

Rotterdam

JACKTANSNAKE

2021-03-04

Contents

1	Motivation	3
1.1	Prepare packages	3
1.2	Loading data	3
1.3	Motivation/ Research Question	4
1.4	Kaplan-Miere	4
1.5	RSF vs. Cox PH model	7

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

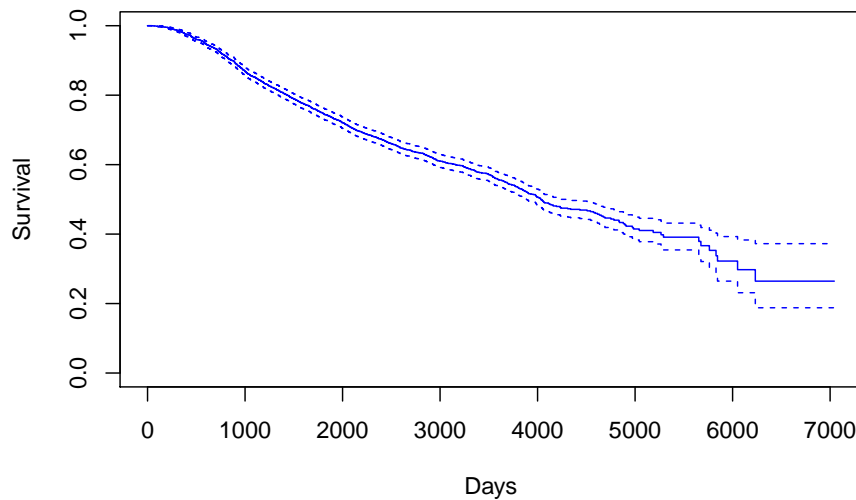
Explore what effects the survival of Breast Cancer patients and what might be a reasonable prediction model for the survival of patients.

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
```

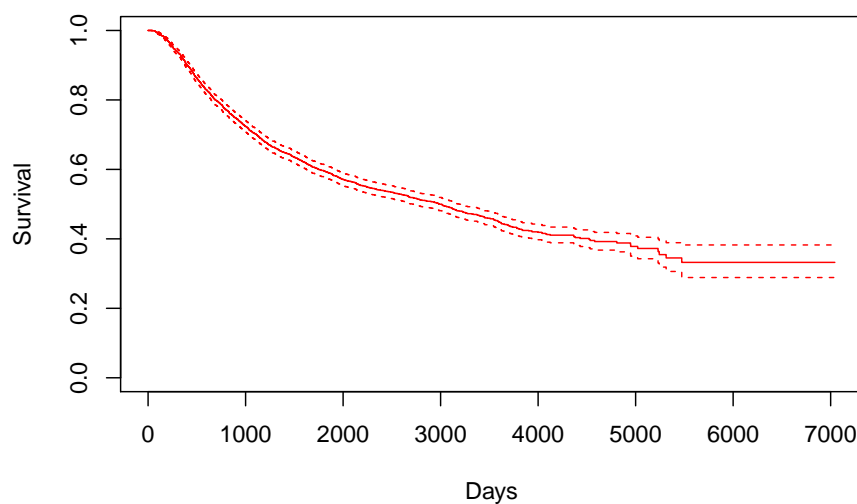
```
## Call: survfit(formula = Surv(rtime, recur) ~ 1, data = rotterdam)
```

```
##
```

```
##      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, "Hormon", "None")),
  head(rotterdam)
```

```
##   pid year age men  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
```

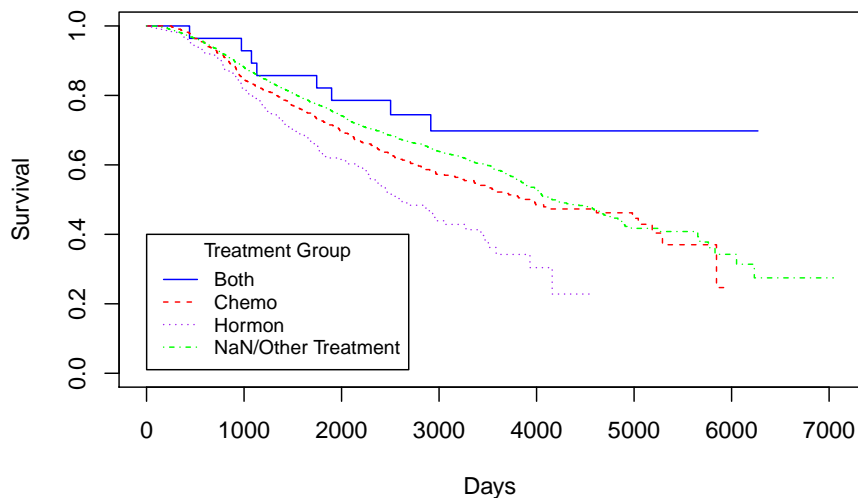
```
KM_Treatment_Death <- survfit(Surv(dtime, death) ~ Treatment, data = rotterdam)
KM_Treatment_Death
```

```
## 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)
```



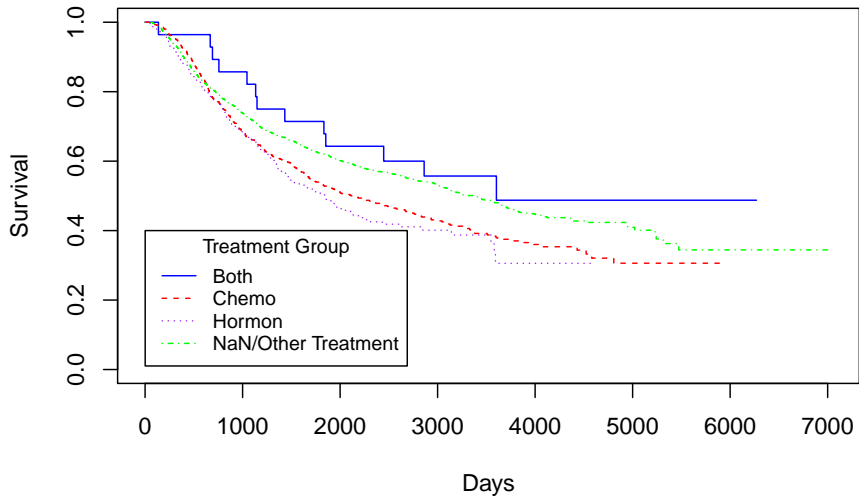
```
KM_Treatment_Recur <- survfit(Surv(rtime, recur) ~ Treatment, data = rotterdam)
KM_Treatment_Recur
```

```
## 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="Days",
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