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Problem Set 7 | **Stat 245**

8.1 In section 1.11, a study was conducted on the effects of ploidy on the prognosis of patients with cancer of the tongue. Tissue samples were examined to determine if the tumor had an aneuploid or diploid DNA profile. Times to death for these two groups of patients are recorded in Table 1.6. To analyze the data, create a single-indicator variable Z which reflects the type of tumor.

- Test the hypothesis of no effect ploidy on survival using the score test. Perform the test using the Breslow, Efron, and discrete method for handling ties. And compare your results.
- Estimate β and its standard error using all three methods of handling ties. Find a 95% confidence interval for the relative risk of death of an individual with an aneuploid tumor as compared to an individual with a diploid tumor.
- Repeat (a) using the likelihood ratio test. Compare your answers to those in part (a).
- Repeat (a) using the Wald test. Compare your answer to those in part (a) and (c).

Solution

- To run this in R, the data in Section 1.11 is available in the KMsurv R package and is named `tongue`. The following code will load the necessary packages and data for the analysis.

```
library(KMsurv)
library(survival)
data(tongue)
```

The data has a variable called `type`, and we can define

$$Z = \begin{cases} 1 & \text{Aneuploid Tumor} \\ 0 & \text{Diploid Tumor} \end{cases}$$

To test the hypothesis we consider the `coxph` function. The following codes will fit the Cox proportional hazards regression model to the data using Breslow, Efron, and discrete method for handling ties.

```
> tongue_breslow <- coxph(Surv(time, delta) ~ type,
+ data = tongue, ties = "breslow")
> tongue_efron <- coxph(Surv(time, delta) ~ type,
+ data = tongue, ties = "efron")
> tongue_exact <- coxph(Surv(time, delta) ~ type,
+ data = tongue, ties = "exact")
```

We can obtain the complete summary of the test above using the `summary` function. But since we are only interested in the score test, we can extract the output using the `sctest` subset list name of the `summary` output. To extract the list of all subset names use `str` function for structure, example `str(summary(tongue_breslow))`. Thus the score tests are the following:

```
> summary(tongue_breslow)$sctest
      test      df      pvalue
2.74639146 1.00000000 0.09747419
> summary(tongue_efron)$sctest
      test      df      pvalue
2.81433788 1.00000000 0.09342544
> summary(tongue_exact)$sctest
      test      df      pvalue
2.7897217 1.00000000 0.0948707
```

All three methods for handling ties have score test p-values greater than .05 (say this is our level of significance). There is no significant difference between the values of the test statistics of the three handling ties.

- The estimate of the β and its standard error are in the subset list name `coefficients` of the `summary` output. So that the following extracts the desired output for all handling ties.

```
> (coeff_breslow <- summary(tongue_breslow)$coefficients)
      coef exp(coef) se(coef)      z Pr(>|z|)
type 0.4609544  1.585587 0.2805353 1.643124 0.1003572
```

```
> (coeff_efron <-summary(tongue_efron)$coefficients)
      coef exp(coef) se(coef)      z Pr(>|z|)
type 0.4663742  1.594203 0.2804476 1.662964 0.09631971
> (coeff_exact <-summary(tongue_exact)$coefficients)
      coef exp(coef) se(coef)      z Pr(>|z|)
type 0.4684064  1.597446 0.2828184 1.656209 0.09767949
```

And the 95% confidence interval for the relative risk is coded as follows:

```
> ci_breslow <- exp(
+   c(coeff_breslow[1] - 1.96 * coeff_breslow[3],
+     coeff_breslow[1] + 1.96 * coeff_breslow[3])
+ )
> ci_breslow
[1] 0.9149419 2.7478080
> ci_efron <- exp(
+   c(coeff_efron[1] - 1.96 * coeff_efron[3],
+     coeff_efron[1] + 1.96 * coeff_efron[3])
+ )
> ci_efron
[1] 0.9200722 2.7622664
> ci_exact <- exp(
+   c(coeff_exact[1] - 1.96 * coeff_exact[3],
+     coeff_exact[1] + 1.96 * coeff_exact[3])
+ )
> ci_exact
[1] 0.9176698 2.7807772
```

- (c) The likelihood ratio test is named `logtest` in the `summary` list of outputs. Thus we have

```
> summary(tongue_breslow)$logtest
      test      df      pvalue
2.6114977 1.0000000 0.1060915
> summary(tongue_efron)$logtest
      test      df      pvalue
2.6735666 1.0000000 0.1020272
> summary(tongue_exact)$logtest
      test      df      pvalue
2.6534747 1.0000000 0.1033238
```

Compared to that in part (a), the test statistics of LRT is slightly less than that in Score test, and in effect the p-value is slightly larger than that in (a).

- (d) The Wald test is named `waldtest` in the `summary` list of outputs. Thus we have

```
> summary(tongue_breslow)$waldtest
      test      df      pvalue
2.7000000 1.0000000 0.1003572
> summary(tongue_efron)$waldtest
      test      df      pvalue
2.77000000 1.00000000 0.09631971
> summary(tongue_exact)$waldtest
      test      df      pvalue
2.74000000 1.00000000 0.09767949
```

Compared to that in part (a) and (c), the test statistics of Wald is between Score test and LRT. The bottomline is that, all three test statistics for three methods of handling ties are close to each other. All have the same conclusion.