

**8. Introduction to Survival Analysis**  
**Illustration – *Stata Users***  
*Spring 2020*

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**1. Illustration**  
**DPCA Study of Primary Biliary Cirrhosis**

**Preliminary – Download from the course website stata data set [pbc.dta](#).**

**DPCA Study of Primary Biliary Cirrhosis**

*source:*

Dickson ER, Grambsch PM and Fleming TR (1989) Prognosis in primary biliary-cirrhosis - model for decision making. *Hepatology*, **10**, 1-7.

**Introduction.**

Bile is a fluid produced in your liver which functions in the digestion of food and, in aids in ridding your body of worn-out red blood cells, cholesterol and toxins. The disease primary biliary cirrhosis is an autoimmune disease in which the body turns against its own cells, in this case bile ducts. As the bile ducts are increasingly damaged, harmful substances can accumulate. This can lead to irreversible scarring of liver tissue (this is cirrhosis). Among other things, the sufferer can experience abdominal pain, internal bleeding and, ultimately, liver failure. Primary biliary cirrhosis is also a risk factor for liver cancer.

This illustration utilizes data from a randomized controlled trial of D-penicillamine (DPCA) for the treatment of primary biliary cirrhosis. A total of n=312 consenting subjects were enrolled and randomized to either active treatment or placebo-control (presumably this group received standard care). Time zero is date of diagnosis and initiation of treatment. Study participants were followed to event of end-stage liver disease or censoring. Thus, these are an example of “right” censored data. Over the approximate 10 years of follow-up, 125 events of death (40%) were observed.

The goal of these analyses was to assess the benefit of randomization to DPCA on survival, overall and after adjustment for selected, important, covariates.

**Data Dictionary/Coding Manual.**

This illustration utilizes the following variables in pbc.dta.

Variable	Codings	Label
<a href="#">years</a>	Continuous (range: 0.11 – 12.47)	Time to death (in years)
<a href="#">status</a>	1 = dead    0 = censored	Event/censoring indicator
<a href="#">rx</a>	1 = DPCA    0 = Control	Treatment/randomization
<a href="#">histol</a>	1=lowest, 2, 3, 4=highest	Severity of liver damage at dx
<a href="#">bilirubin</a>	Continuous, mg/dl	Serum bilirubin

2. Prepare Data for Survival Analysis

```
. use "/Users/cbigelow/Desktop/psc.dta"
(PBC Natural Hx Data)
```

```
. * Check data set (variables of interest only)
. codebook years status rx histol bilirubin, compact
```

Variable	Obs	Unique	Mean	Min	Max	Label
years	312	301	5.49312	.1122519	12.47365	Time to Death (in Years)
status	312	2	.400641	0	1	Alive/Dead
rx	312	2	.4935897	0	1	treatment
histol	312	4	3.032051	1	4	Histologic stage of disease
bilirubin	312	85	3.25609	.3	28	Serum Bilirubin in mg/dl

```
. * ---- Declare Data to be Survival Data -----*
. * Time to event: years
. * Censoring: status (1=dead, 0=censored)
. * Command is stset TIMETOEVENT, failure(CENSORVARIABLE)
```

```
. stset years, failure(status)

      failure event:  status != 0 & status < .
obs. time interval:  (0, years]
exit on or before:   failure
```

```
-----+-----
      312 total observations
      0  exclusions
-----+-----
      312 observations remaining, representing
      125 failures in single-record/single-failure data
1713.854 total analysis time at risk and under observation
              at risk from t =          0
              earliest observed entry t = 0
              last observed exit t = 12.47365
```

```
. * Describe survival data using command stsum
. stsum
```

```
      failure _d:  status
analysis time _t:  years
```

	time at risk	incidence rate	no. of subjects	Survival time		
				25%	50%	75%
total	1713.853528	.0729351	312	4.071184	9.295004	.

**Interpretation:** The 25<sup>th</sup> and 50<sup>th</sup> percentiles of survival are shown. The 25<sup>th</sup> percentile is 4.07 years and says that 25% of participants have survival times less than 4.07 years. The missing value for the 75<sup>th</sup> percentile is the result of the high prevalence of censoring in this cohort.

