# Analyzing Competing Risk Data Using the R timereg Package

## Worked example (Follicular cell lymphoma study)

```
rm(list = ls())
```

```
library(timereg)
```

```
fol <- read.table(
"http://raw.githubusercontent.com/scheike/update-code-for-jss-comp.risk/master/follic.txt",
  sep = ",", header = TRUE)
```

```
head(fol)
```

```
##   age path1 hgb ldh clinstg blktxcat relsite ch rt   survtime stat
## 1  56   NH04 140  NA       2        1       B     Y  0.6981520    1
## 2  36   NH02 130  NA       2        1       D     Y 14.5023956    1
## 3  39   NH02 140  NA       2        3          Y  Y  4.9144422    1
## 4  37   NH03 140  NA       1        1             Y 15.6851472    1
## 5  61   NH04 110  NA       2        2             Y  0.2354552    1
## 6  69   NH02 120  NA       1        1             Y  8.4188912    1
##         dftime dfcens resp stnum
## 1  0.238193018      1   CR     1
## 2 12.418891170      1   CR     2
## 3  0.002737851      1   NR     3
## 4 15.685147159      1   CR     4
## 5  0.002737851      1   NR     5
## 6  8.418891170      1   CR     6
```

```
table(fol$resp,useNA = "always")
```

```
##
##   CR   NR <NA>
##  517   24    0
```

```
table(fol$relsite,useNA = "always")
```

```
##
##         B    D    L <NA>
##  293   18  214   16    0
```

```
table(fol$stat,useNA = "always")
```

```
##
##    0    1 <NA>
##  285  256    0
```

```
evcens <- (fol$resp=="NR" | fol$relsite!="")
                        # no treatment response OR relapse
crcens <- (fol$resp=="CR" & fol$relsite=="" & fol$stat==1)
                        # death AND without relapse AND after Complete treatment response
cause <- ifelse(evcens==1,1,ifelse(crcens==1,2,0))
table(cause)
```

```
## cause
##   0   1   2
## 193 272  76
```

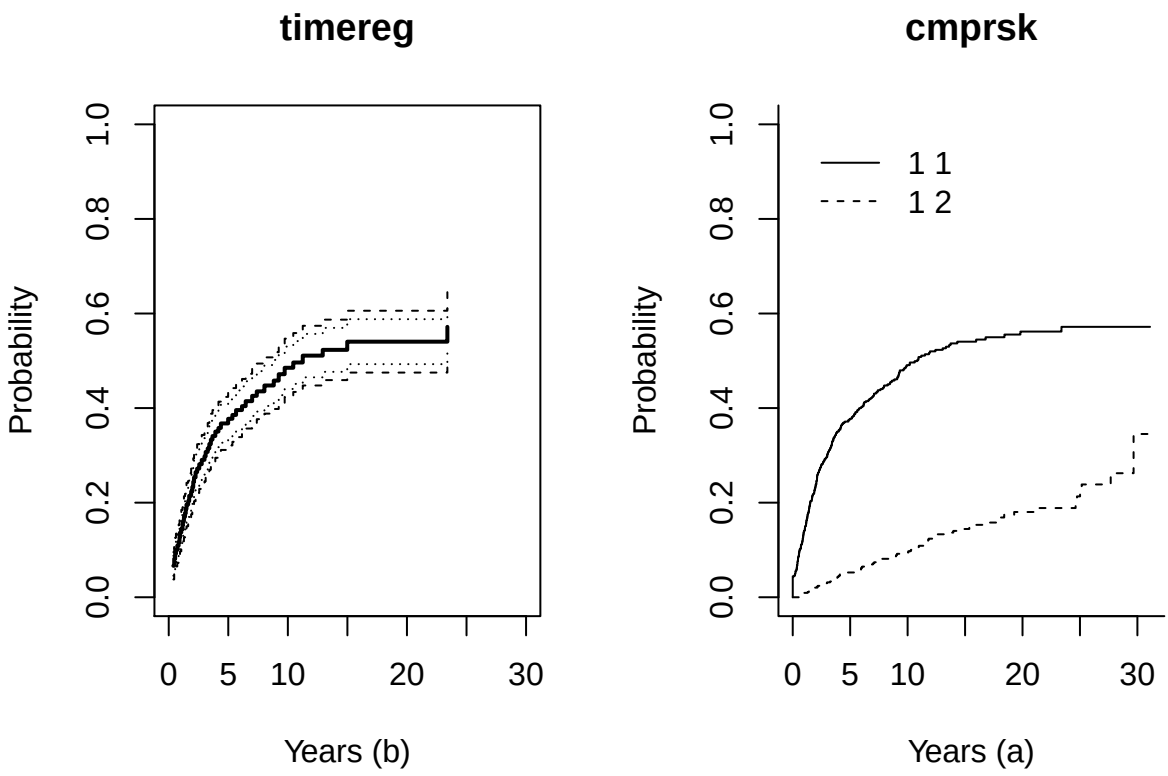
272 no treatment response or relapse 76 competing risk events (death without relapse) 193 censored

```
stage <- as.numeric(fol$clinstg==2)
fol$chemo<-as.numeric(fol$ch=="Y")
times1=sort(unique(fol$dftime[cause==1]))
fol$age <- scale(fol$age)
```

```
library("timereg")
library("cmprsk")
```

```
out1 <-comp.risk(Event(dftime,cause)~ 1,data=fol,cause=1,model="additive")
pout1 <- predict(out1,X=1)
fit<-cuminc(fol$dftime,cause,cencode=0)
```

```
par(mfrow=c(1,2))
plot(pout1,xlim=c(0,30),xlab="Years (b)",main="timereg",uniform=2,se=3)
plot(fit,main="cmprsk",xlab="Years (a)")
```

