MSMS 308 : Practical 01

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Question

Consider the following survival data of 40 patients with myeloma. Compute and plot the estimated survival function, the probability density function, and the hazard function.

Survival Time t (months)	Number of Patients Surviving at Beginning of the Interval	Number of Patients Dying in the Interval
$0-5$	40	5
$5-10$	35	7
$10-15$	28	6
$15-20$	22	4
$20-25$	18	5
$25-30$	13	4
$30-35$	9	4
$35-40$	5	0
$40-45$	5	2
$45-50$	3	1
≥ 50	2	2

R Program, Plot and Interpretation

$$\widehat{S(t)} = \frac{\text{number of patients surviving longer than } t}{\text{total number of patients}}$$

$$\widehat{f(t)} = \frac{\text{number of patients dying in the interval beginning at time } t}{(\text{total number of patients }) \times (\text{ interval width})}$$

$$\widehat{h(t)} = \frac{\text{number of patients dying per unit time in the interval}}{(\text{number of patients surviving at } t) - (\text{ number of deaths in the interval})/2}$$

```r
survival_data <- read.csv('https://raw.githubusercontent.com/sakunisgithub/data_sets/refs/heads/master/msc_semester_3/life_time_prac_1.csv',
                          stringsAsFactors = TRUE)
```

```r
total_number_of_patients <- survival_data$no_at_risk[1]
```

```r
S_t_hat <- survival_data$no_at_risk / total_number_of_patients
```

```r
interval_width <- 5

f_t_hat <- survival_data$no_of_death / (total_number_of_patients * interval_width)

f_t_hat[length(f_t_hat)] = NA
```

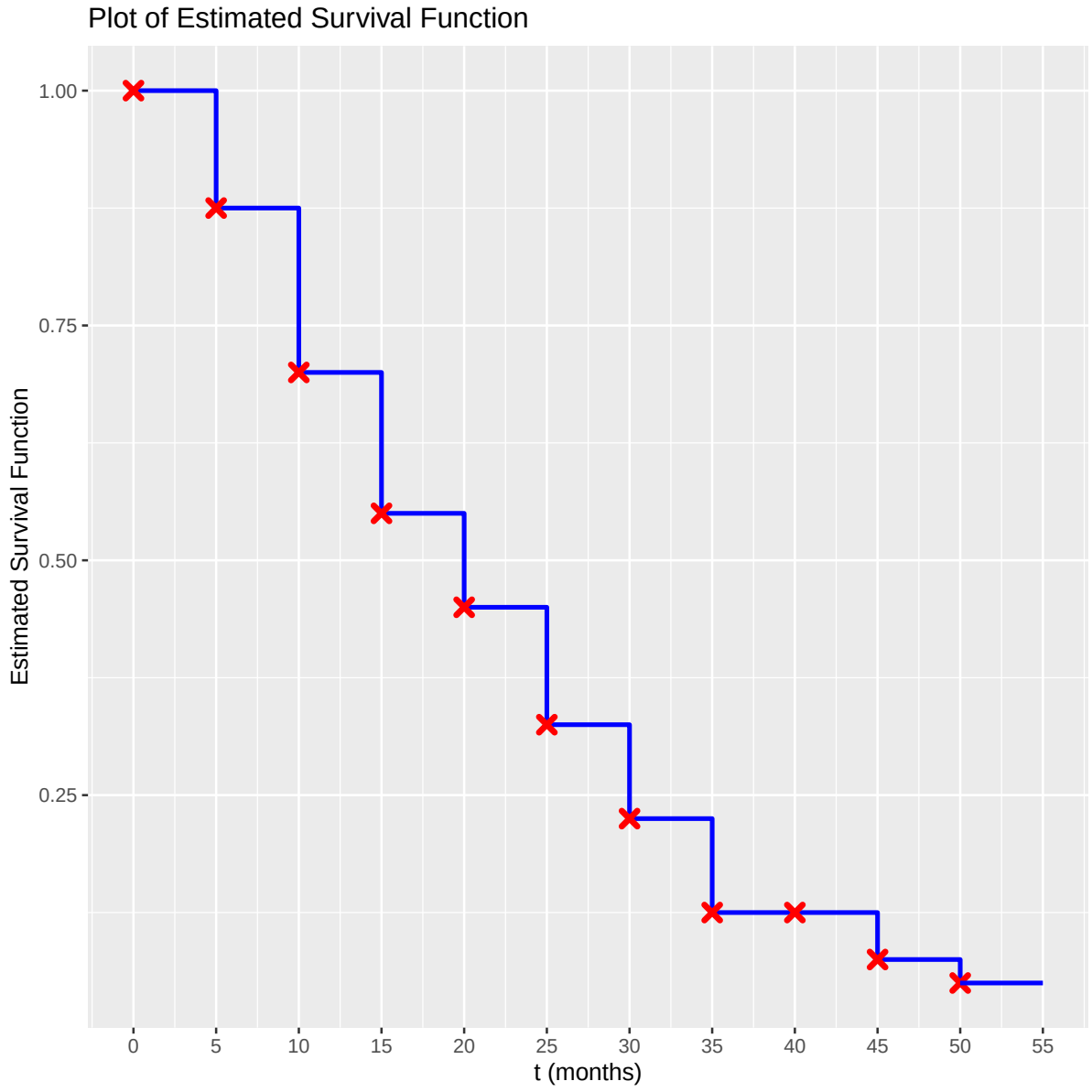
```r
# a = number_of_patients_dying_per_unit_time_in_the_interval

a <- survival_data$no_of_death / interval_width

h_t_hat <- a / (survival_data$no_at_risk - survival_data$no_of_death / 2)

h_t_hat[length(h_t_hat)] = NA
```

```r
analysis_table <- data.frame(survival_data,
                             t = (0:10)*5,
                             S_t_hat = round(S_t_hat, digits = 3),
                             f_t_hat = round(f_t_hat, digits = 3),
                             h_t_hat = round(h_t_hat, digits = 3))
```

```r
analysis_table
```

