

Assignment 4

Survival Analysis



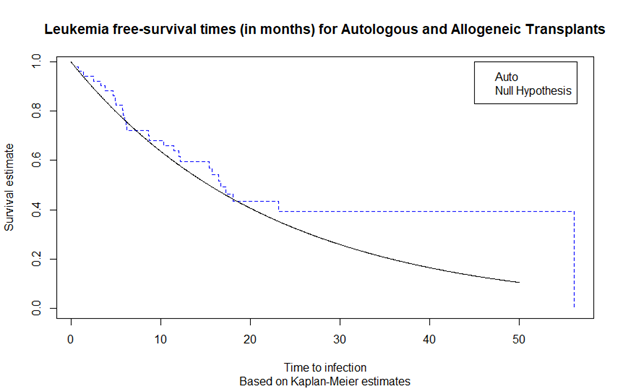
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Question 1

a)



We can see that the null hypothesis line, lies mostly beneath that of the survival estimates. This tells us that it is quite likely that for scenario a), with , that we will accept the null hypothesis.

p-value = 3.8438e-05

b)

This null hypothesis seems less likely from the graph in a), as the estimates seem to be constantly above the null hypothesis line. We will expect a large p-value for this hypothesis.

p-value = 0.9999616

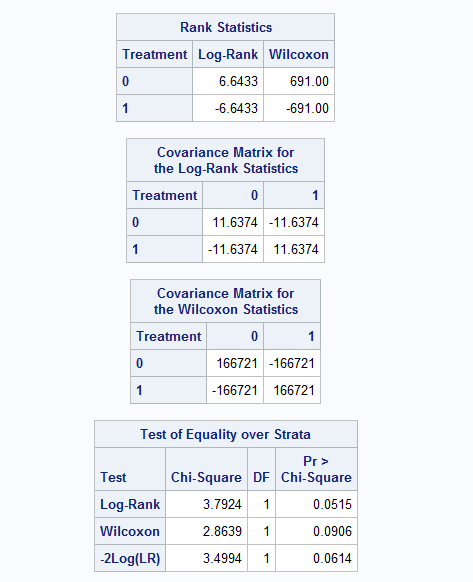
c)

We look at the p-value for guidance on this one, and we see we also have a very small p-value

p-value = 7.687599e-05

We can then deduce that we do not have enough evidence to reject the null hypothesis

Question 2



We would like to test the hypothesis of no difference in the rate of staphylococcus infection between patients whose burns were cared for with a routine bathing care method versus those whose body cleansing was initially performed using 4% chlorhexidine gluconate. We set up the hypothesis as follows:

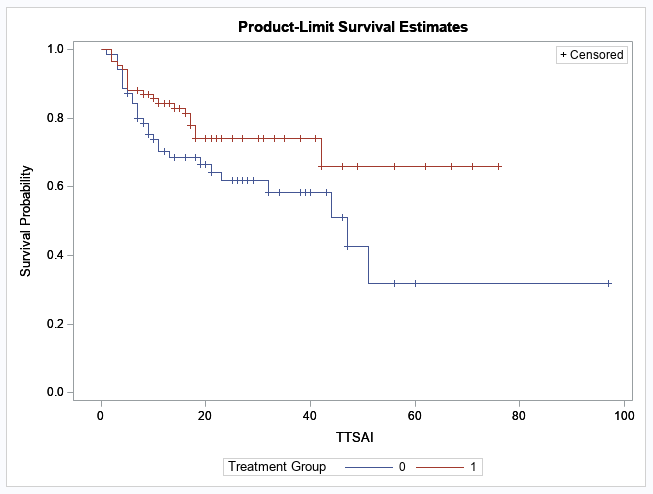
With h1(t) and h2(t) defined as follows

h1(t) : hazard rate of 4% chlorhexidine gluconate cleansing method

h2(t): hazard rate of routine bathing method

So from the above table we can discern a log-rank Chi-square statistic of 3.7924 with a p-value of 0.0515 which is greater than 0.05. This implies we will not reject H0 at 5% significance level and conclude that there is no significant difference between the hazard rates.

For the Gehan-Wilcoxon test, the test statistic is 2.8639 and we have a p-value of 0.0906 and we conclude the same as for the log-rank test. We do not reject H0 and conclude that there is no significant difference between the hazard rates.



