

Multivariate Analysis for the Behavioral Sciences,
Second Edition (Chapman and Hall/CRC, 2019)

Exercises of Chapter 7: Survival Analysis

Kimmo Vehkalahti and Brian S. Everitt

15 November 2018

Exercises

Exercise 7.2

Use the brcancer data (see below) and modify the R code given in the **Examples of Chapter 7** to analyse and visualize the data as instructed.

```
brcancer <- structure(list(
  time = c(23, 47, 69, 70, 100, 101, 148, 181, 198, 208, 212, 224, 5, 8, 10, 13, 18,
           24, 26, 26, 31, 35, 40, 41, 48, 50, 59, 61, 68, 71, 76, 105, 107, 109,
           113, 116, 118, 143, 145, 162, 188, 212, 217, 225),
  event = c(1, 1, 1, 0, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1,
            1, 1, 1, 1, 1, 1, 1, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 0, 0),
  metastized = structure(c(1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 2L,
                           2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L,
                           2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L,
                           2L, 2L, 2L, 2L, 2L),
                        .Label = c("No", "Yes"), class = "factor")),
  .Names = c("time", "event", "metastized"),
  row.names = c(NA, -44L), class = "data.frame")

str(brcancer)
```

```
## 'data.frame':   44 obs. of  3 variables:
## $ time      : num  23 47 69 70 100 101 148 181 198 208 ...
## $ event      : num  1 1 1 0 0 0 1 1 0 0 ...
## $ metastized: Factor w/ 2 levels "No","Yes": 1 1 1 1 1 1 1 1 1 1 ...
```

```
head(brcancer)
```

```
##   time event metastized
## 1   23     1          No
## 2   47     1          No
## 3   69     1          No
## 4   70     0          No
## 5  100     0          No
## 6  101     0          No
```

Exercise 7.3

Use the glioma data (see below) and modify the R code given in the **Examples of Chapter 7** to analyse the data as instructed.

```
glioma <- structure(list(
  no. = c(1L, 2L, 3L, 4L, 5L, 6L, 7L, 8L, 9L, 10L, 11L, 12L, 13L, 14L, 15L, 16L,
    17L, 18L, 19L, 1L, 2L, 3L, 4L, 5L, 6L, 7L, 8L, 9L, 10L, 11L, 12L, 13L,
    14L, 15L, 16L, 17L, 18L),
  age = c(41L, 45L, 48L, 54L, 40L, 31L, 53L, 49L, 36L, 52L, 57L, 55L, 70L, 39L,
    40L, 47L, 58L, 40L, 36L, 27L, 32L, 53L, 46L, 33L, 19L, 32L, 70L, 72L,
    46L, 44L, 83L, 57L, 71L, 61L, 65L, 50L, 42L),
  sex = structure(c(1L, 1L, 2L, 2L, 1L, 2L, 2L, 2L, 2L, 2L, 2L, 1L, 2L, 1L, 1L,
    1L, 2L, 1L, 2L, 2L, 2L, 1L, 2L, 1L, 1L, 1L, 2L, 2L, 2L, 2L,
    1L, 1L, 1L, 2L, 2L, 1L),
    .Label = c("Female", "Male"), class = "factor"),
  histology = structure(c(2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 1L, 1L,
    1L, 1L, 1L, 1L, 1L, 1L, 2L, 2L, 2L, 2L, 2L, 2L, 1L,
    1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L),
    .Label = c("GBM", "Grade3"), class = "factor"),
  group = structure(c(2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L, 2L,
    2L, 2L, 2L, 2L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L, 1L,
    1L, 1L, 1L, 1L, 1L, 1L, 1L),
    .Label = c("Control", "RIT"), class = "factor"),
  event = c(TRUE, FALSE, FALSE, FALSE, FALSE, FALSE, TRUE, FALSE, FALSE, FALSE, FALSE,
    FALSE, FALSE, TRUE, TRUE, FALSE, FALSE, TRUE, TRUE, TRUE, TRUE, TRUE,
    TRUE, TRUE, FALSE, FALSE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE, TRUE,
    TRUE, TRUE, TRUE, TRUE, TRUE),
  time = c(53L, 28L, 69L, 58L, 54L, 25L, 51L, 61L, 57L, 57L, 50L, 43L, 20L, 14L,
    36L, 59L, 31L, 14L, 36L, 34L, 32L, 9L, 19L, 50L, 48L, 8L, 8L, 11L, 12L,
    15L, 5L, 8L, 8L, 6L, 14L, 13L, 25L)),

  .Names = c("no.", "age", "sex", "histology", "group", "event", "time"),
  row.names = c("1", "2", "3", "4", "5", "6", "7", "8", "9", "10", "11", "12",
    "13", "14", "15", "16", "17", "18", "19", "20", "21", "22", "23",
    "24", "25", "26", "27", "28", "29", "30", "31", "32", "33", "34",
    "35", "36", "37"), class = "data.frame")

str(glioma)

## 'data.frame':   37 obs. of  7 variables:
## $ no.          : int  1 2 3 4 5 6 7 8 9 10 ...
## $ age          : int  41 45 48 54 40 31 53 49 36 52 ...
## $ sex          : Factor w/ 2 levels "Female","Male": 1 1 2 2 1 2 2 2 2 2 ...
## $ histology: Factor w/ 2 levels "GBM","Grade3": 2 2 2 2 2 2 2 2 2 2 ...
## $ group        : Factor w/ 2 levels "Control","RIT": 2 2 2 2 2 2 2 2 2 2 ...
## $ event        : logi  TRUE FALSE FALSE FALSE FALSE TRUE ...
## $ time         : int  53 28 69 58 54 25 51 61 57 57 ...
```

