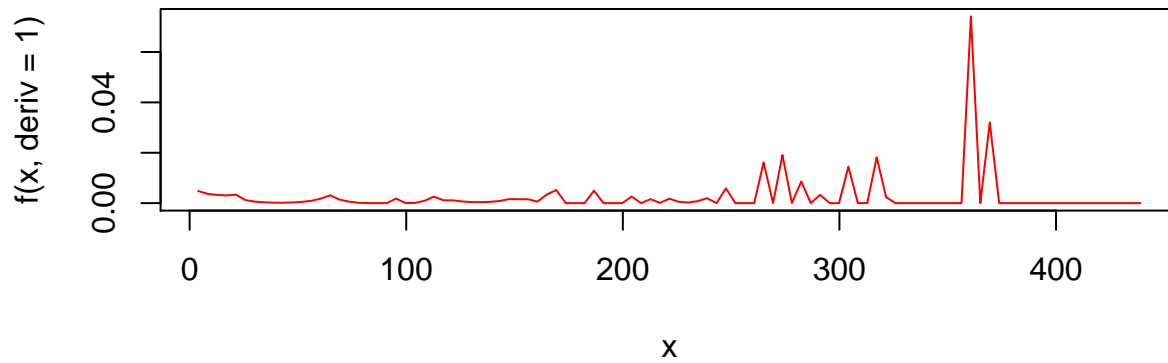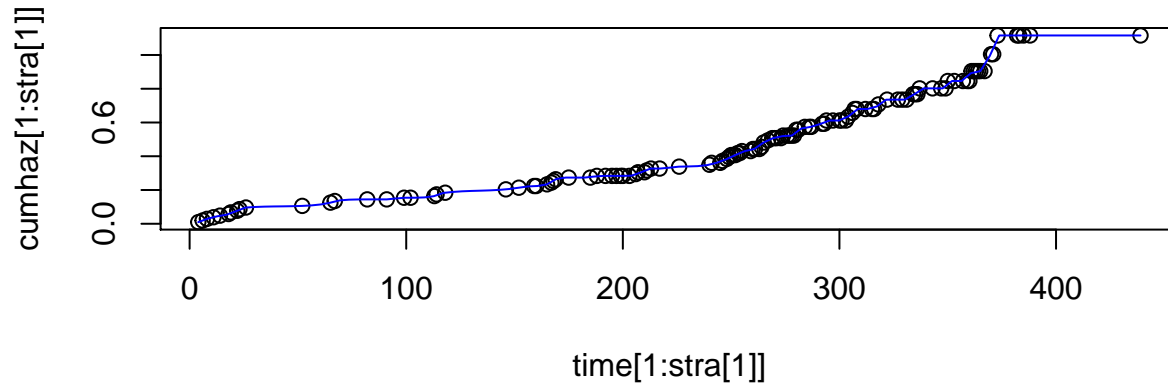
```
plot(survfit(fit),fun="cumhaz", lty = 1:2, xlab = "time", ylab = "Cumhaz")
legend("topleft",legend=c("female","male"), lty = 1:2)
```
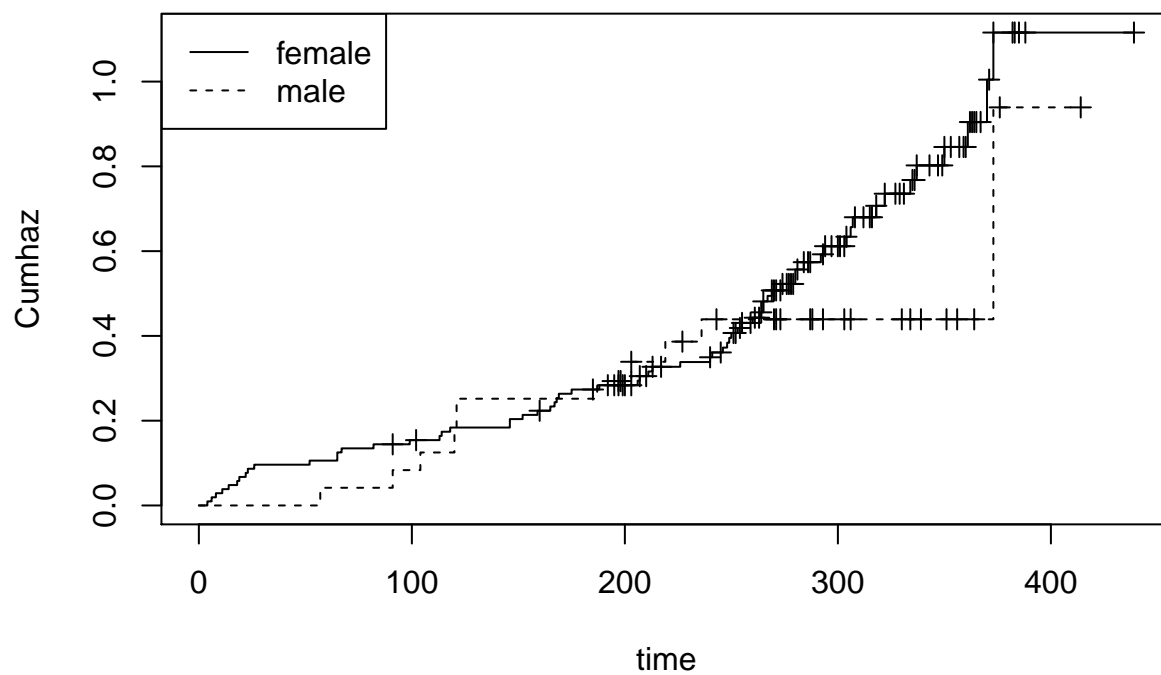


```
temp <- survfit(fit)
time <- temp$time
cumhaz <- temp$cumhaz
stra=temp$strata

par(mfrow=c(2,1),mar=c(4,4,2,2))
```

```r
f=splinefun(time[1:stra[1]],cumhaz[1:stra[1]],method = "monoH.FC")
plot(time[1:stra[1]],cumhaz[1:stra[1]])
curve(f,add = T,col="blue")
curve(f(x,deriv = 1),time[1],time[stra[1]], col="red")
```



```r
