Report 2: Survival Analysis of Primary Biliary Cirrhosis

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1. Introduction

Primary biliary cirrhosis (PBC) is a rare autoimmune liver disease that leading slow but progressive destruction of small bile ducts, which will result in permanent cirrhosis and liver decompensation. Patients may also suffer abdominal pain, diarrhea, and an increased risk of cancer. The dataset is collected from the Mayo Clinic trials of PBC of the liver from 1974 to 1984. 424 PBC patients met the eligibility criteria for a randomized placebo-controlled trial of the drug D-penicillamine (DPCA). The first 312 data entries represent participants of the above trial and their data is mostly complete. The rest 112 patients declined to participate but agreed to record basic measurements and track survival. 6 of these were discarded due to track lost. The purpose of this analysis is to investigate the effect of DPCA on the lifetime of patients with PBC, along with what covariates significantly influence patients' risk of death.

2. EDA

The dataset has 418 data entries, corresponding to 312 trial participants and 106 additional cases. Each entry has 3 basic columns recording their survival time in days, status at endpoint (censored, transplant, dead), and treatments by DPCA/placebo. Besides, each entry has 15 covariates describing a patient's personal information (age, sex), clinical assay indexes, and other complications. The dataset contains 276 complete cases without missing values among trial participants. The sex ratio of the dataset is at least 9:1 (female to male) and 125 of the 312 trial participants died at the endpoint. To formalize the analysis, both censored and transplant status are considered alive. The variable table is shown in Appendix and we conduct the survival analysis on the complete cases.

2.1 Univariate Analysis

Combining the results in Table 1 and Figure 1, we can clearly see that covariates bili, chol, copper, alk.phos, ast, trig, and protime have typical right-skewed distributions, which I will apply the log transformation to them to compensate for a normal distribution in survival analysis. The median survival time and patient ages are 1788 days after registration and 49.71 years respectively. The death rate of complete cases (40.22%) is fairly close to the original trial data (40.06%) and the number of patients treated with DPCA and placebo is nearly identical (Table 2, 3). The sex ratio is 7.11:1 (female to male).

	time	age	bili	chol	albumin	copper	alk.phos	ast	trig	platelet	protime
mean	1979.167	49.800	3.334	371.261	3.517	100.768	1996.612	124.119	124.978	261.772	10.736
sd	1112.380	10.523	4.601	234.788	0.405	88.269	2115.478	56.720	65.281	93.129	1.008
median	1788.000	49.710	1.400	310.000	3.545	74.000	1277.500	116.625	108.000	257.000	10.600
\min	41.000	26.278	0.300	120.000	1.960	4.000	289.000	28.380	33.000	62.000	9.000
max	4556.000	78.439	28.000	1775.000	4.400	588.000	13862.400	457.250	598.000	563.000	17.100
1st Qu.	1185.750	41.513	0.800	249.500	3.310	42.750	922.500	82.458	85.000	200.000	10.000
3rd Qu.	2689.750	56.585	3.525	401.000	3.772	129.250	2068.250	153.450	151.250	318.250	11.200
IQR	1504.000	15.072	2.725	151.500	0.462	86.500	1145.750	70.992	66.250	118.250	1.200
MAD	1131.224	10.633	1.186	106.747	0.348	53.374	756.867	52.299	45.961	87.473	0.890

Table 1: Summary statistics of numerical variables

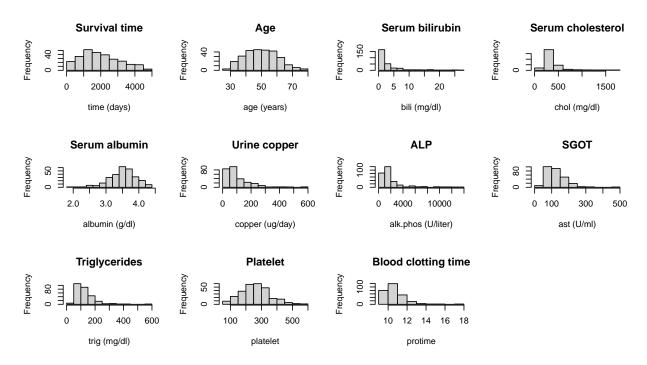


Figure 1: Histograms of numerical variables

2.2 Bivariate Analysis

We test the correlation matrix for available variable pairs. A visualized result is provided in Figure 2. we have the following key strong linear correlations (signif. level 0.05):

- time and status has a negative PCC of -0.35, which confirms our data setting and clinical observations. bili and time have a negative PCC of -0.43, which is reasonable since an elevated level of serum bilirubin is a sign of liver damage or disease that the liver is not clearing the toxic chemical properly.
- ascites and edema have a positive PCC of 0.63, which is reasonable since they are both typical symptoms of liver diseases.

