Rotterdam

JACKTANSNAKE

2021-03-05

Contents

Chapter 1

Motivation

1.1 Prepare packages

1.2 Loading data

```
data(rotterdam)
```

Variable name	Description
pid	patient identifier
year	year of cancer incidence
age	age
meno	menopausal status (0= premenopausal, 1= postmenopausal)
size	tumor size, a factor with levels <=20, 20-50, >50
grade	tumor grade
nodes	number of positive lymph nodes
pgr	progesterone receptors (fmol/l)
er	estrogen receptors (fmol/l)
hormon	hormonal treatment (0=no, 1=yes)
chemo	chemotherapy
rtime	days to recurrence or last follow-up
recur	0= no recurrence, 1= recurrence
dtime	days to death or last follow-up
death	0= alive, 1= dead

1.3 Motivation/ Research Question

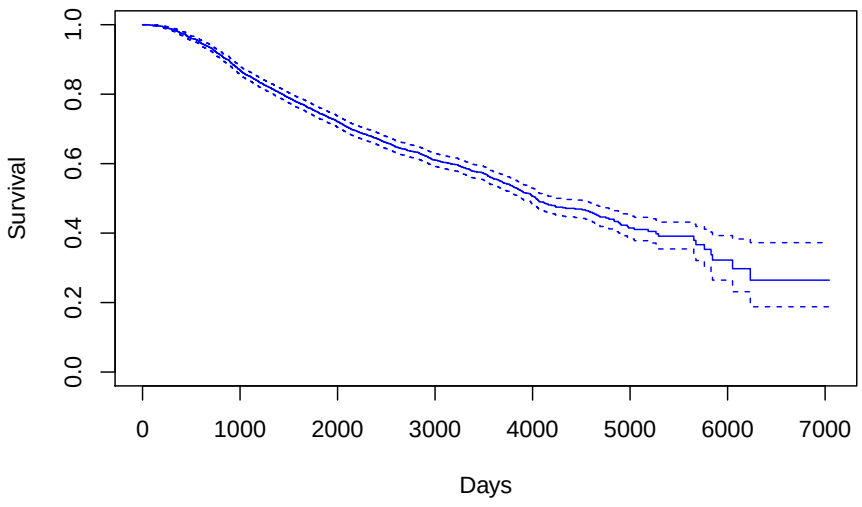
Explore what effects the survival of Breast Cancer patients and what might be a reasonable prediction model for the survival of patients.

1.4 Kaplan-Miere

```
KM_None_Death <- survfit(Surv(dtime, death) ~ 1, data = rotterdam)
KM_None_Death
```

```
## Call: survfit(formula = Surv(dtime, death) ~ 1, data = rotterdam)
##
##       n  events  median 0.95LCL 0.95UCL
##    2982    1272    4033    3888    4309
```

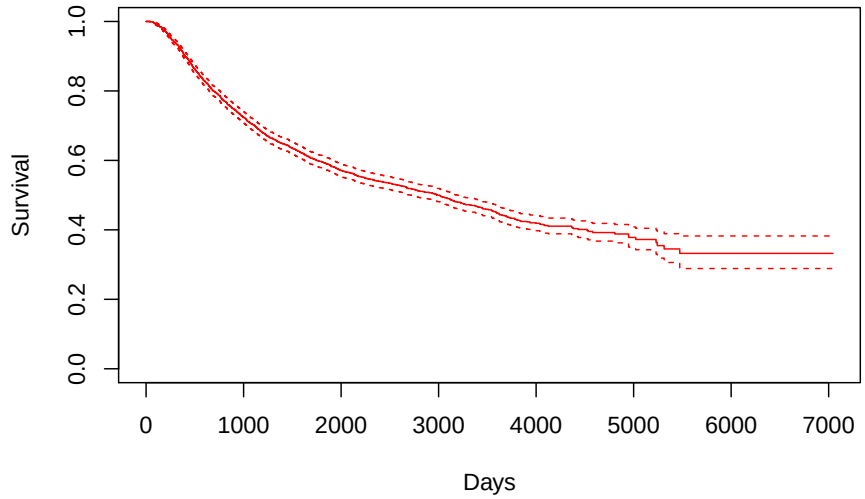
```
plot(KM_None_Death, conf.type = "plain", col = "blue", xlab="Days", ylab="Survival")
```




```
KM_None_Recur <- survfit(Surv(rtime, recur) ~ 1, data = rotterdam)
KM_None_Recur
```

```
## Call: survfit(formula = Surv(rtime, recur) ~ 1, data = rotterdam)
##
##       n  events  median 0.95LCL 0.95UCL
##    2982    1518    2983    2719    3193
```

```
plot(KM_None_Recur, conf.type = "plain", col = "red", xlab="Days", ylab="Survival")
```




```
rotterdam <- rotterdam %>%
  mutate(Treatment = ifelse(chemo == 1 & hormon == 0, "Chemo", ifelse(chemo == 0 & hormon == 1, '
head(rotterdam)
```

