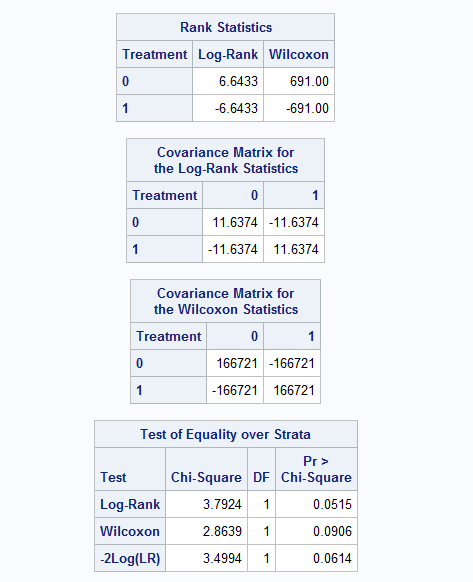
Question 1

a)

b)

c)

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:

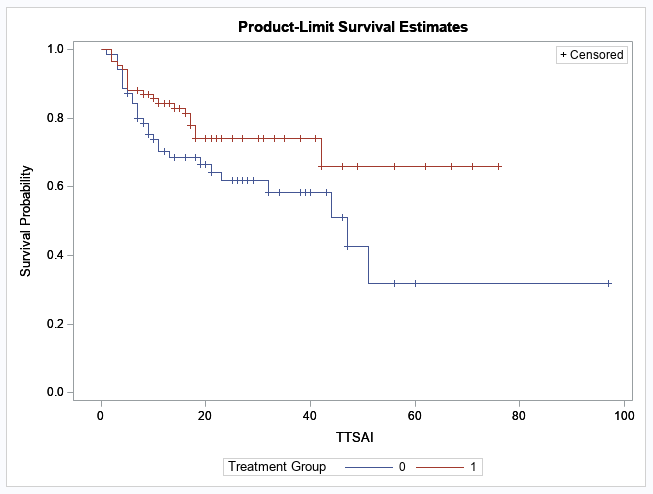
With h1(t) and h2(t) defined as follows

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

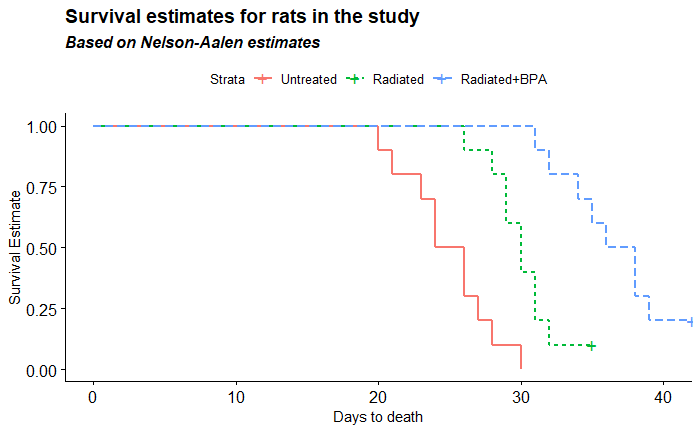
With h1(t), h2(t) and h3(t) defined as follows

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.

Appendix A

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

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

event = data$Censored)~offset(exp(-0.045\*data$Surv\_Time)),

subset = data$Treatment==1,

type="kaplan-meier")

df\_summary <- fortify(surv\_obj)

etau <- sum(-log(df\_summary$surv))

x <- seq(0, 1, length.out=48)

dat <- data.frame(x=x, px=dexp(x, rate=0.045))

ggsurv <- ggsurvplot(surv\_obj , data = data, xlab="Time to infection",

ylab="Survival estimate",

legend.labs = c("Auto"), linetype = 'strata') +

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

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

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

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

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

print(ggsurv)

dchisq(etau, 1)

pchisq(0.045, df = 1, lower.tail = FALSE)