Besides, we notice that *status* have linear correlations with almost all clinical indicators and symptoms (Fig.7). Therefore, we will consider all covariates at this stage. The paired scatter plots for quantitative variables are shown in Appendix, Table 7.

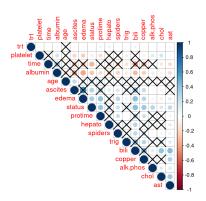


Figure 2: Visualized correlation matrix

Table 2: Frequency table (a)

Var	class	freq.	%
status	alive	165	59.78
	dead	111	40.22
trt	DPCA	136	49.28
	placebo	140	50.72
sex	male	34	12.32
	female	242	87.68
ascites	no	257	93.12
	yes	19	6.88
hepato	no	134	48.55
	yes	142	51.45

Table 3: Frequency table (b)

Var	class	freq.	%
spiders	no	196	71.01
	yes	80	28.99
edema	no	234	84.78
	treated	25	9.06
	yes	17	6.16
stage	1	12	4.35
	2	59	21.38
	3	111	40.22
	4	94	34.06

3. Survival Analysis

3.1 Kaplan-Meier (KM) Estimator

The Kaplan-Meier estimator is defined as: $\hat{S}(t) = \prod_{t_i < t} (1 - \frac{d_i}{r_i})$, r_i is the number of individuals at risk just before t_i (including censored individuals at t_i), and d_i is the number of individuals experiencing the event at time t_i . First, we investigate whether a significant difference in survival curves exists between two groups of patients with different treatments. The null and alternative hypothesis are: $H_0: S_{DPCA}(t) = S_p(t), H_1: S_{DPCA}(t) \neq S_p(t)$, where H_0 states there is no significant difference in survival time between patients who receive

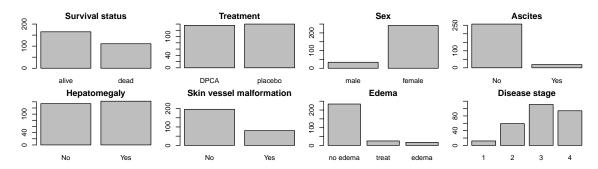


Figure 3: Frequency distribution of categorical variables

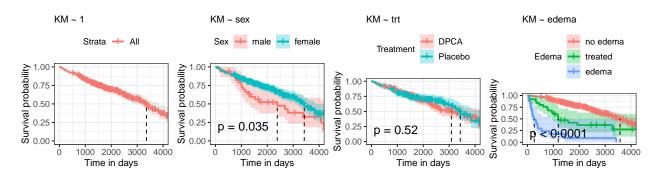


Figure 4: Survival plots by KM estimator

DPCA and placebo, H_1 states there is a significant difference between the above groups. We consider p < 0.05 to indicate statistical significance. The KM survival curve and log-rank test are shown in Figure 4 and Table 4. Since p = 0.5 > 0.05, we do not reject the null hypothesis, which means there is no significant difference in survival curves between DPCA and placebo treatment for complete patient cases. Then we investigate the difference regarding patients' sex. The null and alternative hypothesis are: $H_0: S_m(t) = S_f(t)$, $H_1: S_m(t) \neq S_f(t)$, where H_0 states there is no significant difference in survival time between male and female patients, H_1 states there is a significant difference. since p = 0.03 < 0.05, we reject the null hypothesis and the survival time indeed has a significant difference between sex groups. This difference can be clearly captured as the survival curve of the female group is generally above the male group, indicating a higher survival probability at large t. A similar analysis on the edema also rejects the null hypothesis, revealing a significant difference in survival curves.