f=splinefun(time[(stra[1]+1):sum(stra)],cumhaz[(stra[1]+1):sum(stra)],method = "monoH.FC")
plot(time[(stra[1]+1):sum(stra)],cumhaz[(stra[1]+1):sum(stra)])
time[(stra[1]+1):sum(stra)]
```

```
## [1]  57  91 104 120 121 187 197 198 203 219 227 236 243 270 271 273 287
## [18] 288 293 303 306 330 334 339 351 356 364 373 376 414
```

```r
curve(f(x,deriv = 1),time[stra[1]+1],time[sum(stra)], col="red")
```
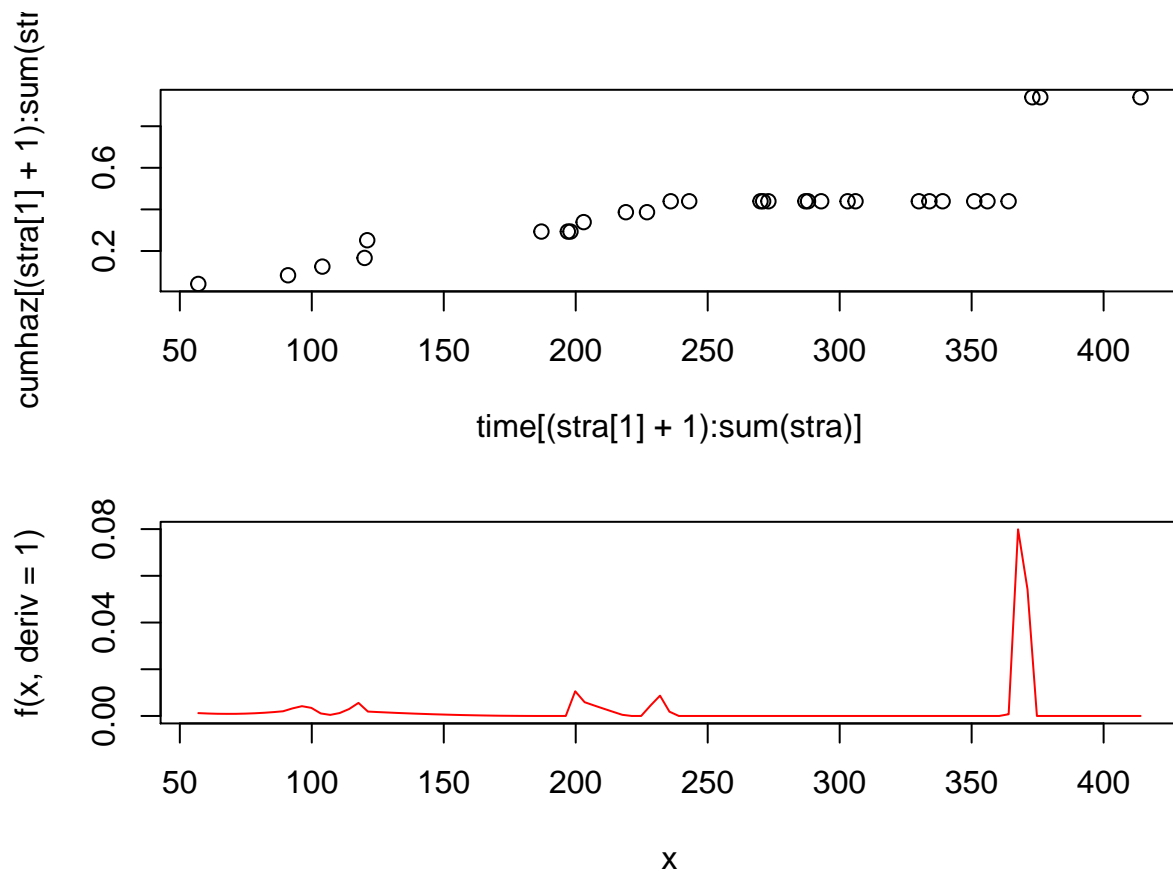
```
# res=data.frame(x=time[(stra[2]+1):sum(stra)],y=c(0,diff(cumhaz[(stra[2]+1):sum(stra)])))
# plot(predict(loess(y~x,res),data.frame(x=seq(time[stra[2]+1]:time[sum(stra)]))),pch=20,col="blue",cex=
# plot(res)
```