# **Biostatistics in Research Practice**

# **Exercise: Analysis of the VenUS I trial in Stata 9**

In this exercise we shall explore some of the functions which Stata provides for the analysis of time to event data. The data come from the VenUS I trial of four layer elastic bandaging for venous leg ulcers. Load the file, venusi.dta, and start Stata.

# **Date functions**

Inspect the file. You will see that there are the following variables:

1.	id	Identity code
2.	centre	Centre Code
3.	arm	Treatment arm
4.	sex	Sex
5.	duration	Duration of ulcer
6.	episodes	Previous episodes of ulceration
7.	mobility	Mobility
8.	ankcirc	Ankle circumference
9.	area	Area of ulcer (sq cm)
10.	age	Age
11.	heal_dat	Healing date
12.	entrance	Entrance date
13.	last_dat	Last date

To carry out the analysis, we need two variables: the time from trial entrance to healing or censoring, and a variable which says whether the patient has healed or has been censored.

This is easy in Stata. The dates are already in date format, so we can just subtract one from another to get the time difference in days. We will first compute the difference between healing data and entrance date in days, which we will call time1. You should have:

```
gen time1 = heal_dat - entrance
```

Now repeat this to get the number of days from entrance to the last date. Make variable

gen time2 = last\_dat - entrance

Have a look at **time1** and **time2**. We need to combine them to make a third time variable, which we can call **time**. This will be the time to the event (healing) or the last time seen, whichever is earlier. If there is a healing date, the patient healed and **time = time1**. If healing date is missing, the patient did not heal and **time = time2**. To do this, you can make **time = time1** then replace **time** by **time2** if **time1** is missing.

```
gen time = time1
replace time = time2 if time1 == .
```

Note the double "==" for "is equal to". A single "=" means "make equal to". Note the "." for missing data. I labelled this variable "**Time to healing (days)**":

label var time "Time to healing (days)"

We could also have generated time more efficiently by

```
gen time = heal_dat - entrance
replace time = last_dat - entrance if time1 == .
```

Have a look at the dates and times. Try case number 9, Id = 1022. The dates are 10 Jun 99 to 24 Jun 99, which I would think of as a difference of 14 days. Variable **time** = 13.50269 days. I don't know why Stata does this, but we shall round them up:

replace time = int(time + 1)

to make the analysis consistent with that published. "int" is the integer part function, so for case number 9 we add 1 to give 14.50269 then chop of the fractional part to give 14.

# Healed or censored?

Finally, we will need a variable for status, healed or censored. We want all non-missing **time1** subjects to have **status** = 1, healed, and all missing **time1** subjects to have **status** = 0, not healed or censored.

gen status = 1

replace status = 0 if time1 == .

# Kaplan Meier survival estimates

In Stata 9, there is a special set of commands for survival analysis. They start with "st" for "survival times". To see them, try:

help st

To use them, we have to tell Stata what the survival time and outcome variables are. The command is:

```
stset time, failure(status)
```

Note the warning about "1 obs. end on or before enter()". This tells us that one observation has a zero or negative survival time. To see what this is, you could try:

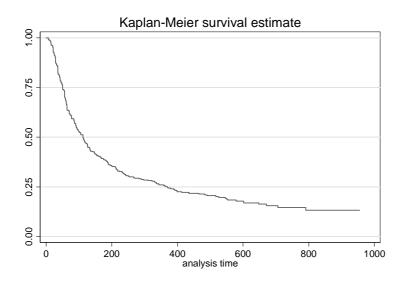
list if time<=0

This will show that case number 28, Id = 1062, was only seen on the entrance date. This subject will contribute nothing to the analysis and we can ignore it.

We can now do the Kaplan Meier analysis. This is done using the sts command. Just type st:

sts

You will get a Kaplan Meier curve for the whole dataset:



I had used

#### set scheme s1mono

so that I could print this. You might like

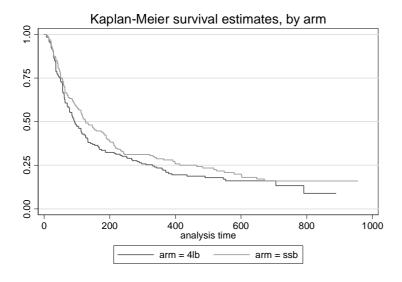
### set scheme s1color

better on the screen. We get exactly the same by

### sts graph

We can get the survival curves for each treatment arm by

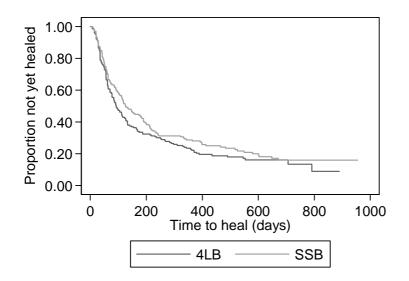
### sts graph, by(arm)