1-pchisq(0.045, df = 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

20 0 0 1 15 0 0 0 0 1 0 4 24 1 32 0 32 0

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

32 0 0 1 19 1 0 1 0 0 0 3 16 0 16 0 16 0

33 0 0 1 15 0 0 1 0 0 0 2 10 0 10 0 3 1

34 0 0 1 5 0 0 1 0 1 0 3 6 0 6 0 4 1

35 0 1 1 35 0 0 1 0 0 0 4 8 1 43 0 7 1

36 0 0 1 2 1 0 1 0 0 0 1 1 1 27 0 27 0

37 0 1 1 5 0 0 1 0 0 0 2 18 0 18 0 18 0

38 0 0 1 55 1 0 1 0 0 1 4 6 1 5 1 47 1

39 0 0 0 10 0 0 0 1 0 0 2 19 1 29 0 29 0

40 0 0 1 15 0 0 1 0 0 0 4 5 0 5 0 5 0

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

43 0 0 1 25 1 1 1 1 0 1 4 14 1 4 1 7 1

44 0 0 1 95 1 1 1 1 1 1 4 9 0 9 0 3 1

45 0 1 1 30 0 0 0 0 1 0 4 1 1 39 0 39 0

46 0 0 1 15 1 0 1 0 0 0 4 10 0 10 0 10 0

47 0 0 1 20 0 1 1 1 0 0 4 6 1 5 1 46 0

48 0 1 1 6 0 0 1 0 0 0 2 13 1 28 0 28 0

49 0 0 1 15 0 0 1 0 0 1 4 11 1 21 0 21 0

50 0 0 1 7 0 0 1 1 0 0 1 8 1 17 1 38 0

51 0 0 1 13 0 0 1 1 1 0 4 10 0 10 0 10 0

52 0 0 1 25 1 0 1 0 0 1 4 6 1 40 0 5 1

53 0 0 1 25 1 0 1 0 1 1 4 18 1 22 0 9 1

54 0 1 1 20 1 0 1 0 0 1 4 16 1 16 1 21 1

55 0 1 1 25 0 0 1 1 0 0 4 7 1 26 0 26 0

56 0 0 1 95 1 0 1 1 1 1 4 14 0 14 0 14 0

57 0 0 1 17 1 0 1 0 0 0 4 16 0 16 0 16 0

58 0 0 1 3 0 0 1 0 1 0 3 4 0 4 0 1 1

59 0 0 1 15 1 0 1 0 0 0 4 19 0 6 1 19 0

60 0 0 1 65 1 1 1 1 1 1 4 21 1 8 1 10 1

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63 0 0 1 45 1 0 1 1 0 1 4 11 1 24 1 40 0

64 0 1 0 35 0 0 1 1 0 0 4 4 1 5 1 47 0

65 0 0 1 85 1 1 1 1 0 1 4 12 1 8 1 9 1

66 0 1 1 15 0 1 0 1 0 1 4 11 1 35 0 19 1

67 0 0 1 70 0 1 1 1 1 0 2 23 1 8 1 60 0

68 0 0 1 6 1 0 0 0 0 1 4 7 0 7 0 7 0

69 0 0 1 20 0 0 1 0 0 0 4 19 1 26 0 6 1

70 0 1 1 36 1 0 1 0 1 1 4 16 1 20 1 23 1

71 1 1 1 50 1 1 1 0 1 0 4 15 0 1 1 15 0

72 1 0 1 21 1 0 1 0 0 0 4 6 1 13 1 23 0

73 1 0 1 16 1 0 1 0 0 0 4 2 1 9 0 9 0

74 1 1 1 3 0 0 1 0 0 0 4 6 1 14 0 14 0

75 1 0 1 5 1 0 1 0 0 0 3 8 0 8 0 2 1

76 1 0 1 32 0 1 1 1 0 1 4 18 1 51 0 18 1

77 1 0 1 38 0 1 1 1 0 0 4 12 1 22 0 22 0

78 1 0 1 16 1 0 1 0 0 0 4 7 1 16 0 16 0

79 1 1 1 9 0 1 0 1 0 0 4 6 1 2 1 2 1

80 1 0 1 17 0 1 1 0 0 0 2 10 1 10 1 22 0

81 1 0 1 22 1 0 1 0 0 0 4 12 1 20 0 5 1

82 1 0 1 10 0 0 1 0 0 0 4 5 1 5 1 14 0

83 1 0 1 12 1 0 1 0 0 0 4 12 0 12 0 12 0

84 1 0 1 80 1 1 1 1 1 1 4 6 1 4 1 41 0

85 1 1 1 15 0 0 1 1 0 0 4 9 1 9 1 21 0

86 1 0 1 50 1 0 1 0 0 1 4 18 1 7 1 56 0

87 1 0 1 50 1 1 1 1 1 1 4 7 1 42 1 67 0

88 1 0 1 15 1 0 1 0 0 0 3 11 0 11 0 11 0

89 1 0 1 8 1 0 1 0 0 0 4 9 1 17 0 17 0

90 1 1 1 45 1 1 1 1 0 0 1 11 1 11 1 18 1

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94 1 0 1 40 0 1 1 1 0 0 4 11 1 8 1 31 0