### 3. Model Free Approaches

#### a. Descriptives

```
. * Continuous variables
. sort rx
. tabstat years bilirubin, by(rx) statistics(n mean sd min q max) columns(statistics) format(%8.2f)
longstub
```

rx	variable	N	mean	sd	min	p25	p50	p75	max
Placebo	years	158.00	5.52	3.00	0.11	3.37	5.19	7.24	12.47
	bilirubin	158.00	2.87	3.63	0.30	0.80	1.40	3.20	20.00
DPCA	years	154.00	5.47	3.16	0.14	3.15	4.96	7.59	12.38
	bilirubin	154.00	3.65	5.28	0.30	0.70	1.30	3.60	28.00
Total	years	312.00	5.49	3.08	0.11	3.26	5.04	7.40	12.47
	bilirubin	312.00	3.26	4.53	0.30	0.80	1.35	3.45	28.00

```
. * Discrete variables
. fre rx histol status
```

```
rx -- treatment
```

		Freq.	Percent	Valid	Cum.
Valid	0 Placebo	158	50.64	50.64	50.64
	1 DPCA	154	49.36	49.36	100.00
	Total	312	100.00	100.00	

```
histol -- Histologic stage of disease
```

		Freq.	Percent	Valid	Cum.
Valid	1	16	5.13	5.13	5.13
	2	67	21.47	21.47	26.60
	3	120	38.46	38.46	65.06
	4	109	34.94	34.94	100.00
	Total	312	100.00	100.00	

```
status -- Alive/Dead
```

		Freq.	Percent	Valid	Cum.
Valid	0 Censored	187	59.94	59.94	59.94
	1 Dead	125	40.06	40.06	100.00
	Total	312	100.00	100.00	

```
. tab2 rx status, row column
-> tabulation of rx by status
```

```
+-----+
| Key |
+-----+
|     |
|     |
| frequency |
| row percentage |
| column percentage |
+-----+
```

treatment	Alive/Dead		Total
	Censored	Dead	
Placebo	93	65	158
	58.86	41.14	100.00
	49.73	52.00	50.64
DPCA	94	60	154
	61.04	38.96	100.00
	50.27	48.00	49.36
Total	187	125	312
	59.94	40.06	100.00
	100.00	100.00	100.00

**Interpretation:**

Among n=158 randomized to PLACEBO, there were 65 deaths (41%)

Among n=154 randomized to active treatment DPCA, there were 60 deaths (40%)

**b. Kaplan-Meier Curve Estimation**

Note – must have previously issued command `stset` to declare data as survival data see again, page 3)

- . \* Single Group Kaplan-Meier Curve Estimation
- . \* Command is `sts list`
- . `sts list`

```
failure _d: status
analysis time _t: years
```

*Kaplan-Meier Estimates*

Time	Beg. Total	Fail	Net Lost	Survivor Function	Std. Error	[95% Conf. Int.]	
.1123	312	1	0	0.9968	0.0032	0.9775	0.9995
.1396	311	1	0	0.9936	0.0045	0.9746	0.9984
.1944	310	1	0	0.9904	0.0055	0.9705	0.9969
.2108	309	1	0	0.9872	0.0064	0.9662	0.9952

--- rows omitted ---

12.19	7	0	1	0.3406	0.0528	0.2398	0.4438
12.21	6	0	1	0.3406	0.0528	0.2398	0.4438
12.23	5	0	1	0.3406	0.0528	0.2398	0.4438
12.32	4	0	1	0.3406	0.0528	0.2398	0.4438
12.34	3	0	1	0.3406	0.0528	0.2398	0.4438
12.38	2	0	1	0.3406	0.0528	0.2398	0.4438
12.47	1	0	1	0.3406	0.0528	0.2398	0.4438

- . \* Two Group Kaplan-Meier Curve Estimation
- . \* Command is `sts list, by(GROUPVAR)` Note: Must have sorted by GROUPVAR first
- . `sort rx`
- . `sts list, by(rx)`

```
failure _d: status
analysis time _t: years
```

*Kaplan-Meier Estimates*

Time	Beg. Total	Fail	Net Lost	Survivor Function	Std. Error	[95% Conf. Int.]	
Placebo							
.1123	158	1	0	0.9937	0.0063	0.9559	0.9991
.1944	157	1	0	0.9873	0.0089	0.9503	0.9968
.3587	156	1	0	0.9810	0.0109	0.9423	0.9938
.3833	155	1	0	0.9747	0.0125	0.9340	0.9904

---- rows omitted --

DPCA							
.1396	154	1	0	0.9935	0.0065	0.9548	0.9991
.2108	153	1	0	0.9870	0.0091	0.9491	0.9967
.3012	152	1	0	0.9805	0.0111	0.9408	0.9937