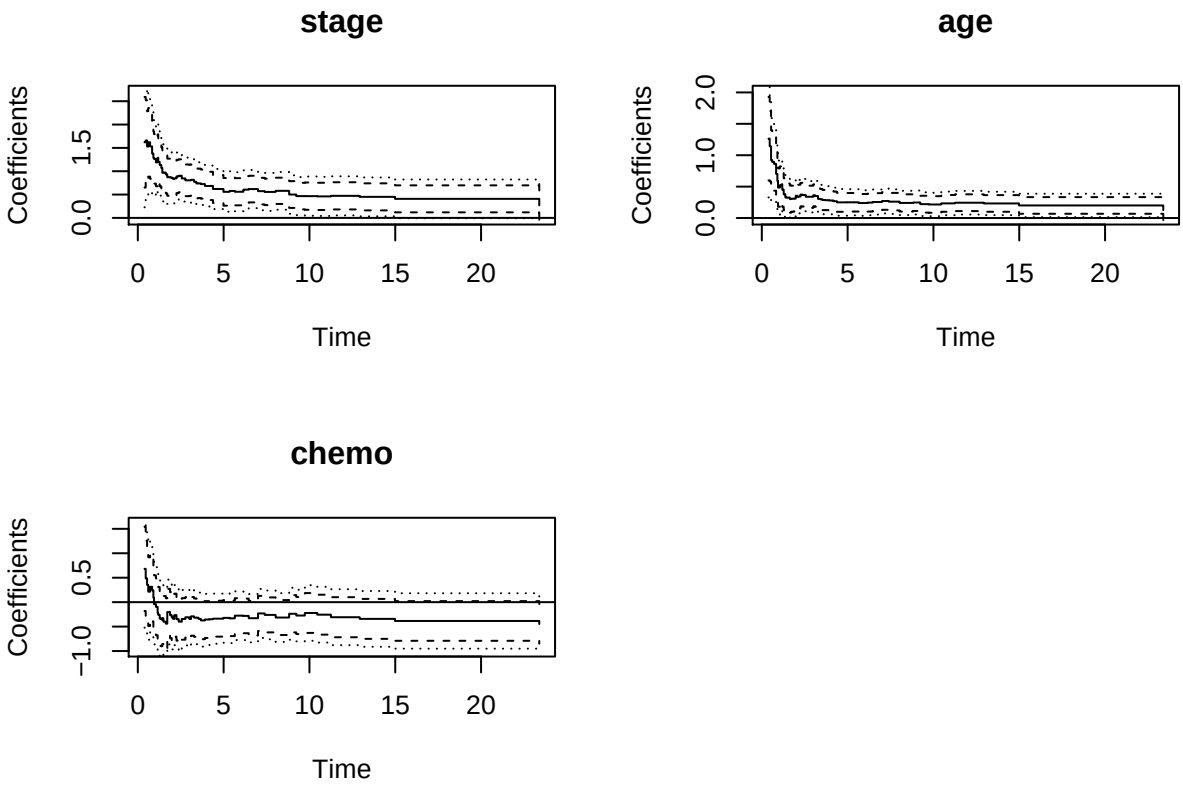



```
## problems with convergence when hgb included
outf<-comp.risk(Event(dftime,cause)~stage+age+chemo,
data=fol,cause=1,n.sim=5000,model="prop",cens.model="cox")
summary(outf)
```