Question 3

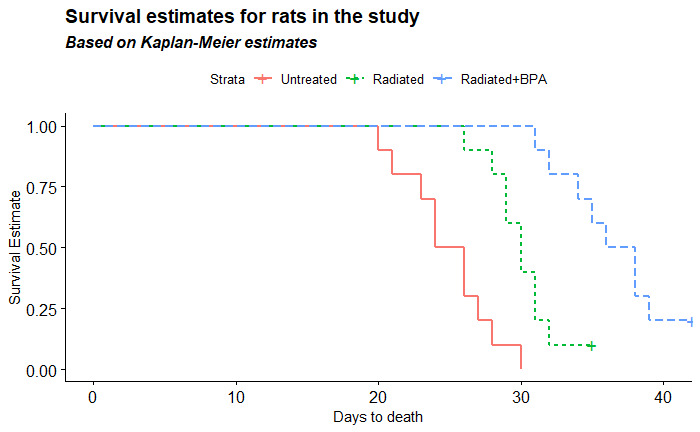
With h1(t), h2(t) and h3(t) defined as follows

h1(t) : hazard rate of untreated rats

h2(t): hazard rate of radiated rats

h3(t) : hazard rate of radiated+bpa treated rats

a)



We can see that the untreated rats clearly have a lower survival rate, with their drop beginning at around 20 days, whereas the radiated rats seem to survive slightly longer, only beginning with a drop in survival around 30 days, whereas the radiated+bpa treated rats seem to be fairing best. From this plot, it would appear that the overall best treatment would be the radiated+bpa treatment, but further investigation and study is needed to confirm.

b)

For the pair-wise test, we split the data into groups of two, comparing the Untreated against the Radiated rats, we have the following:

Log rank ꭕ2 = 11.412, p-value = 0.0007

We therefore reject the null hypothesis and conclude that there is indeed a difference in the hazard rate between the untreated and radiated rats.

For the second pair-wise test, we again split the data into groups of two, comparing the Untreated against the Radiated+BPA rats, we have the following:

Log rank ꭕ2 = 21.671, p-value = 0.0001

We therefore reject the null hypothesis and conclude that there is indeed a difference in the hazard rate between the untreated and radiated rats.

Again, we split the data into groups of two, comparing the Radiated rats against the Radiated+BPA rats, we have the following:

Log rank ꭕ2 = 10.148, p-value = 0.0014

We therefore reject the null hypothesis and conclude that there is indeed a difference in the hazard rate between the untreated and radiated rats.

Appendix A

data <- read.table('Section1\_9.dat',col.names = c('Surv\_Time','Treatment','Censored'),colClasses = c('numeric', 'numeric', 'numeric'))

surv\_obj <- survfit(Surv(time = data$Surv\_Time,

event = data$Censored)~data$Treatment,

subset = data$Treatment==2,

type="kaplan-meier")

surv\_summary <- summary(surv\_obj)

surv.estimates <- surv\_obj$surv

surv.times <- surv\_obj$time

x <- seq(0, 50, length.out=1000)

y <- exp(-0.045\*x)

plot(x=surv.times, y=surv.estimates, type='s', xlab="Time to infection", ylab="Survival estimate",

main = "Leukemia free-survival times (in months) for Autologous and Allogeneic Transplants",

sub = "Based on Kaplan-Meier estimates", col = "blue", lty=2)

lines(x = x,y, lwd=1.5, lty=1)

legend(45,1,legend = c("Auto","Null Hypothesis"))

stat <- (sum(surv\_summary$n.event) - sum(0.045\*surv\_summary$time))^2/sum(0.045\*surv\_summary$time)

norm.stat <- sqrt(stat)

1-pnorm(q = norm.stat, mean = 0, sd = 1)

pnorm(q = norm.stat, mean = 0, sd = 1)

pchisq(stat, df = 1, lower.tail = FALSE)

kmp <-survfit(Surv(rat\_data$death\_times,rat\_data$censored)~rat\_data$treatment,type="kaplan-meier")

ggsurv\_rats <- ggsurvplot(kmp, data = rat\_data, xlab="Days to death",

ylab="Survival Estimate",

legend.labs = c("Untreated", "Radiated", "Radiated+BPA"),

linetype = 'strata') +

labs(title = "Survival estimates for rats in the study",

subtitle = "Based on Nelson-Aalen estimates")

ggsurv\_rats <- ggpar(ggsurv\_rats,

font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv\_rats)

rats\_1\_2 <- rat\_data[rat\_data$treatment == 1 | rat\_data$treatment == 2,]

rats\_1\_3 <- rat\_data[rat\_data$treatment == 1 | rat\_data$treatment == 3,]

rats\_2\_3 <- rat\_data[rat\_data$treatment == 2 | rat\_data$treatment == 3,]

rats\_surv\_1\_2 <- survdiff(Surv(time = rats\_1\_2$death\_times,

event = rats\_1\_2$censored)~rats\_1\_2$treatment)