---- rows omitted --

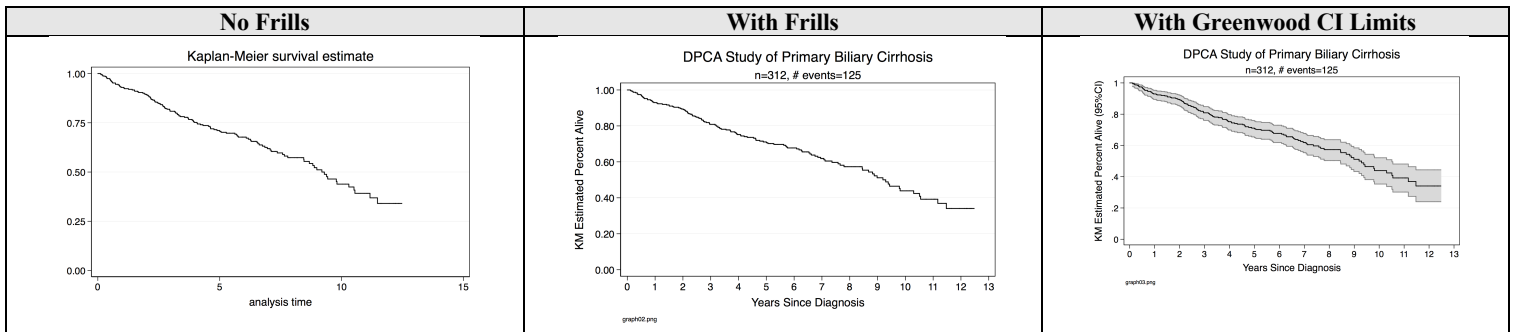
**c. Kaplan-Meier Curve Plot**

```

. * ---- Single Group: Kaplan Meier Curve ----*
. * --- no frills plot ---*
. sts graph

. * with frills --*
. sts graph, xlabel(0(1)13) ylabel(0(.20)1) xtitle("Years Since Diagnosis") ytitle("KM Estimated Percent Alive") title("DPCA Study of Primary Biliary Cirrhosis") subtitle("n=312, # events=125") caption("graph02.png", size(vsmall))

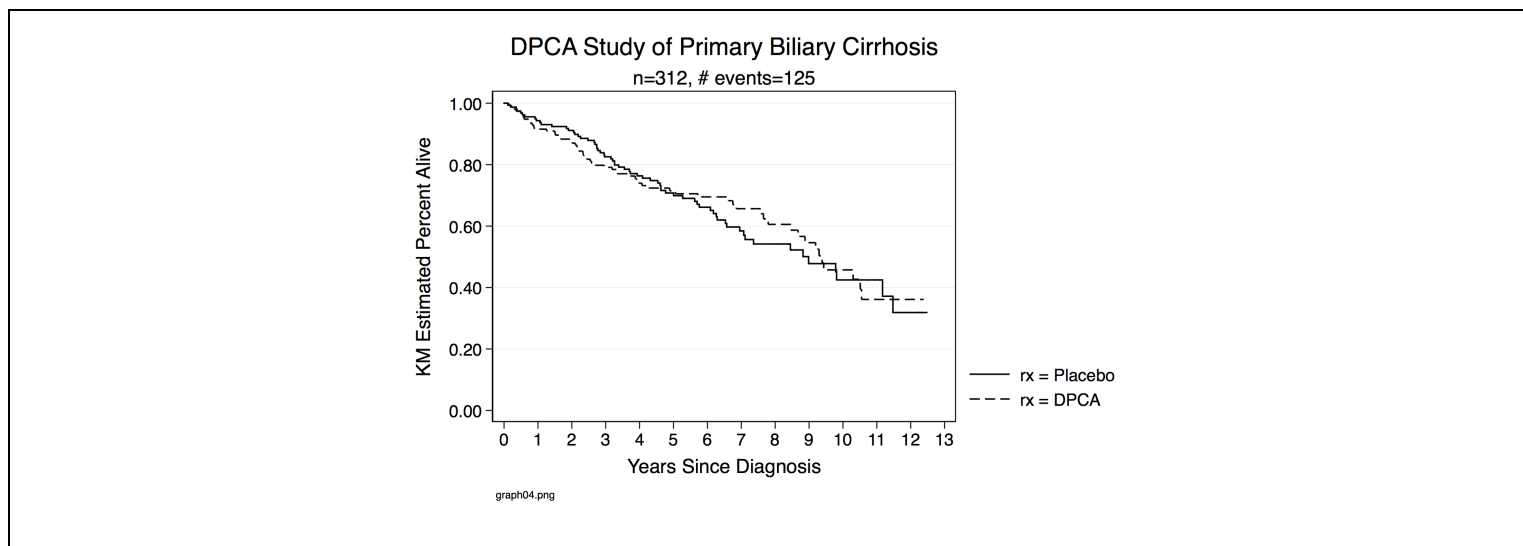
. * With Greenwood CI limits
. sts graph, gwood legend(off) xlabel(0(1)13) ylabel(0(.20)1) xtitle("Years Since Diagnosis") ytitle("KM Estimated Percent Alive (95%CI)") title("DPCA Study of Primary Biliary Cirrhosis") subtitle("n=312, # events=125") caption("graph03.png", size(vsmall))
    
```



```

. * Two Group Kaplan-Meier Curve Estimation
. * Command is sts graph, by(GROUPVAR) OPTION OPTION OPTION Note: Must have sorted by GROUPVAR first
. sort rx
. sts list, by(rx)

. * with frills ---*
. sts graph, by(rx) xlabel(0(1)13) ylabel(0(.20)1) xtitle("Years Since Diagnosis") ytitle("KM Estimated
Percent Alive") title("DPCA Study of Primary Biliary Cirrhosis") subtitle("n=312, # events=125")
caption("graph04.png", size(vsmall))
    
```