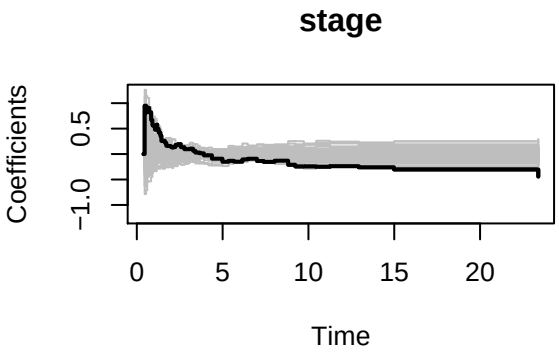
```
## Competing risks Model
##
## Test for nonparametric terms
##
## Test for non-significant effects
##             Supremum-test of significance p-value H_0: B(t)=0
## (Intercept)                         12.10              0.0000
## stage                                5.04              0.0000
## age                                  4.07              0.0008
## chemo                                2.18              0.1830
##
## Test for time invariant effects
##                   Kolmogorov-Smirnov test p-value H_0:constant effect
## (Intercept)                        2.980                       0.0000
## stage                              0.950                       0.0200
## age                                0.853                       0.0016
## chemo                              0.760                       0.0246
##                     Cramer von Mises test p-value H_0:constant effect
## (Intercept)                       13.200                       0.0000
## stage                              2.660                       0.0002
## age                                0.457                       0.0028
```

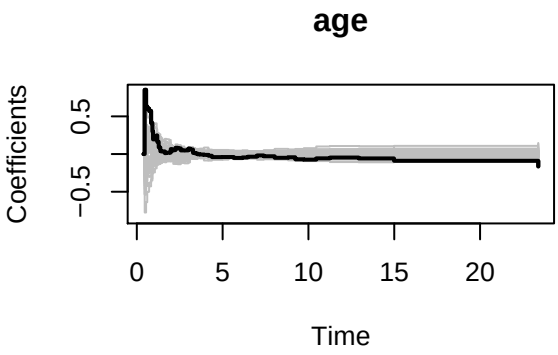
```
## chemo                          0.482                    0.3360
```

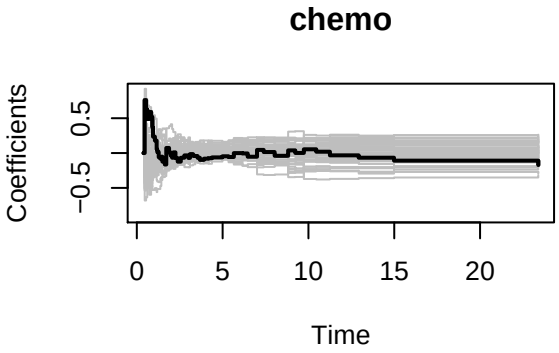
```
par(mfrow=c(2,2))
plot(outf,specific.comps=2:4,pointwise.ci=2,sim.ci=3)
```




```
par(mfrow=c(2,2))
 plot(outf,specific.comps=2:4,score=1)
```




```
outf1<-comp.risk(Event(dftime,cause)~stage+age+const(hgb)+chemo,
data=fol,cause=1,times=times1,model="prop")
summary(outf1)
```

```
## Competing risks Model
##
## No test for non-parametric terms
## Parametric terms :
##                Coef.      SE Robust SE      z P-val lower2.5% upper97.5%
## const(hgb) 0.000387 0.00406   0.00406 0.0953 0.924  -0.00757    0.00834
##
```

```
outfg<-comp.risk(Event(dftime,cause)~const(stage)+const(age)+
const(hgb)+const(chemo),data=fol,cause=1,times=times1,model="prop",cens.model="cox")
summary(outfg)
```

```
## Competing risks Model
##
## No test for non-parametric terms
## Parametric terms :
##                   Coef.      SE Robust SE       z    P-val lower2.5%
## const(stage)  0.678000 0.13900   0.13900  4.8800 1.05e-06   0.40600
## const(age)    0.280000 0.07210   0.07210  3.8900 1.02e-04   0.13900
## const(hgb)    0.000149 0.00413   0.00413  0.0362 9.71e-01  -0.00795
```

```
## const(chemo) -0.302000 0.17600   0.17600 -1.7200 8.59e-02  -0.64700
##               upper97.5%
## const(stage)    0.95000
## const(age)      0.42100
## const(hgb)      0.00824
## const(chemo)    0.04300
##
```