Exercise 7.4

Source of the data: Palotie, U., Eronen, A. K., Vehkalahti, K. and Vehkalahti, M. M. (2017). Longevity of 2- and 3-surface restorations in posterior teeth of 25- to 30-year-olds attending Public Dental Service—A 13-year observation. *Journal of Dentistry*, 62, 13–17. <https://doi.org/10.1016/j.jdent.2017.05.012>

(Acknowledgements, p.17: “The authors acknowledge the Helsinki City Public Dental Service for handing their data at disposal. *Tuomo Maisala* is thanked for picking out the cases and *Marjut Grainger* for invaluable help with data cleaning.”)

```
teeth <- read.csv(file = "data/teeth.csv", row.names = 1)
head(teeth)
```

##	ID	Gender	Age	ISOcode	Reint	Survyear	Type4	Material	Type2
## 1	1	1	30	24	0	2.510	1	2	1
## 2	2	1	30	26	0	2.510	3	2	2
## 3	3	1	30	16	1	0.301	3	2	2
## 4	4	2	30	14	1	0.545	1	2	1
## 5	5	2	30	15	1	9.033	1	2	1
## 6	6	1	28	15	1	12.526	1	2	1

```
tail(teeth)
```

##	ID	Gender	Age	ISOcode	Reint	Survyear	Type4	Material	Type2
## 5537	5537	2	25	14	1	0.348	1	2	1
## 5538	5538	2	25	36	0	0.504	4	2	2
## 5539	5539	2	25	37	0	0.504	4	2	2
## 5540	5540	1	25	27	1	9.732	3	2	2
## 5541	5541	1	25	46	1	9.438	4	2	2
## 5542	5542	2	25	36	0	9.068	4	2	2

```
# Set maximum longevity to 13 years and censor all at the end of the last year:
```

```
teeth$Survyear[teeth$Survyear > 13] <- 13
teeth$Reint[teeth$Survyear == 13] <- 0
```

- ID: Tooth ID
- Gender: 1=Male, 2=Female
- Age: Patient age in years (2002)
- ISOcode: Tooth code (ISO)
- Reint: Re-intervention: 0=No, 1=Yes
- Survyear: Longevity of restoration in years
- Type4: 1=Upper premolar, 2=Lower premolar, 3=Upper molar, 4=Lower molar
- Material: 1=Amalgam, 2=Composite
- Type2: 1=Premolar, 2=Molar