### d. Log Rank Test of Equality of Survival Distributions

```

. * ---- Log Rank Test (NULL: equality of survival distributions among rx groups)
. * Command is sts test GROUPVAR
. sts test rx

      failure _d: status
      analysis time _t: years
    
```

Log-rank test for equality of survivor functions

rx	Events observed	Events expected
Placebo	65	63.22
DPCA	60	61.78
Total	125	125.00

chi2(1) = 0.10  
 Pr>chi2 = 0.7498

**Interpretation:** Do NOT reject. Assumption of the null hypothesis has NOT led to an unlikely result (p-value = .75). We have no statistically significant evidence that the survival distributions are not the same.



### 4. Cox PH Model Regression

Recall. The Cox PH model models the hazard of event (in this case death) at time “t” as the product of a baseline hazard times  $\exp(\text{linear model in the predictors } X_1, X_2, \dots X_p)$ . Here,  $p=3$  because we have 3 predictors of interest:

$$h(t; X_1, \dots, X_p) = h_0(t) \exp[\beta_1 X_1 + \dots + \beta_p X_p]$$

- $X_1 = \mathbf{rx}$ , 0/1 indicator of randomization
- $X_2 = \mathbf{histol}$ , ordinal measure of degree of tissue damage at diagnosis
- $X_3 = \mathbf{bilirubin}$ , continuous (mg/dl)

Note. The predictor **histol** is an ordinal predictor. So we will need to replace it with appropriately defined design variables prior to modeling.

#### a. Fit Cox PH Model

```
. * Single Predictor Model: rx (User coded as 0/1 already)
. stcox rx
```

Cox regression -- Breslow method for ties

```
No. of subjects =          312          Number of obs   =          312
No. of failures =           125
Time at risk   = 1713.853528
Log likelihood = -639.92903          LR chi2(1)       =           0.10
                                          Prob > chi2     =           0.7498
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]
rx	.9444768	.1692173	-0.32	0.750	.6647918 1.341828

**Interpretation:** Relative to control patients, patients treated with DPCA have lower hazard of death (HR = .94) at all times of follow-up. This very small benefit is not statistically significant (p-value = .75). Notice that the 95% CI for the HR includes the null value of 1.

```
. * Single Predictor Model: rx (Stata defined design variable)
. stcox i.rx
```

Cox regression -- Breslow method for ties

```
No. of subjects =          312          Number of obs   =          312
No. of failures =           125
Time at risk   = 1713.853528
Log likelihood = -639.92903          LR chi2(1)       =           0.10
                                          Prob > chi2     =           0.7498
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]
rx DPCA	.9444768	.1692173	-0.32	0.750	.6647918 1.341828

**Interpretation:** SAME. Relative to control patients, patients treated with DPCA have lower hazard of death (HR = .94) at all times of follow-up. This very small benefit is not statistically significant (p-value = .75). Notice that the 95% CI for the HR includes the null value of 1.

```
. * Single Predictor Model:  histol (user created design variables)
. generate histol2=0
. replace histol2=1 if histol==2
(67 real changes made)

. generate histol3=0
. replace histol3=1 if histol==3
(120 real changes made)

. generate histol4=0
. replace histol4=1 if histol==4
(109 real changes made)

. stcox histol2 histol3 histol4

      failure _d:  status
      analysis time _t:  years

Cox regression -- Breslow method for ties

No. of subjects =          312          Number of obs   =          312
No. of failures =           125
Time at risk   = 1713.853528
Log likelihood = -613.62114          LR chi2(3)       =          52.72
                                          Prob > chi2     =          0.0000

-----+-----
      _t | Haz. Ratio  Std. Err.      z    P>|z|     [95% Conf. Interval]
-----+-----
      histol2 |  4.987976   5.143153    1.56  0.119    .6610611   37.63631
      histol3 |  8.580321   8.685371    2.12  0.034    1.179996   62.39165
      histol4 | 21.38031   21.57046    3.04  0.002    2.959663   154.4493
-----+-----
```