Var.	Cat.	N	Observed	Expected	(O-E)^2/E	(O-E)^2/V	Chisq.	p
44	DPCA	136	57	53.7	0.209	0.405	0.4	0.5
trt	placebo	140	54	57.3	0.195	0.405	0.4	0.5
2015	$_{ m male}$	34	21	13.7	3.878	4.47	4.5	0.03
sex	female	242	90	97.3	0.546	4.47	4.0	
	no edema	234	79	100.95	4.77	53.09		
edema	treated	25	16	8.06	7.83	8.46	113	< 2e-16
	$_{ m edema}$	17	16	1.99	98.74	101.59		

Table 4: Log-rank stats table

3.2 Cox Proportional Hazards (Cox PH) Model

Var.	Chisq.	exp(coef)	se(coef)	Z	p	C-index	likelihood	log-rank	Wald
age	0.0323	1.0328	0.0092	3.509	< 0.001				
edema:treated	0.1887	1.2076	0.2904	0.650	0.516				
edema:edema	0.9053	2.4727	0.3386	2.674	0.008		179 0	249.7,	173,
bili	0.7343	2.0839	0.1220	6.017	< 2e-09	0.849	173.8, p<2e-16	p<2e-16	p<2e-16
albumin	-0.7948	0.4517	0.2582	-3.078	0.002				
copper	0.3834	1.4673	0.1468	2.612	0.009				
protime	2.6860	14.6730	1.1867	2.263	0.024				

Table 5: AIC model selection result

Since we consider the effect of covariates have on the risk of death (or survival time in reverse) and some of them are quantitative, we fit a Cox PH model to measure the hazard

function instead of the survival function in KM estimator. The hazard function can be expressed as $h(t) = h_0(t) \times exp(\beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_p x_p)$, where t represents the survival time, h(t) is the hazard function determined by p covariates $(x_1, x_2, ..., x_p)$ and the coefficients $(b_1, b_2, ..., b_p)$ measure the impact of them. h_0 is the baseline hazard equals to $h(t)|_{x_i=0, i\in[p]}$. The estimated Cox PH model should satisfy the following assumptions:

Var.	Chisq.	df	p
age	0.954	1	0.329
$_{\rm edema}$	5.769	2	0.056
bili	0.782	1	0.377
albumin	0.312	1	0.577
copper	0.776	1	0.378
protime	3.805	1	0.051
GLOBAL	2.6860	7	0.068

Table 6: Test for proportional hazards

- $\beta_i, i \in [p]$ is constant over time (proportional hazard)
- Linear form of the covariates and no outliers which are poorly predicted by the model

Global Schoenfeld Test p: 0.06777

Seta(t) for protime Beta(t) for albumin Beta(t) for edema Schoenfeld Individual Test p: 0.3288 Schoenfeld Individual Test p: 0.0559 Beta(t) for age 2500 3100 3400 2500 3100 Schoenfeld Individual Test p: 0.3765 Schoenfeld Individual Test p: 0.5766 Beta(t) for bili 3100 3100 Beta(t) for copper Schoenfeld Individual Test p: 0.3784 Schoenfeld Individual Test p: 0.0511 2500 3100

Figure 5: Schoenfeld residual plots

We use backward elimination to select the best model regarding its explainability and complexity of covariates. Starting from a full model, we minimize the AIC (see Appendix) and each time eliminate 1 covariate which gives the minimum value if deleted. We fit the model by maximum partial likelihood. The selection result is shown in Table 5, with its goodness-of-fit test passed and a concordance of 0.849 showing its strong robustness. Model assessments are shown in Table 6 and Figures 5, 6. We do not reject the null hypothesis that selected covariates follow a proportional hazard pattern. $\beta(t)$ has no time-related pattern in Schoenfeld plots and ensures proportional hazard. The martingale residual plots regarding selected covariates generally follow a linear pattern, and the linear prediction of deviance is fairly symmetric around 0 except at the very end. The model satisfies the assumptions and explains the trial cases properly. However, we see that 10 outliers (abs. value \geq 2) exist in the deviance residual plot, indicating the model has poor explainability on them and the model is not perfectly fit on the trials.

