Applied Survival Analysis - January 2016

Lab 3: Comparing survival curves between groups

In this lab, we are going to understand how to produce a Kaplan-Meier plot of survival estimates for more than one subgroup on the same graph, and compute a *Logrank* or *Wilcoxon* test in R.

(a) Using the following artificial data from two treatment groups

compare the survival of the two groups by computing the *Logrank* test using the **survdiff** function in R. What's your conclusion? **Optional:** Write an R program to construct tables like that on page 22 of today's notes.

- (b) We are going to work on data from a leukemia remission study (Garrett 1997). The data consist of 42 patients who are monitored over time to see how long (weeks) it takes them to go out of remission (remiss: 1 = yes, 0 = no). Half of the patients received a new experimental drug and the other half received a standard drug (trt: 1=6-MP, 0=Control). This dataset is called leukem.csv. Import the data in R. Use the factor function to encode the trt variable as a factor (please, see ?factor for more details).
 - (i) Use the survfit function to get the KM estimates in both groups. After using information from (a), guess what the syntax would be.
 - (ii) Plot the survival estimates of the two treatment groups using the plot function. Which group seems to be doing better? Comment on the graph.
 - (iii) Compare the survival between the two groups in terms of the *Logrank* and *Wilcoxon* test using the **survdiff** function. What do you conclude from these tests? Why do you think that there is a difference in the p-values of the two tests? Explain your opinion.
 - (iv) How could you informally check the proportional hazards assumption? Any ideas?