**Interpretation:** Recall. Higher score on histol (valid scores = 1, 2, 3, 4) represent greater level of liver tissue damage present at diagnosis. This model shows that higher (“worse”) values of histol at diagnosis are associated with poorer prognosis (Hazard ratio estimates increase from 1 to 4.98 to 8.58 to 21.4, relative to the referent group histol=1). This is highly statistically significant. Caveat: Note that the confidence intervals are wide.

```
. * Single Predictor Model:  histol (Stata generated design variables)
. stcox i.histol

      failure _d:  status
      analysis time _t:  years

Cox regression -- Breslow method for ties

No. of subjects =          312          Number of obs   =          312
No. of failures =           125
Time at risk   = 1713.853528
Log likelihood = -613.62114          LR chi2(3)       =          52.72
                                          Prob > chi2     =          0.0000

-----+-----
      _t | Haz. Ratio  Std. Err.      z    P>|z|     [95% Conf. Interval]
-----+-----
      histol
      2 |  4.987976   5.143153    1.56  0.119    .6610611   37.63631
      3 |  8.580321   8.685371    2.12  0.034    1.179996   62.39165
      4 | 21.38031   21.57046    3.04  0.002    2.959663   154.4493
-----+-----
```

**Interpretation:** SAME. Higher (“worse”) values of histol at diagnosis are associated with poorer prognosis (Hazard ratio estimates increase from 1 to 4.98 to 8.58 to 21.4, relative to the referent group histol=1). This is highly statistically significant. Caveat: Note that the confidence intervals are wide.

```
. * Single Predictor Model: bilirubin
. stcox bilirubin
```

```
failure _d: status
analysis time _t: years
```

```
Iteration 0: log likelihood = -639.97989
Iteration 1: log likelihood = -611.85115
Iteration 2: log likelihood = -597.6878
Iteration 3: log likelihood = -597.6845
Refining estimates:
Iteration 0: log likelihood = -597.6845
```

Cox regression -- Breslow method for ties

```
No. of subjects =          312          Number of obs   =          312
No. of failures =           125
Time at risk   = 1713.853528
Log likelihood = -597.6845
LR chi2(1)     =           84.59
Prob > chi2    =           0.0000
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]
bilirubin	1.160509	.0151044	11.44	0.000	1.131279 1.190494

**Interpretation:** Associated with each 1 unit (1 mg/dl) increase in bilirubin is an increased risk of death at all times of follow-up (HR = 1.16, 95% CI = 1.13 – 1.19). This is highly statistically significant (p-value << .0001).

```
. * Use option nohr to obtain betas instead of hazard ratios
. stcox bilirubin, nohr
```

```
failure _d: status
analysis time _t: years
```

Cox regression -- Breslow method for ties

```
No. of subjects =          312          Number of obs   =          312
No. of failures =           125
Time at risk   = 1713.853528
Log likelihood = -597.6845
LR chi2(1)     =           84.59
Prob > chi2    =           0.0000
```

_t	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
bilirubin	.1488587	.0130153	11.44	0.000	.1233492 .1743683

## b. Multivariable Model Development

```
. *----- LR Tests -----*
```

```
. * --- rx controlling for histol -----*
```

```
. quietly: stcox i.histol
. eststo model_histol
```

```
. quietly: stcox i.histol i.rx
. eststo model_histolrx
```

```
. lrtest model_histol model_histolrx
```

```
Likelihood-ratio test          LR chi2(1) =      0.67
(Assumption: model_histol nested in model_histolrx)  Prob > chi2 = 0.4138
```

**Interpretation:** Do not reject. After adjustment for histol, randomization to DPCA is NOT associated with survival (LR Test p-value = .41)

```
. * --- rx controlling for bilirubin -----*
```

```
. quietly: stcox bilirubin
. eststo model_bili
```

```
. quietly: stcox bilirubin i.rx
. eststo model_bilirx
```

```
. lrtest model_bili model_bilirx
```

```
Likelihood-ratio test          LR chi2(1) =      1.20
(Assumption: model_bili nested in model_bilirx)      Prob > chi2 = 0.2732
```

**Interpretation:** Do not reject. After adjustment for bilirubin, randomization to DPCA is NOT associated with survival (LR Test p-value = .27)

```
. * --- rx controlling for both histol and bilirubin
```

```
. quietly: stcox i.histol bilirubin
. eststo model_both
```

```
. quietly: stcox i.histol bilirubin i.rx
. eststo model_bothrx
```

```
. lrtest model_both model_bothrx
```

```
Likelihood-ratio test          LR chi2(1) =      0.76
(Assumption: model_both nested in model_bothrx)      Prob > chi2 = 0.3837
```

**Interpretation:** Do not reject. After adjustment for both histol and bilirubin, randomization to DPCA is NOT associated with survival (LR Test p-value = .38)

## c. Side-by-side Comparison of Models