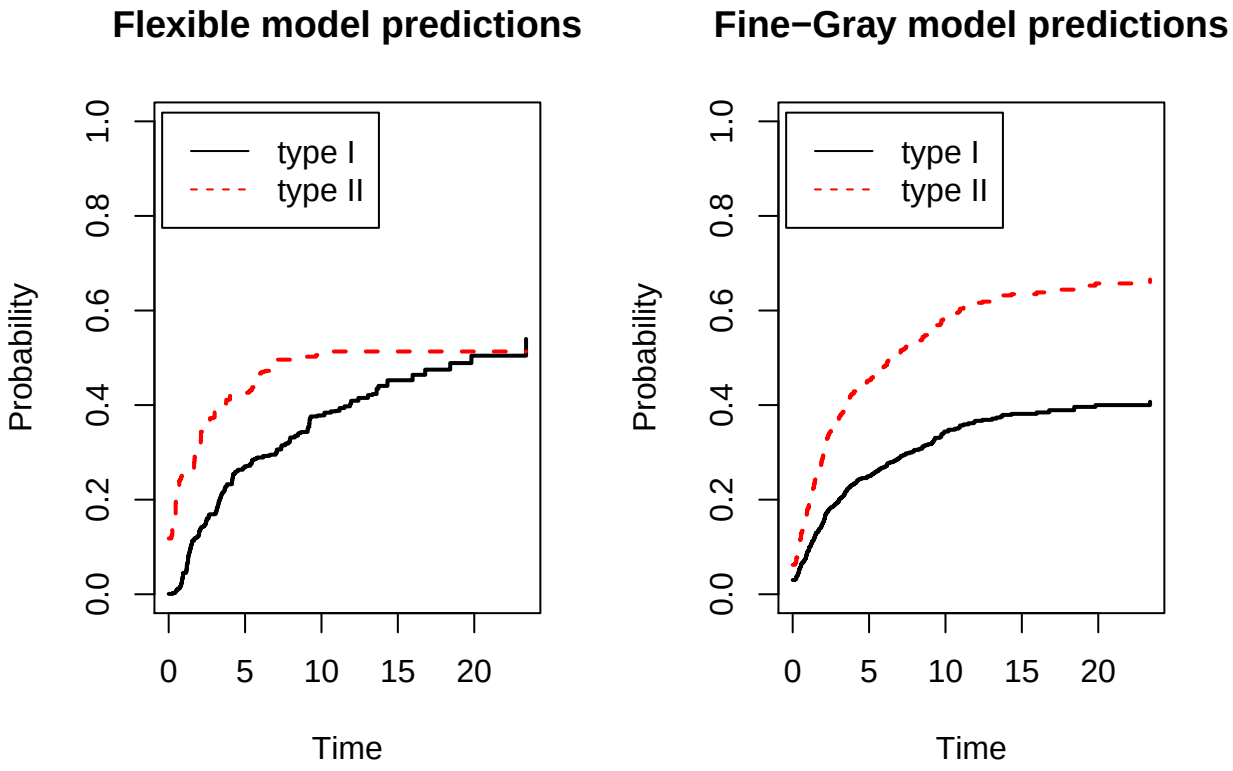
```
## predictions for fg model and outf1
newdata=data.frame(stage=c(0,1),age=c(-1,0.3),hgb=rep(138,2),chemo=c(0,1))
```

```
poutf1<-predict(outf1,newdata)
poutfg<-predict(outfg,newdata)
```

