STAT40810: Stochastic Models: Assignment 3

Ian Towey

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Question 1

The model choosen that was:

 $Survival \sim log BUN + HGB * platelet$

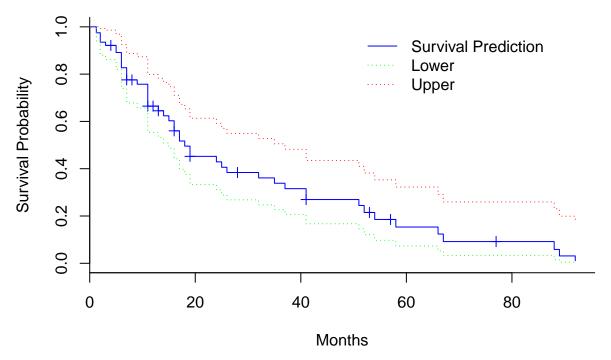
.

The model was discovered by fitting each covariate separately reviewing significance of p-value at $\alpha = 0.05$. Then adding interaction pairs and again reviewing significance of p-value at $\alpha = 0.05$.

```
## Call:
## coxph(formula = Surv(time, vstatus) ~ logBUN + HGB:platelet,
##
       data = myeloma)
##
    n= 65, number of events= 48
##
##
                    coef exp(coef) se(coef)
                                                 z Pr(>|z|)
##
                           4.90052 0.61291 2.593 0.00951 **
## logBUN
                 1.58934
## HGB:platelet -0.06885
                           0.93346
                                   0.03242 -2.124 0.03368 *
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
##
                exp(coef) exp(-coef) lower .95 upper .95
## logBUN
                   4.9005
                              0.2041
                                         1.474
                                                 16.2913
## HGB:platelet
                   0.9335
                              1.0713
                                         0.876
                                                  0.9947
## Concordance= 0.669 (se = 0.051)
## Rsquare= 0.171
                    (max possible= 0.991)
                                 on 2 df.
## Likelihood ratio test= 12.16
                                            p=0.00229
## Wald test
                        = 13.49
                                 on 2 df,
                                            p=0.001174
## Score (logrank) test = 13.99
                                on 2 df,
                                            p=0.0009179
```

The model summary is displayed above. Things of note in this the output include:

- The number of patients at the start of the study was 65.
- At the end of the study there was 48 events, therefore 17 right-cencored patients.
- Covariate logBUN (log BUN at diagnosis) and interaction covariates HGB (hemoglobin at diagnosis)
 * PLATELET (platelets at diagnosis: 0=abnormal, 1=normal) are significient at α = 0.05 level.
- The level of BUN at diagnosis time increases the hazard by 1.5 per month
- The level of interaction covariate slightly decreases the hazard
- The "Concordance" value, is a measure of the predictive discrimination of a covariate.
- The "Rsquared" value, reflects the improvement in the fit of the model with the covariate compared to the null model.
- The hypothesis tests Likelihood ratio test, Wald test and Score test all test the hypothesis that $H_0: \beta=0$ at the $\alpha=0.05$ level. The results of these there test shows the test statistic for all three tests are much greater than 0 so we reject the H_0

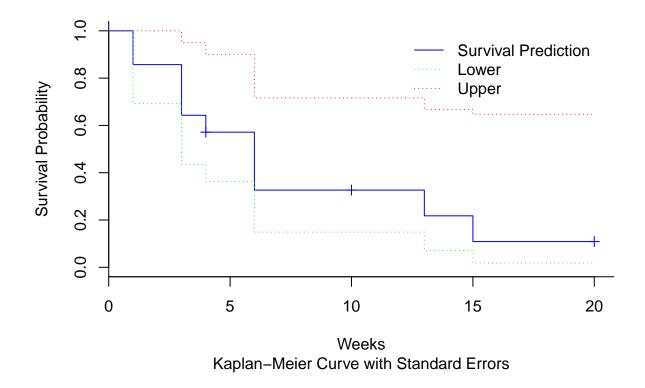


Analysis of the survival function plot above, we see that the media survival time (in months) for a patient is approximately 20 months. The probability of survival for a patient after 80 months is about 10%

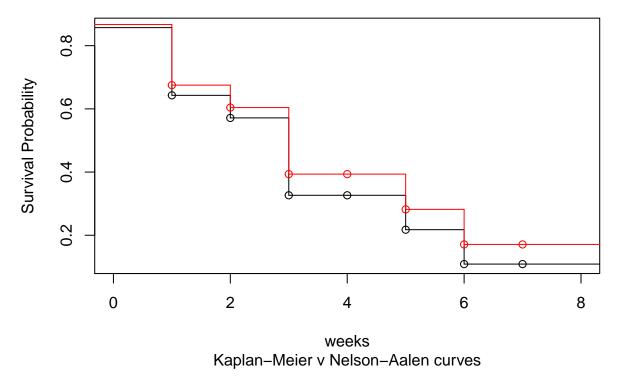
Question 2

(a) Kaplan-Meier estimate of the survival function and curve plot of the survival function.

```
## Call: survfit(formula = survdat ~ 1, se = TRUE)
##
##
    time n.risk n.event survival std.err lower 95% CI upper 95% CI
##
              14
                       2
                             0.857
                                    0.0935
                                                  0.6921
                                                                  1.000
       1
       3
              12
                       3
                                                   0.4351
                                                                  0.950
##
                             0.643
                                    0.1281
##
       4
               9
                       1
                             0.571
                                    0.1323
                                                   0.3630
                                                                  0.899
##
       6
               7
                       3
                             0.327
                                    0.1309
                                                  0.1488
                                                                  0.716
##
               3
                             0.218
                                    0.1246
                                                  0.0709
                                                                  0.668
      13
                       1
               2
##
      15
                       1
                             0.109
                                    0.0990
                                                  0.0183
                                                                  0.647
```



(b) Comparison of the Kaplan-Meier v Nelson-Aalen estimators



The Kaplan-Meier estimator is unbiased for the survival function. The Nelson–Aalen estimator is unbiased for cumulative hazard. The Nelson–Aalen estimator is always larger than negative log of the Kaplan– Meier estimator.