```
. quietly: stcox i.rx
. eststo model1
```

```
. quietly: stcox bilirubin i.rx
. eststo model2
```

```
. quietly: stcox i.histol i.rx
. eststo model3
```

```
. quietly: stcox bilirubin i.histol i.rx
. eststo model4
```

```
. * Display Betas and Summary Statistics
. estout model1 model2 model3 model4, stats(n chi2 bic, star(chi2)) prehead("Betas")
```

Betas

	model1	model2	model3	model4
	b	b	b	b
0b.rx	0	0	0	0
1.rx	-.0571242	-.2006959	-.1469394	-.1579999
bilirubin		.1513976		.1475188
1b.histol			0	0
2.histol			1.628527	1.52564
3.histol			2.176732	1.92305
4.histol			3.09258	2.796094
n				
chi2	.1017198	85.79155***	53.38545***	127.504***
bic	1285.601	1205.654	1249.546	1181.171

**KEY:**  
 Chi2 = Value of LR test comparing the model fit (“full”) to intercept only (“reduced”)  
 bic = Schwarz’ Bayesian Information Criterion = It is a function of the log-likelihood. Smaller values indicate a better fit.

```
. * Display Hazard Ratios and Model Fit Statistics. Option eform produces hazard ratios *
. estout model1 model2 model3 model4, eform stats(n chi2 bic, star(chi2)) prehead("Hazard Ratios")
```

Hazard Ratios

	model1	model2	model3	model4
	b	b	b	b
0b.rx	1	1	1	1
1.rx	.9444768	.8181612	.8633463	.8538499
bilirubin		1.163459		1.158955
1b.histol			1	1
2.histol			5.096362	4.598085
3.histol			8.817444	6.841793
4.histol			22.03384	16.38054
n				
chi2	.1017198	85.79155***	53.38545***	127.504***
bic	1285.601	1205.654	1249.546	1181.171

### 5. Regression Diagnostics for Cox PH Model

#### a. Test of Proportional Hazards