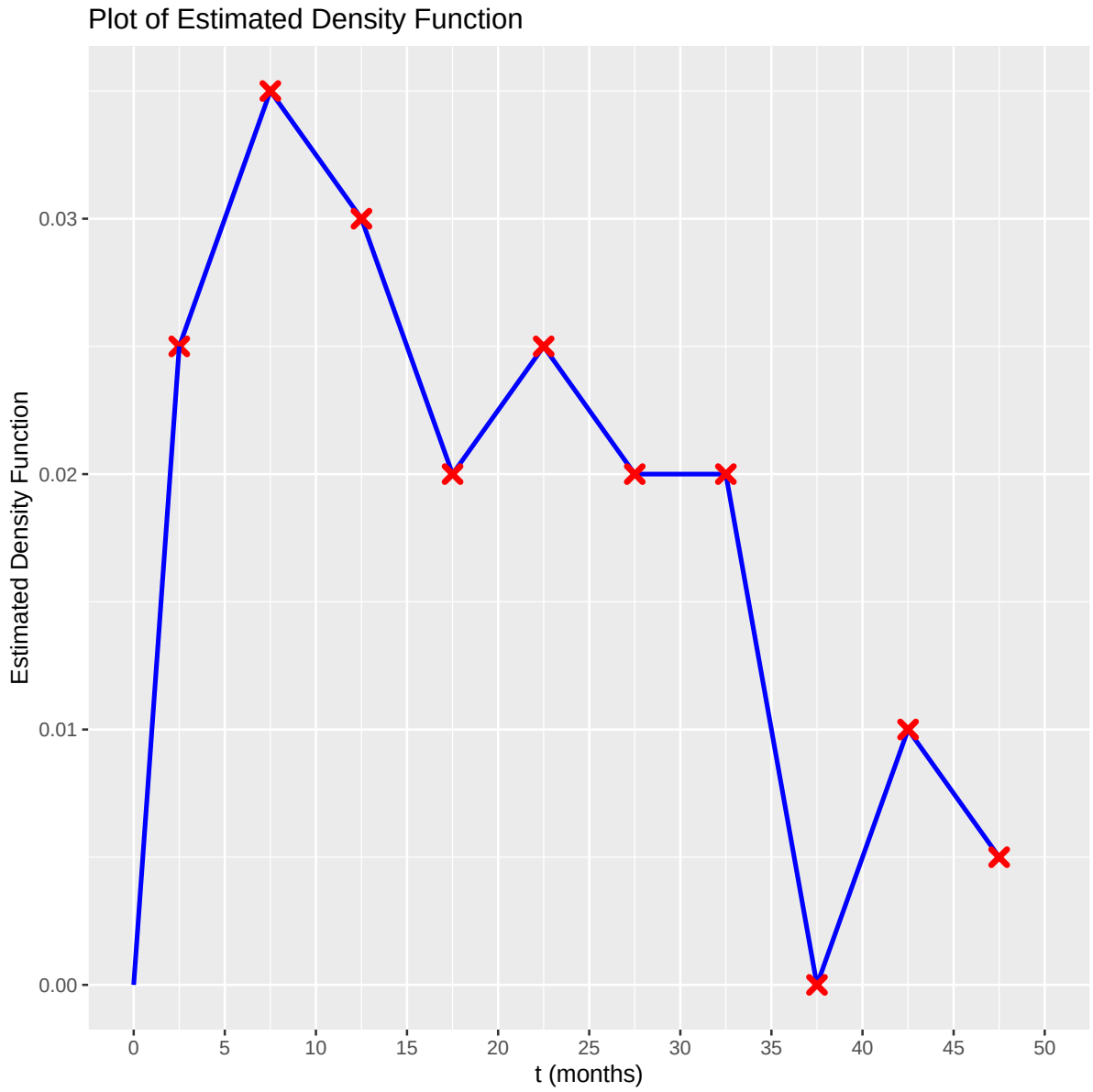
```
##    survival_time no_at_risk no_of_death  t S_t_hat f_t_hat h_t_hat
## 1            0--5         40           5  0   1.000   0.025   0.027
## 2           5--10         35           7  5   0.875   0.035   0.044
## 3          10--15         28           6 10   0.700   0.030   0.048
## 4          15--20         22           4 15   0.550   0.020   0.040
## 5          20--25         18           5 20   0.450   0.025   0.065
## 6          25--30         13           4 25   0.325   0.020   0.073
## 7          30--35          9           4 30   0.225   0.020   0.114
## 8          35--40          5           0 35   0.125   0.000   0.000
## 9          40--45          5           2 40   0.125   0.010   0.100
## 10         45--50          3           1 45   0.075   0.005   0.080
## 11           >=50          2           2 50   0.050      NA      NA
```

```r
t_last <- max(analysis_table$t)

S_t_hat_last <- analysis_table %>% filter(t == t_last) %>% pull(S_t_hat)

analysis_table %>%
  ggplot(aes(x = t, y = S_t_hat)) +
  geom_step(direction = "hv", linewidth = 1, color = "blue") +
  geom_point(size = 2, color = "red", shape = 4, stroke = 2) +
  annotate("segment", x = t_last, xend = t_last + 5,
           y = S_t_hat_last, yend = S_t_hat_last, color = "blue", linewidth = 1) +
  scale_x_continuous(limits = c(0, 55), breaks = seq(0, 55, 5)) +
  labs(x = "t (months)",
       y = "Estimated Survival Function",
       title = "Plot of Estimated Survival Function")
```