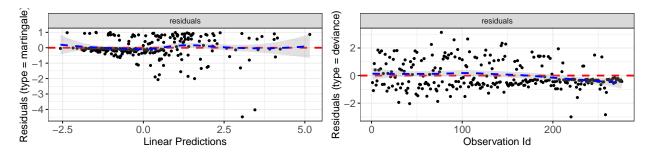


Figure 6: Martingale residual and deviance plot

3.3 Cox PH Model Estimation

Estimated model (0.05 signif. level, after log transformation):

 $\hat{h}(t) = \hat{h}_0(t) \times exp(0.03 \times age + 0.91 \times edema + 0.73 \times bili - 0.79 \times albumin + 0.38 \times copper + 2.69 \times protime)$

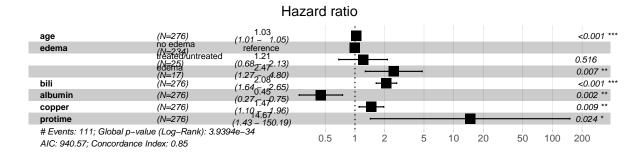


Figure 7: Forest plot of estimated model

- Blood clotting time (*protime*) has an HR of 14.67, indicating bleeding will considerably increase the risk of death for PBC patients. A higher level of urine copper and serum bilirubin, edema, and older age will all increase the risk; whereas a higher level of serum albumin will decrease the risk, which corresponds well to the current clinical study.
- The estimated model excludes treatment method and sex as they all failed the significance test in the full model. This confirms the KM estimator of DPCA's irrelevance with PBC patients' survival time but delivers a different result for sex since in the KM estimator the survival curves have a significant difference.

4. Summary

The analysis focuses on 276 complete cases of PBC and use both the KM and Cox PH model to estimate the survival function and the hazard function. The result shows that treatment with DPCA does not have a significant effect on patients' survival time. The model selected by backward AIC explains that a higher age, a higher level of urine copper and serum bilirubin, having edema will increase the risk and a higher level of serum bilirubin

will decrease the risk. To expand data modeling, we can train a random forest or construct parametric models to compare with the explainability of Cox PH model.

Appendix

AIC: The Akaike information criterion (AIC) is an estimator of prediction error and thereby relative quality of statistical models for a given dataset. It deals with the trade-off between the goodness of fit of the model and the simplicity of the model and provides a means for model selection. Let k be the number of estimated parameters in the model, and \hat{L} be the maximum value of the likelihood function for the model: AIC = $2k - 2\ln(\hat{L})$.

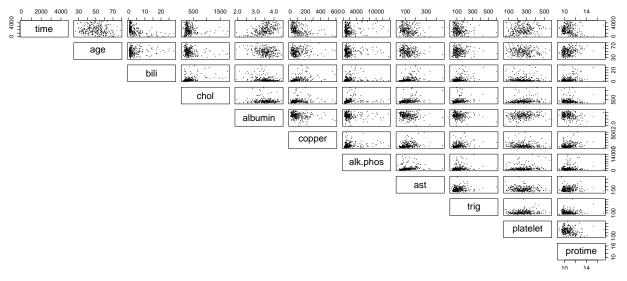


Figure 8: Paired plots

Variable	Type	Description
id	N/A	case number, discard in analysis
time	Quant.	response variable, number of days between registration & earlier status
status	Qual.	0=alive, 1=dead
trt	Qual.	treatment, 0=DPCA, 1=placebo
age	Quant.	patient's age in years at registration
sex	Qual.	patient's sex, m=male, f=female
ascites	Qual.	presence of ascites, 0=No, 1=Yes
hepato	Qual.	presence of hepatomegaly, 0=No, 1=Yes
spiders	Qual.	blood vessel malformations in the skin, 0=No, 1=Yes
edema	Qual.	0=no edema, 0.5=untreated/successfully treated, 1=edema despite diuretic therapy
bili	Quant.	serum bilirunbin (mg/dl)
copper	Quant.	urine copper (ug/day)
chol	Quant.	serum cholesterol (mg/dl)
albumin	Quant.	serum albumin (g/dl)
alk.phos	Quant.	alkaline phosphotase (U/liter)
ast	Quant.	aspartate aminotransferase, or SGOT (U/ml)
trig	Quant.	triglycerides (mg/dl)
platelet	Quant.	platelet count
protime	Quant.	standardized blood clotting time
stage	Qual.	histologic stage of disease (biopsy)

Table 7: Table of variables