```
. * Test of proportional hazards
. quietly: stcox bilirubin i.histol i.rx
. estat phtest, detail
```

Test of proportional-hazards assumption

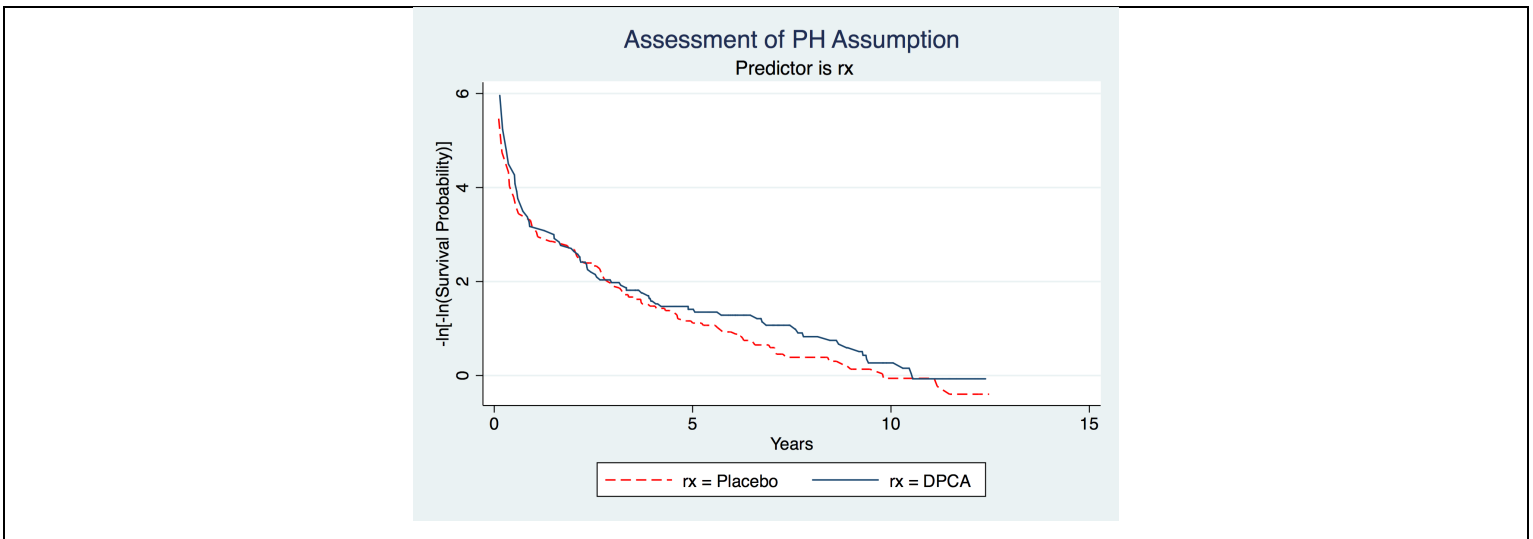
Time: Time

	rho	chi2	df	Prob>chi2
bilirubin	0.09686	0.88	1	0.3485
1b.histol	.	.	1	.
2.histol	0.01775	0.04	1	0.8424
3.histol	0.00187	0.00	1	0.9834
4.histol	-0.04811	0.29	1	0.5914
0b.rx	.	.	1	.
1.rx	-0.09026	0.99	1	0.3204
global test		13.19	5	0.0216

**Interpretation:** The global test is significant (p-value = .02) ... but ....  
 For each predictor, do not reject the assumption of proportional hazards

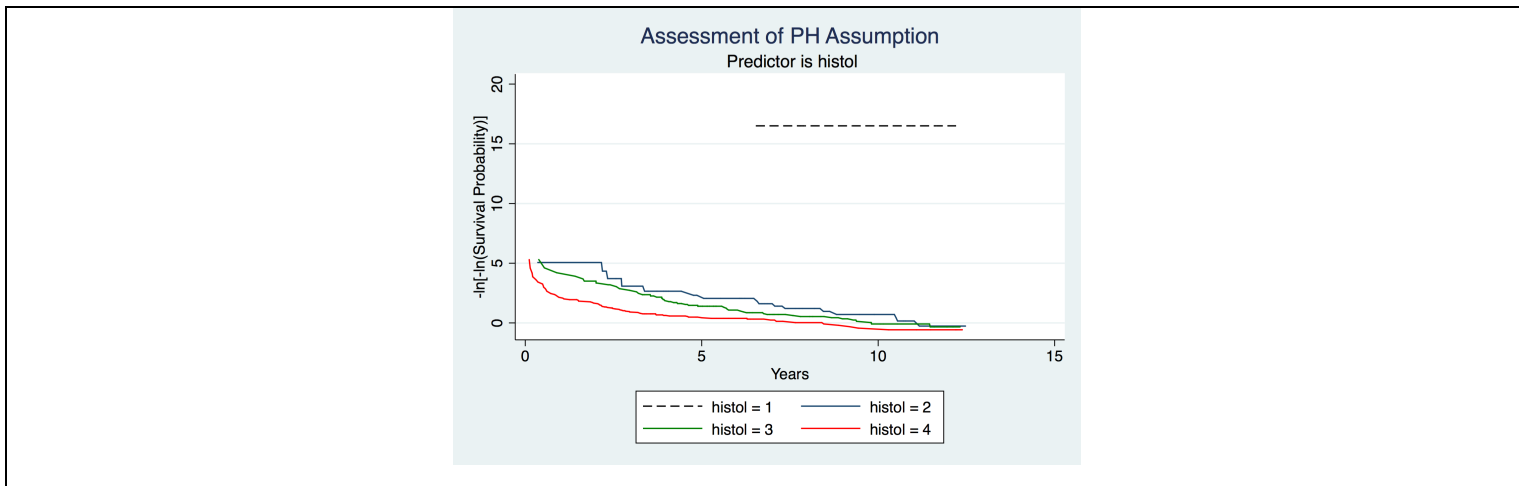
#### b. Graphical Assessment of Proportional Hazards

```
. * Assessment of PH Assumption: Randomization/Treatment
. stphtest, by(rx) adjust(bilirubin histol) noltime plotlopts(symbol(none) color(red) lpattern(dash))
plot2opts(symbol(none) color(navy)) title("Assessment of PH Assumption") subtitle(" Predictor is rx") xtitle("Years")
```



**Interpretation:** Looks reasonable.  
**Note:** adjust(bilirubin histol) tells Stata to set these variables to their mean values  
 The option noltime tells Stata to plot time on the horizontal, not the logarithm of time.

