

# Homework 9

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Consider the colon data in the R package "survival". It gives adjuvant chemotherapy data for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are two records per person, one for recurrence (etype=1) and one for death (etype=2). Other important variables include:

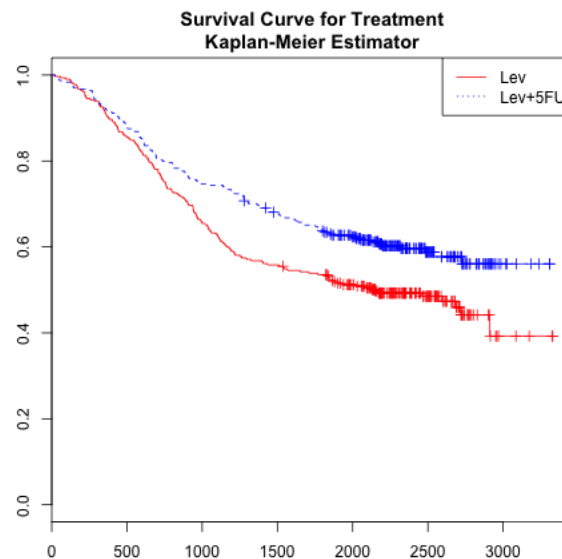
- rx: Treatment: Obs(ervation), Lev(amisole), Lev(amisole)+5-FU
- sex: 1=male
- age: in years
- time: days until event or censoring
- status: censoring status

For the following, consider survival to be Days until Death, i.e., etype=2.

## Problem 1

Using the Kaplan-Meier method, estimate the survival curve for each treatment group: Lev(amisole) and Lev(amisole)+5-FU.

Using Kaplan-Meier method, fit the survival estimator, the estimated survival curve is as follows:



## Problem 2

Estimate the median survival time for each of the two treatment groups, using the estimated survival curves.

Using Kaplan-Meier survival curve, the result is as follows:

Kaplan-Meier Estimated Curve

Call: `survfit(formula = Surv(time, status) ~ rx, data = survival_colon)`

	n	events	median	0.95LCL	0.95UCL
rx=Lev	310	161	2152	1540	NA
rx=Lev+5FU	304	123	NA	2725	NA

So the estimated median is:

Table 1: Estimated Median for two treatment groups

Treatment	Lev	Lev+5FU
Median	2152	NA

The median is calculated as the smallest survival time for which the survivor function is less than or equal to 0.5.

- For treatment Lev, the estimated median is 2152.
- For treatment Lev+5FU, since it never gets to the point where  $s(t) \leq 0.5$ , then the median for treatment Lev+5FU is NA.

## Problem 3

Using the log-rank test, determine whether there is a difference in survival between the two groups.

Using Log-rank test, the null hypothesis and alternative hypothesis are:

$H_0$ : there is no difference between the two treatment of survival curves

$H_1$ : there is difference between the two treatment of survival curves

the result is as follows:

Log-rank Test Result

Call:

`survdif(formula = Surv(time, status) ~ rx, data = survival_colon)`

	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V
rx=Lev	310	161	137	4.24	8.21
rx=Lev+5FU	304	123	147	3.95	8.21

Chisq= 8.2 on 1 degrees of freedom, p= 0.00417

Since the p-value of log-rank test is 0.00417, then we should reject the null hypothesis, i.e., concluding that there is a difference in survival between the two groups.

## Problem 4

Using a Cox proportional hazards model, estimate the hazard ratio for Levamisole relative to 5-FU, adjusting for Age and Sex.

Using Cox proportional hazards model and adjusting for Age and Sex, the result is as follows:

## Cox proportional hazards model adjusting for age and sex Result

Call:

coxph(formula = Surv(time, status) ~ rx\_d + age + sex, data = survival\_colon)

n= 614, number of events= 284

	coef	exp(coef)	se(coef)	z	Pr(> z )
rx_d	0.344635	1.411474	0.120079	2.870	0.0041 **
age	0.000920	1.000921	0.005119	0.180	0.8574
sex	-0.043126	0.957791	0.118948	-0.363	0.7169

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Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

	exp(coef)	exp(-coef)	lower .95	upper .95
rx_d	1.4115	0.7085	1.1155	1.786
age	1.0009	0.9991	0.9909	1.011
sex	0.9578	1.0441	0.7586	1.209

Concordance= 0.549 (se = 0.018 )

Rsquare= 0.014 (max possible= 0.996 )

Likelihood ratio test= 8.38 on 3 df, p=0.0388

Wald test = 8.29 on 3 df, p=0.04033

Score (logrank) test = 8.37 on 3 df, p=0.03892

Since we want to get the hazard ratio for Levamisole relative to 5-FU, then we simply set the Lev+5FU as the baseline.

Since from the result we can see, the hazard ratio for the second group relative to the first group, that is, rxLev relative to rxLev+5FU with adjusting for age and sex is 1.4115.

## Problem 5

**Give a 95% confidence interval for the hazard ratio in 4.**

From the result above, we can see that the 95% confidence interval for hazard ratio in Problem 4 is:

[1.1155, 1.786]

**R Code:**

```

rm(list = ls())
library(survival)
data("colon")

#Meier Estimator for treatment Lev, Lev+5FU
survival_colon <- subset(colon, etype==2 & rx %in% c("Lev", "Lev+5FU"))
fit_trt <- survfit(formula = Surv(time, status) ~ rx, data = survival_colon, type = "kaplan-meier")
sink('/Users/raymond/Drive/STAT W4201/HW9/meiersum.txt')
summary(fit_trt)
sink()

#Plot the survival curve
png(filename = "/Users/raymond/Drive/STAT W4201/HW9/meiercurve.png")
plot(fit_trt, lty = c(1,2), col = c("red", "blue"))
title(main="Survival Curve for Treatment")
title(main="Kaplan-Meier Estimator", line=0.5)
legend("topright", c("Lev", "Lev+5FU"), col=c("red", "blue"), lty=c(1,3))
dev.off()

#Estimate the median
sink('/Users/raymond/Drive/STAT W4201/HW9/meier.txt')
fit_trt
sink()

#Log-rank test for difference
log_rank <- survdiff(Surv(time, status) ~ rx, data=survival_colon)

sink('/Users/raymond/Drive/STAT W4201/HW9/logrank.txt')
log_rank
sink()

#Cox proportional hazards model
survival_colon$rx_d <- as.numeric(survival_colon$rx=="Lev")
cox <- coxph(Surv(time, status) ~ rx_d + age + sex, data=survival_colon)
sink('/Users/raymond/Drive/STAT W4201/HW9/cox.txt')
summary(cox)
sink()

```