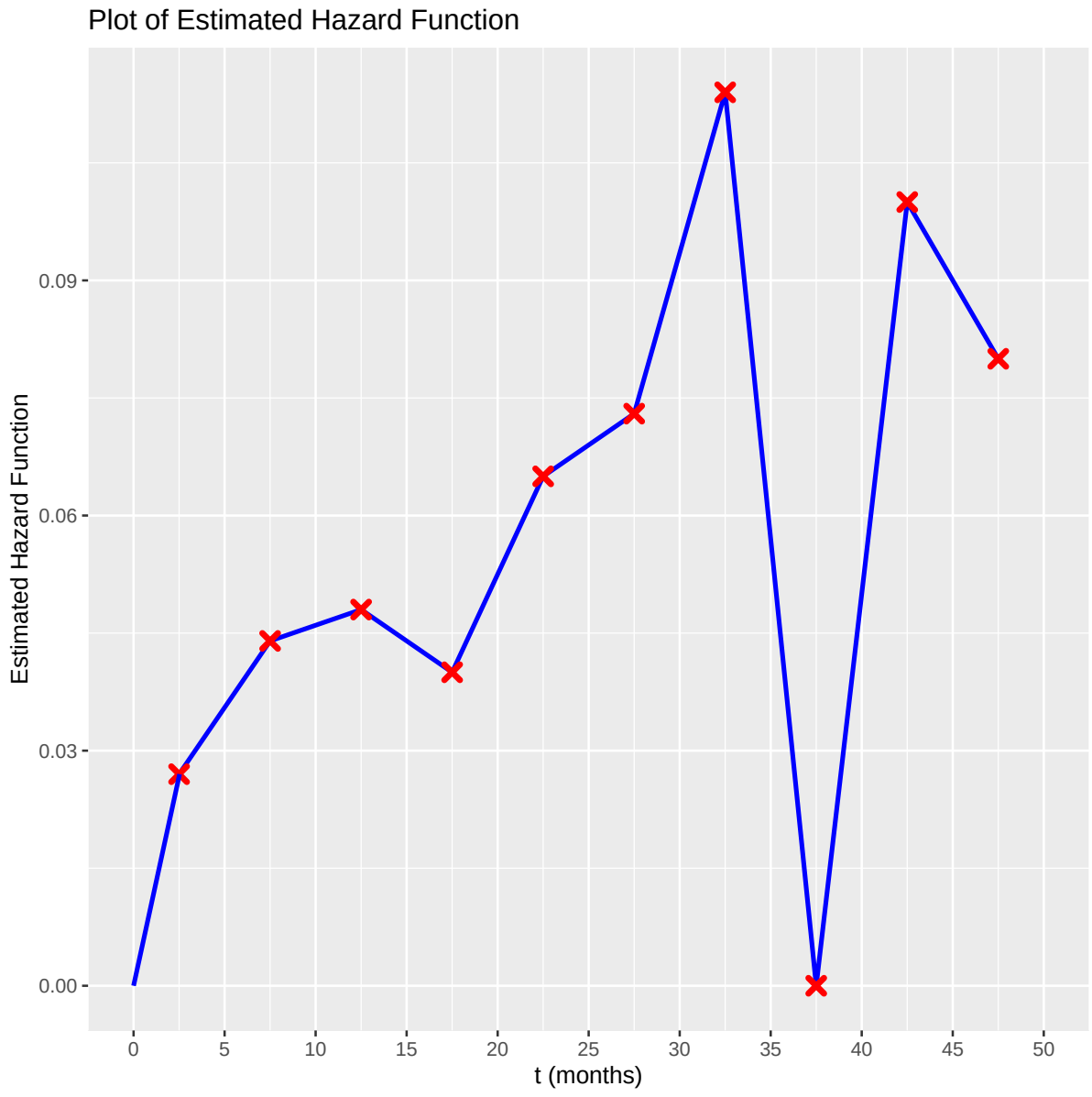
✎ The median survival time for myeloma patients is approximately 17.5 months.

```r
t_first <- min(analysis_table$t)

f_t_hat_first <- analysis_table %>% filter(t == t_first) %>% pull(f_t_hat)

analysis_table[-dim(analysis_table)[1],] %>%
  ggplot(aes(x = t+2.5, y = f_t_hat)) +
  geom_line(linewidth = 1, col = "blue") +
  geom_point(size = 2, col = "red", shape = 4, stroke = 2) +
  annotate("segment", x = t_first, xend = t_first + 2.5,
           y = 0, yend = f_t_hat_first, color = "blue", linewidth = 1) +
  scale_x_continuous(limits = c(0, 50), breaks = seq(0, 50, 5)) +
  labs(x = "t (months)",
       y = "Estimated Density Function",
       title = "Plot of Estimated Density Function")
```



✎ Death due to myeloma is most likely occur in 5 to 10 months.

```r
h_t_hat_first = analysis_table %>% filter(t == t_first) %>% pull(h_t_hat)

analysis_table[-dim(analysis_table)[1],] %>%
  ggplot(aes(x = t+2.5, y = h_t_hat)) +
  geom_line(linewidth = 1, col = "blue") +
  geom_point(size = 2, col = "red", shape = 4, stroke = 2) +
  annotate("segment", x = 0, xend = h_t_hat_first + 2.5,
           y = 0, yend = h_t_hat_first, color = "blue", linewidth = 1) +
  scale_x_continuous(limits = c(0, 50), breaks = seq(0, 50, 5)) +
  labs(x = "t (months)",
       y = "Estimated Hazard Function",
       title = "Plot of Estimated Hazard Function")
```



✎ The hazard function shows an increasing trend and reaches its peak in 30 to 35 months, so risk of death increases over time.