rats\_surv\_1\_2$chisq

pchisq(rats\_surv\_1\_2$chisq,1,lower.tail = FALSE)

rats\_surv\_1\_3 <- survdiff(Surv(time = rats\_1\_3$death\_times,

event = rats\_1\_3$censored)~rats\_1\_3$treatment)

rats\_surv\_1\_3$chisq

pchisq(rats\_surv\_1\_3$chisq,1,lower.tail = FALSE)

rats\_surv\_2\_3 <- survdiff(Surv(time = rats\_2\_3$death\_times,

event = rats\_2\_3$censored)~rats\_2\_3$treatment)

rats\_surv\_2\_3$chisq

pchisq(rats\_surv\_2\_3$chisq,1,lower.tail = FALSE)

**data** burn\_data;

label TimeFollowed='Time (in days) until infection'

Treatment='Treatment Group'; input Patient\_ID Treatment Gender Race Perc\_Area\_Burned BSI\_Head BSI\_Butt BSI\_Trunk BSI\_Upper BSI\_Lower BSI\_Resp TOB TTE Excision\_Ind TTPAT PAT TTSAI SAI @@;

cards;

1 0 0 0 15 0 0 1 1 0 0 2 12 0 12 0 12 0

2 0 0 1 20 0 0 1 0 0 0 4 9 0 9 0 9 0

3 0 0 1 15 0 0 0 1 1 0 2 13 0 13 0 7 1

4 0 0 0 20 1 0 1 0 0 0 2 11 1 29 0 29 0

5 0 0 1 70 1 1 1 1 0 0 2 28 1 31 0 4 1

6 0 0 1 20 1 0 1 0 0 0 4 11 0 11 0 8 1

7 0 0 1 5 0 0 0 0 0 1 4 12 0 12 0 11 1

8 0 0 1 30 1 0 1 1 0 0 4 8 1 34 0 4 1

9 0 0 1 25 0 1 0 1 1 0 4 10 1 53 0 4 1

10 0 0 1 20 0 1 0 1 0 0 4 7 0 1 1 7 0

11 0 0 1 30 1 0 1 0 0 1 4 7 1 21 1 44 1

12 0 0 0 20 0 0 1 0 0 1 4 20 0 1 1 20 0

13 0 0 1 25 0 0 1 1 1 0 4 12 1 32 0 32 0

14 0 0 1 70 0 0 0 0 0 1 4 16 0 16 0 16 0

15 0 0 1 20 1 0 1 0 0 0 4 39 0 39 0 39 0

16 0 0 0 10 1 0 1 0 0 1 4 23 1 34 0 34 0

17 0 0 1 10 1 0 0 0 0 0 4 8 0 8 0 8 0

18 0 0 1 15 0 0 0 0 0 0 4 15 0 15 0 6 1

19 0 0 1 10 0 0 0 0 0 1 4 8 0 8 0 8 0

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21 0 0 1 16 0 0 1 0 0 0 4 25 1 22 1 43 0

22 0 1 1 55 1 0 1 1 0 0 4 14 1 3 1 56 0

23 0 0 1 20 1 0 1 1 0 0 4 24 1 47 0 11 1

24 0 0 0 30 0 0 0 1 1 0 4 6 1 43 0 43 0

25 0 0 1 40 0 1 0 1 1 0 1 25 0 3 1 25 0

26 0 0 1 15 1 0 1 1 0 0 4 12 0 12 0 12 0

27 0 1 1 50 0 0 1 0 0 1 4 15 1 53 0 32 1

28 0 0 1 40 1 0 1 1 0 0 4 18 1 52 0 51 1

29 0 1 1 45 0 1 1 1 1 0 4 13 1 11 1 21 0

30 0 1 0 40 0 1 1 1 1 0 2 29 0 2 1 29 0

31 0 0 1 28 0 0 1 0 0 0 2 7 0 7 0 3 1

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41 0 1 1 20 1 0 1 0 0 1 4 1 1 4 1 97 0

42 0 1 0 30 1 0 1 1 0 1 4 15 1 28 0 28 0

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151 1 1 1 20 1 0 1 0 0 0 4 7 1 6 1 17 1

152 1 0 1 15 0 0 0 1 1 1 4 19 1 3 1 42 0

153 1 0 1 10 0 0 1 0 0 0 4 10 0 10 0 2 1

154 1 0 1 35 1 1 1 0 0 0 4 10 1 27 0 27 0

;

**run**;

**proc** **print** data=burn\_data;

**run**;

**proc** **lifetest** data=burn\_data plot=(s);

time TTSAI\*SAI(**0**);

strata Treatment;

**run**;