Homework 10

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```
library(survival)
library(MASS)
library(survminer)
library(KMsurv)
library(tidyverse)
```

Problem 1

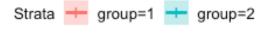
Input data

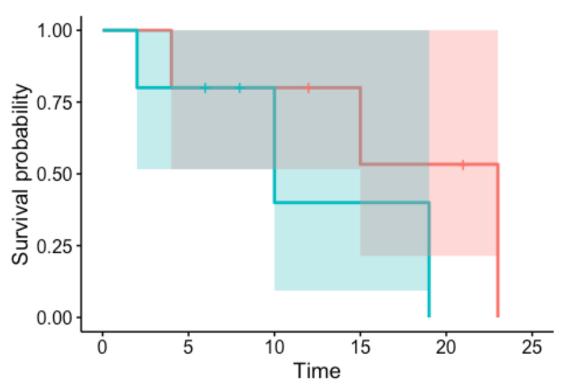
```
time = c(4, 12, 15, 21, 23, 2, 6, 8, 10, 19)
cens = c(1, 0, 1, 0, 1, 1, 0, 0, 1, 1)
group = c(rep(1, 5), rep(2, 5))
data1 = data.frame(time = time, cens = cens, group = group)
data1
##
      time cens group
## 1
         4
              1
                    1
                    1
## 2
        12
              0
## 3
        15
              1
                    1
## 4
        21
              0
                    1
## 5
        23
              1
                    1
                    2
## 6
        2
              1
                    2
## 7
         6
              0
## 8
         8
              0
                    2
## 9
                    2
        10
              1
## 10
        19
                    2
```

Using the log-rank test to test hypotheses.

 H_0 : $h_1(t) = h_2(t)$ for all t; H_1 : $h_1(t) \neq h_2(t)$ for some t.

```
survdiff(Surv(time,cens)~group, data=data1) # Log rank test
## Call:
## survdiff(formula = Surv(time, cens) ~ group, data = data1)
##
           N Observed Expected (O-E)^2/E (O-E)^2/V
##
                    3
                          4.14
## group=1 5
                                   0.313
                                              1.15
                          1.86
## group=2 5
                    3
                                   0.697
                                               1.15
##
## Chisq= 1.1 on 1 degrees of freedom, p= 0.3
```





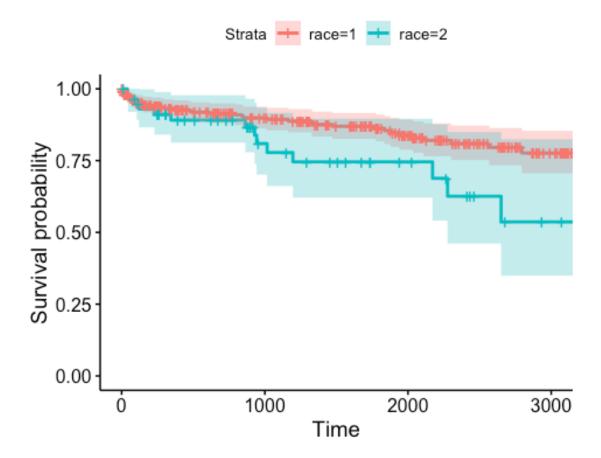
Calculating by using R, we can get that $Z^2 = 1.1$ and corresponding p - value = 0.3. As p-value is larger than 0.05, we fail to reject the null hypothesis and conclude that $h_1(t) = h_2(t)$ for all t. The plot of survival probability of two groups are shown above.

Problem 2

```
data("kidtran")
head(kidtran)
     obs time delta gender race age
##
## 1
                                   46
       1
            1
                   0
                          1
## 2
       2
            5
                   0
                          1
                                   51
                                1
## 3
       3
            7
                   1
                          1
                                   55
       4
            9
                          1
                                   57
## 4
                   0
       5
## 5
           13
                   0
                          1
                                   45
           13
## 6
                                   43
female_kid = kidtran %>%
  filter(gender == 2)
male kid = kidtran %>%
filter(gender == 1)
```

For female:

```
ggsurvplot( survfit(Surv(time, delta) ~ race, data = female_kid),
conf.int=TRUE)
```



Using the log-rank test to test hypotheses.

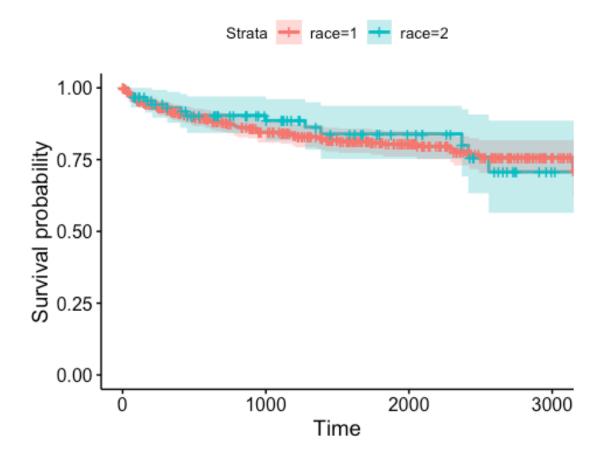
 H_0 : $h_1(t) = h_2(t)$ for all t; H_1 : $h_1(t) \neq h_2(t)$ for some t.