```
. * Assessment of PH Assumption: Histol
. sthplot, by(histol) adjust(bilirubin rx) noltime plotlopts(symbol(none) color(black) lpattern(dash)) plot2opts(
symbol(none) color(navy)) plot3opts(symbol(none) color(green)) plot4opts(symbol(none) color(red)) title("Assessment of
PH Assumption") subtitle(" Predictor is histol") xtitle("Years")
```



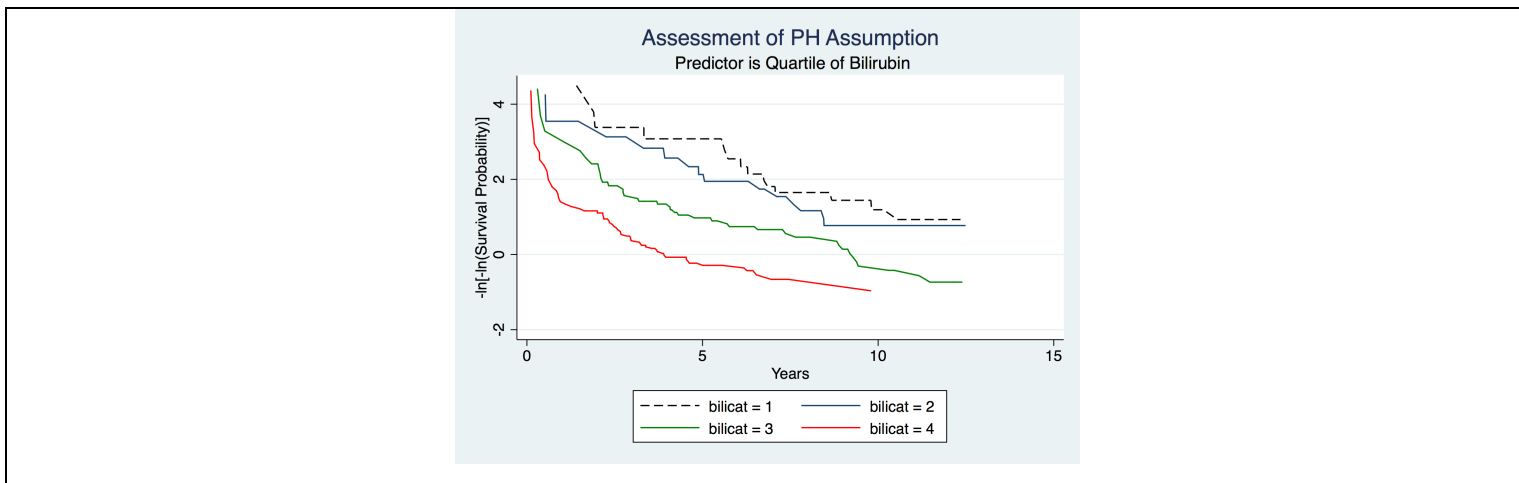
**Interpretation:** Looks reasonable, except for the group, histol=1. I checked on this (not shown); there was just 1 death in this group

```
. * Assessment of PH Assumption: Bilirubin, using Quartile Groupings
. centile bilirubin, c(25,50,75)
```

Variable	Obs	Percentile	Centile	-- Binom. Interp. -- [95% Conf. Interval]	
bilirubin	312	25	.8	.7	.9
		50	1.35	1.2	1.8
		75	3.475	3.12635	4.5

```
. generate bilicat=bilirubin
. recode bilicat (min/0.8=1) (0.81/1.35=2) (1.351/3.475=3) (3.4751/max=4) if bilirubin !=.
(bilicat: 307 changes made)
```

```
. sthplot, by(bilicat) adjust(rx) noltime plotlopts(symbol(none) color(black) lpattern(dash)) plot2opts(symbol(none)
color(navy)) plot3opts(symbol(none) color(green)) plot4opts(symbol(none) color(red)) title("Assessment of PH
Assumption") subtitle(" Predictor is Quartile of Bilirubin") xtitle("Years")
```



**Interpretation:** Looks reasonable.

**c. Test of Overall Goodness of Fit**

Note #1. This test utilizes a command **stcoxgof** that must be downloaded from the internet

Note #2. The command **stcoxgof** will not work with factor variables. Therefore, in fitting my model, I replaced **histol** with the 0/1 indicators of levels 2, 3, and 4. See again page 10.

Note #3. The command **stcoxgof** also requires that you have saved thie martingale residuals. This is accomplished with the option **mgale(NAMEYOU PROVIDE)**

```
. findit stcoxgof
```

```
----- not shown: Downloading of stcoxgof -----
```

```
. stcox bilirubin histol2 histol3 histol4 rx, mgale(mgale)
```

```
. stcoxgof
```

```
Goodness-of-fit test for the inclusion of design variables based on 3 quantiles of risk
(Added variables version of the Groennesby and Borgan test)
```

```
Score test                chi2(2)    =    2.318
                          Prob > chi2 =    0.3137
```

```
Likelihood-ratio test    LR chi2(2) =    2.356
                          Prob > chi2 =    0.3079
```

```
(Table collapsed on quantiles of linear predictor)
```

Quantile of Risk	Observed	Expected	z	p-Norm	Observations
1	19	22.87	-.809	.418	108
2	36	34.409	.271	.786	102
3	70	67.721	.277	.782	102
Total	125	125			312

**Interpretation:** Good. Do not reject. We do not have statistically significant evidence of a poor fit (p-value = .31).

**Caveat:** It is quite possible that that additional regression diagnostics will reveal issues!