

Survival Analysis Assignment

I'm trying to solve a problem for my survival analysis class. Basically it consists of data on survival probabilities with several covariates. And we're trying to compare the difference in survival probabilities from two treatments. The coding should be done in R. The questions I need to answer are below. And the data set is posted. My deadline is tonight (Thursday evening) around midnight (eastern time). Let me know if you can help and what your fee is.

The pbc.txt data is a modified Mayo Clinic primary biliary cirrhosis data. Primary biliary cirrhosis is a rare autoimmune liver disease. Some variables have missing data.

age:	in years
alb:	serum albumin
alkphos:	alkaline phosphatase
bili:	serum bilirunbin
edema:	presence of edema 1 unsuccessfully treated edema
time:	survival time
protime:	standardised blood clotting time
spiders:	blood vessel malformations in the skin
status:	censoring status
trt:	1 = control, 2 = treatment

We would like to test if treatment significantly effect survival and build a statistical model that incorporates influential covariates associated with disease outcome.

1. Compare the Kaplan-Meier survival curves for the two treatment groups. Plot the curves and conduct an appropriate test of significance.
2. Fit a main effects Cox proportional hazards model, stratified on treatment and conduct a stepwise AIC procedure (*) which includes up to all two-way interactions. Report the final model from this procedure.
3. In the model selected above, log transform all the continues covariates and refit the model on the log-transformed variables. Which model provides a better fit? Explain.
4. For your final chosen model, please calculate the estimated two year survival probabilities for a new subject in the control and treatment arms, with all the continuous covariates set at their mean level.

(*) Here is an example of a code to run a stepwise AIC procedure, please modify it as needed:

```
library(MASS)
attach(pbc)
pbc.all<-coxph(Surv(time,status)~.,data=pbc) # Initial model
pbc.2level <- stepAIC(pbc.all,~.^2) # up to two-way interaction
pbc.2level $anova # Shows stepwise model path
```