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98 1 1 1 26 0 0 1 0 0 1 4 8 1 3 1 35 0

99 1 0 1 10 0 1 1 1 0 0 4 13 1 21 0 21 0

100 1 1 1 85 1 1 1 1 0 1 4 11 0 3 1 11 0

101 1 0 1 75 1 0 1 1 1 0 4 29 1 49 0 16 1

102 1 0 0 5 0 0 1 0 1 0 1 13 0 13 0 13 0

103 1 0 1 20 1 0 1 0 0 0 4 1 1 12 0 12 0

104 1 1 1 8 0 1 0 1 1 0 4 6 1 6 1 13 0

105 1 1 1 10 0 0 1 0 0 1 4 6 1 23 0 23 0

106 1 0 1 10 0 0 0 0 1 1 4 3 1 31 0 31 0

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109 1 0 1 10 1 0 0 0 1 0 4 5 1 18 0 18 0

110 1 0 1 18 0 0 1 1 1 0 4 6 1 5 1 33 0

111 1 0 1 20 1 0 1 1 0 0 4 9 1 8 1 17 0

112 1 0 1 80 1 1 1 1 1 1 4 4 1 11 1 13 0

113 1 0 0 17 1 0 1 1 1 1 4 5 1 4 1 35 0

114 1 0 0 35 1 0 1 0 0 0 4 7 1 7 1 71 0

115 1 0 1 50 1 0 1 0 1 1 4 11 0 11 0 3 1

116 1 0 0 20 0 0 1 0 0 0 4 6 1 31 1 42 1

117 1 0 1 25 0 1 1 1 0 0 3 8 0 8 0 5 1

118 1 0 1 20 0 0 0 1 0 1 1 3 1 2 1 30 0

119 1 0 1 20 0 0 1 1 0 0 4 6 1 38 0 38 0

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121 1 0 0 15 1 0 1 0 0 0 2 20 0 20 0 20 0

122 1 0 1 15 0 0 1 0 1 0 4 30 0 2 1 30 0

123 1 0 1 15 0 0 1 0 0 0 4 2 1 7 0 7 0

124 1 0 1 20 0 0 1 1 0 0 2 8 1 6 1 22 0

125 1 0 1 13 1 0 1 0 0 0 4 13 0 4 1 5 1

126 1 0 1 25 1 0 1 0 0 1 4 13 1 1 1 31 0

127 1 0 1 25 0 0 1 1 0 1 4 17 0 17 0 10 1

128 1 0 1 8 1 0 1 0 0 0 4 14 0 14 0 14 0

129 1 1 1 30 1 0 1 0 0 1 4 13 0 5 1 13 0

130 1 0 1 40 0 1 1 1 1 0 4 24 0 7 1 17 1

131 1 1 1 12 0 1 1 1 1 0 1 14 1 21 0 21 0

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134 1 0 1 15 0 0 1 0 0 0 4 17 1 17 0 11 1

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141 1 1 1 35 1 0 1 0 0 1 4 6 1 5 1 49 0

142 1 0 0 10 0 0 1 0 0 0 4 12 0 12 0 12 0

143 1 0 1 8 0 0 1 0 1 0 3 14 0 1 1 14 0

144 1 0 1 13 0 0 0 0 1 0 4 32 1 38 0 38 0

145 1 1 0 10 0 1 1 1 0 0 2 12 1 13 1 41 0

146 1 0 1 8 0 0 0 1 1 0 4 10 1 18 0 18 0

147 1 0 1 7 1 0 1 0 0 0 4 8 0 8 0 8 0

148 1 0 1 52 1 0 1 1 1 1 4 15 1 39 1 76 0

149 1 1 1 14 0 1 1 1 1 0 4 8 1 62 0 62 0

150 1 1 1 7 0 0 1 0 0 0 1 5 1 17 0 17 0

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**;