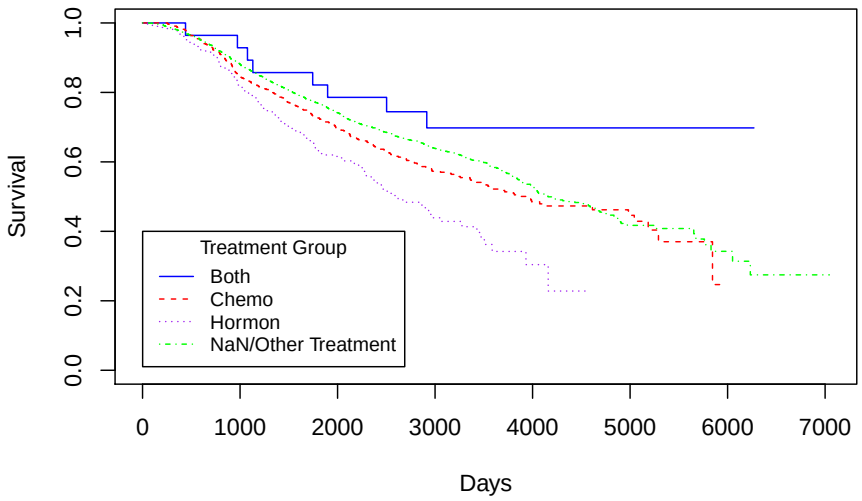
```
##   pid year age meno  size grade nodes pgr  er hormon chemo rtime recur dtime
## 1   1 1992  74    1  <=20     3     0  35 291      0     0  1799     0  1799
## 2   2 1984  79    1 20-50     3     0  36 611      0     0  2828     0  2828
## 3   3 1983  44    0  <=20     2     0 138   0      0     0  6012     0  6012
## 4   4 1985  70    1 20-50     3     0   0  12      0     0  2624     0  2624
## 5   5 1983  75    1  <=20     3     0 260 409      0     0  4915     0  4915
## 6   6 1983  52    0  <=20     3     0 139 303      0     0  5888     0  5888
##   death           Treatment
## 1     0 NaN/Other Treatment
## 2     0 NaN/Other Treatment
## 3     0 NaN/Other Treatment
## 4     0 NaN/Other Treatment
## 5     0 NaN/Other Treatment
```

```
## 6     0 NaN/Other Treatment
```

```
KM_Treatment_Death <- survfit(Surv(dtime, death) ~ Treatment, data = rotterdam)
KM_Treatment_Death
```

```
## Call: survfit(formula = Surv(dtime, death) ~ Treatment, data = rotterdam)
##
##                                   n events median 0.95LCL 0.95UCL
## Treatment=Both                   28      8     NA      NA      NA
## Treatment=Chemo                 552    250   3954    3425    5186
## Treatment=Hormon                311    151   2591    2361    3276
## Treatment=NaN/Other Treatment  2091    863   4159    4015    4654
```

```
plot(KM_Treatment_Death, conf.type = "plain", col = c("blue", "red", "purple", "green")
legend(1, 0.4, legend=c("Both", "Chemo","Hormon", "NaN/Other Treatment"),
       col=c("blue", "red", "purple", "green"), lty=1:4, cex=0.8,
       title="Treatment Group", text.font=6)
```

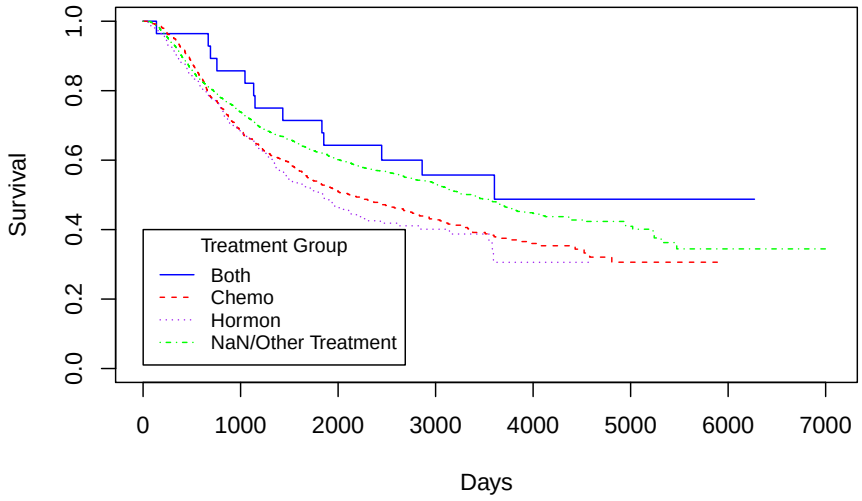



```
KM_Treatment_Recur <- survfit(Surv(rtime, recur) ~ Treatment, data = rotterdam)
KM_Treatment_Recur
```

```
## Call: survfit(formula = Surv(rtime, recur) ~ Treatment, data = rotterdam)
##
```

```
##                                    n events median 0.95LCL 0.95UCL
## Treatment=Both                    28     13   3603    1853      NA
## Treatment=Chemo                  552    324   2141    1749    2672
## Treatment=Hormon                 311    169   1841    1468    2234
## Treatment=NaN/Other Treatment   2091   1012   3376    3087    3649
```

```
plot(KM_Treatment_Recur, conf.type = "plain", col = c("blue", "red", "purple", "green"), xlab="Da
legend(1, 0.4, legend=c("Both", "Chemo","Hormon", "NaN/Other Treatment"),
       col=c("blue", "red", "purple", "green"), lty=1:4, cex=0.8,
       title="Treatment Group", text.font=6)
```



1.5 RSF vs. Cox PH model

hkhkhjg