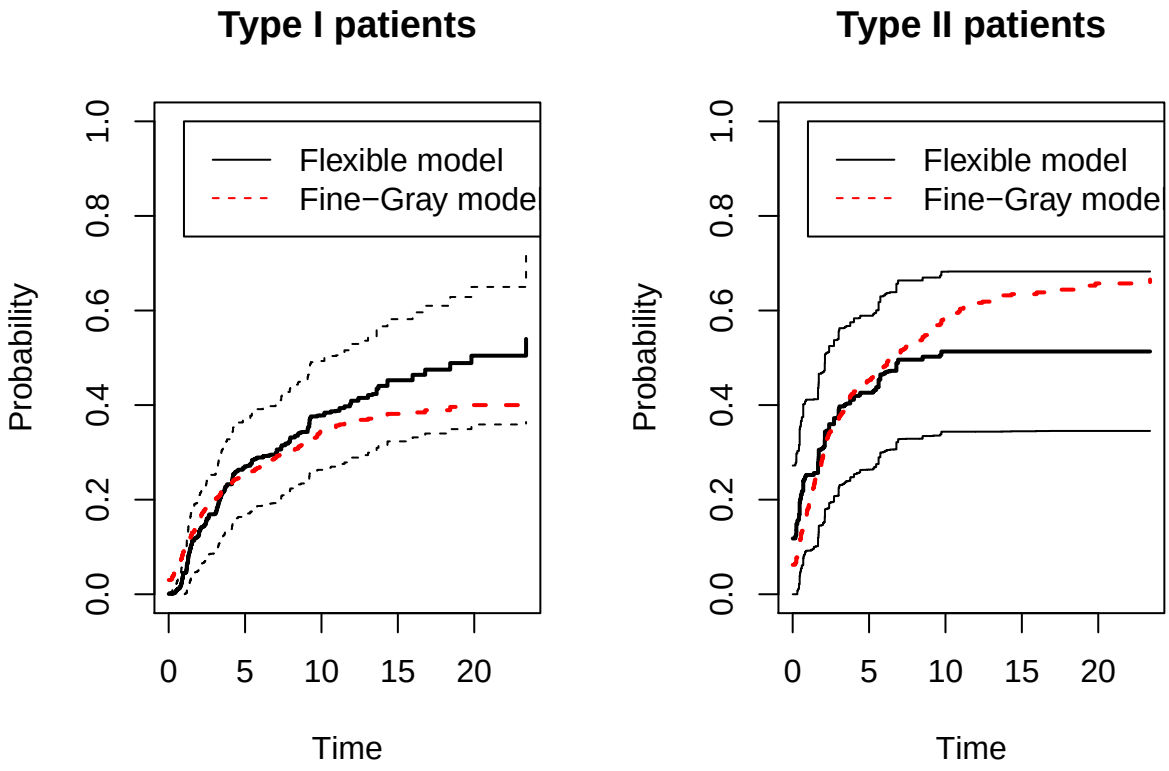
```
newdata
```

```
##   stage  age hgb chemo
## 1     0 -1.0 138     0
## 2     1  0.3 138     1
```

```
par(mfrow=c(1,2))
plot(poutf1,multiple=1,se=0,uniform=0,col=1:2,lty=1:2)
legend("topleft",inset = .02 ,lty = 1:2,col = 1:2,c("type I","type II"))
title(main="Flexible model predictions")

plot(poutfg,multiple=1,se=0,uniform=0,col=1:2,lty=1:2)
legend("topleft",inset = .02,lty = 1:2,col = 1:2,c("type I","type II"))
title(main="Fine-Gray model predictions")
```




```
par(mfrow=c(1,2))
plot(poutf1,se=0,uniform=2,col=1,lty=1,specific.comps=1)
plot(poutfg,new=0,se=0,uniform=0,col=2,lty=2,specific.comps=1)

title(main="Type I patients")
legend(1,1.0,c("Flexible model","Fine-Gray model"),lty=1:2,col=1:2)

plot(poutf1,se=0,uniform=1,col=1,lty=1,specific.comps=2)
plot(poutfg,new=0,se=0,uniform=0,col=2,lty=2,specific.comps=2)
title(main="Type II patients")
legend(1,1.0,c("Flexible model","Fine-Gray model"),lty=1:2,col=1:2)
```


Type I patients
Type II patients
Flexible model
Fine−Gray mode
Probability
Time
0.0
0.2
0.4
0.6
0.8
1.0
0
5
10
15
20