```
survdiff(Surv(time,delta) ~ race, data = female kid)
## Call:
## survdiff(formula = Surv(time, delta) ~ race, data = female_kid)
##
            N Observed Expected (O-E)^2/E (O-E)^2/V
##
                          44.79
                    39
## race=1 280
                                     0.748
                                                4.85
## race=2 59
                    14
                           8.21
                                     4.076
                                                4.85
##
   Chisq= 4.8 on 1 degrees of freedom, p= 0.03
```

Calculating by using R, we can get that $Z^2=4.8$ and corresponding p-value=0.03. As p-value is smaller than 0.05, we reject the null hypothesis and conclude that $h_1(t)\neq h_2(t)$ for some t.

For male:

```
ggsurvplot( survfit(Surv(time, delta) ~ race, data = male_kid),
conf.int=TRUE)
```



Using the log-rank test to test hypotheses.

 $H_0: h_1(t) = h_2(t)$ for all t; $H_1: h_1(t) \neq h_2(t)$ for some t.

```
survdiff(Surv(time,delta) ~ race, data = male kid)
## Call:
## survdiff(formula = Surv(time, delta) ~ race, data = male_kid)
##
            N Observed Expected (O-E)^2/E (O-E)^2/V
##
                           71.9
## race=1 432
                    73
                                    0.0168
                                               0.097
## race=2 92
                    14
                           15.1
                                    0.0801
                                               0.097
##
  Chisq= 0.1 on 1 degrees of freedom, p= 0.8
```

Calculating by using R, we can get that $Z^2 = 0.1$ and corresponding p - value = 0.8. As p-value is larger than 0.05, we fail to reject the null hypothesis and conclude that $h_1(t) = h_2(t)$ for all t.

Problem 3

Get data.

```
data("larynx")
larynx_data = larynx %>%
 mutate(z1 = ifelse(stage == 2, 1, 0),
         z2 = ifelse(stage == 3, 1, 0),
         z3 = ifelse(stage == 4, 1, 0))
head(larynx data)
     stage time age diagyr delta z1 z2 z3
##
## 1
         1 0.6 77
                       76
                              1
                                 0
                                    0
## 2
         1 1.3
                53
                       71
                              1
                                 0
                                    0
                                       0
## 3
        1 2.4 45
                       71
                              1
                                    0 0
## 4
         1 2.5 57
                       78
                              0
                                 0
                                    0
                                       0
## 5
         1 3.2 58
                       74
                              1
                                 0
                                    0 0
         1 3.2 51
                       77
## 6
                              0 0 0
```

We fit following model(using Breslow method for tie handling):

```
h(t) = h_0(t)exp(\beta_1 Z_1 + \beta_2 Z_2 + \beta_3 Z_3 + \beta_4 Z_4 + \beta_5 Z_1 \times Z_4)
```

```
fit=coxph(Surv(time,delta)~z1+z2+z3+age+z1*age,data=larynx data,ties='breslow
')
summary(fit)
## Call:
## coxph(formula = Surv(time, delta) \sim z1 + z2 + z3 + age + z1 *
##
       age, data = larynx_data, ties = "breslow")
##
##
     n= 90, number of events= 50
##
##
                coef exp(coef)
                                  se(coef)
                                                z Pr(>|z|)
## z1
          -7.3820143
                      0.0006223 3.4027542 -2.169
                                                    0.0301 *
           0.6218044 1.8622853 0.3558078 1.748
## z2
                                                    0.0805 .
## z3
           1.7534270 5.7743576 0.4239595 4.136 3.54e-05 ***
           0.0059729 1.0059908 0.0148792 0.401
                                                    0.6881
## age
## z1:age 0.1116674 1.1181409 0.0476728 2.342
                                                    0.0192 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
##
          exp(coef) exp(-coef) lower .95 upper .95
## z1
          0.0006223 1606.8231 7.900e-07
                                            0.4903
## z2
          1.8622853
                        0.5370 9.272e-01
                                            3.7403
          5.7743576
## z3
                        0.1732 2.516e+00
                                           13.2550
## age
          1.0059908
                        0.9940 9.771e-01
                                            1.0358
                        0.8943 1.018e+00
                                            1.2277
## z1:age 1.1181409
##
## Concordance= 0.682 (se = 0.045 )
## Rsquare= 0.235 (max possible= 0.988)
```

```
## Likelihood ratio test= 24.11 on 5 df, p=2e-04
## Wald test = 23.77 on 5 df, p=2e-04
## Score (logrank) test = 27.98 on 5 df, p=4e-05
```

Explain of results:

 $\beta_1 + \beta_5$: the log hazard ratio for subjects in stage II versus stage I is (-7.382+0.112*a) given they have same age, where a is the age of subjects.

 β_2 : the log hazard ratio for subjects in stage III versus stage I is 0.621 given they have same age.

 β_3 : the log hazard ratio for subjects in stage IV versus stage I is 1.753 given they have same age.

 β_4 : when patients are not in stage II, the log hazard ratio for subjects with one unit changes in age is 0.006 given they are in same stage.

 $\beta_4 + \beta_5$: when patients are in stage II, the log hazard ratio for subjects with one unit changes in age is 0.118.

Relative risk:

For the hazard of dying for a stage II patient of age 50 is

$$h_2(t) = h_0(t)exp(-7.382 \times 1 + 0.111 \times 1 \times 50)$$

For the hazard of dying for a stage I patient of age 50 is

$$h_1(t) = h_0(t) exp(0)$$

So the hazard ratio is

$$HR(t) = \frac{h_2(t)}{h_1(t)} = 0.16$$