This can be improved quite a lot. We can relabel the horizontal axis, label the vertical axis, change the number interval, make the numbers horizontal, remove the grid lines, remove the title, change the legend, and make the text bigger:

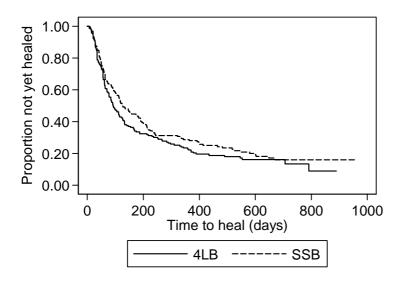
# sts graph, by(arm) xtitle("Time to heal (days)") ytitle(Proportion not yet healed) ylabel(0 (0.2) 1, angle(horiz) nogrid) title("") legend(order(1 2) label(1 "4LB") label(2 "SSB")) scale(1.5)

Of course, this command all goes on one line. The options are all standard graph options, apart from "by(arm)". We get:



For printing, it is often better to make one curve dashed and make them both black:

```
sts graph, by(arm) clpattern(solid dash) clcolor(black
black) xtitle("Time to heal (days)") ytitle(Proportion
not yet healed) ylabel(0 (0.2) 1, angle(horiz) nogrid)
title("") legend(order(1 2) label(1 "4LB") label(2
"SSB")) scale(1.5)
```

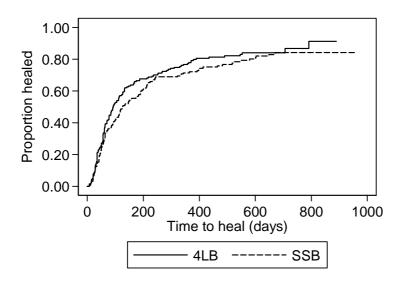


We add "clpattern(solid dash) clcolor(black black)" because the lines are connect lines ("cl"). We have to set colour and pattern for both of them. (Of course, Stata speaks American and likes "color", not "colour". Barbarians, or sensible, whichever you like.)

We can get the proportion healed instead of the proportion yet to heal using the "failure" option:

```
sts graph, by(arm) failure clpattern(solid dash)
clcolor(black black) xtitle("Time to heal (days)")
ytitle(Proportion healed) ylabel(0 (0.2) 1, angle(horiz)
nogrid) title("") legend(order(1 2) label(1 "4LB")
label(2 "SSB")) scale(1.5)
```

We get:



It is "failure" of course because this is called the failure function, though for us healing is a success.

### Log-rank test

We can test the null hypothesis that the two treatments are the same using a log-rank test. This is also done using sts:

sts test arm

You should get:

```
. sts test arm
```

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

Log-rank test for equality of survivor functions

	Events	Events
arm	observed	expected
41b ssb	154 144	140.86 157.14
Total	298	298.00
	chi2(1) Pr>chi2	= 2.35 = 0.1250

The sts command will also give you all the survival estimates at every time, Greenwood confidence bounds, etc., as options.

### **Cox regression**

Carry out Cox regression of survival on treatment arm and area of ulcer. You can do this by the stcox command:

### stcox arm area

This gives:

```
. stcox arm area
         failure _d: status
   analysis time _t: time
Iteration 0: log likelihood = -1566.596
Iteration 1: log likelihood = -1553.6348
Iteration 2: log likelihood = -1548.8007
Iteration 3: log likelihood = -1547.6302
Iteration 4: log likelihood = -1547.574
Iteration 5: log likelihood = -1547.5738
Refining estimates:
Iteration 0: log likelihood = -1547.5738
Cox regression -- Breslow method for ties
                                                    Number of obs =
No. of subjects =
                            385
                                                                             385
                         -
298
No. of failures =
Time at risk = 76522
                                                   LR chi2(2) = 38.04
Prob > chi2 = 0.0000
Log likelihood = -1547.5738
```

	Haz. Ratio			1 1	[95% Conf.	Interval]
arm	.7931181 .9733582	.0922428	-1.99	0.046	.6314512 .9611442	

The hazard ratio for **arm** tells us that treatment arm changing from 0 (4LB) to 1 (SSB) reduces the probability of healing on any given day by a factor 0.793. Alternatively, treatment arm changing from 1 (SSB) to 0 (4LB) increases the probability of healing on any given day by a factor 1/0.793 = 1.26. The difference is significant, just.

We could get the hazard ratio the other way up by recoding the **arm** variable to 1 for SSB and 2 for 4LB. I made a new variable, arm2 = 2 - arm:

gen arm2 = 2 - arm

stcox arm2 area

We get:

. stcox arm2 area failure \_d: status analysis time \_t: time Iteration 0: log likelihood = -1566.596 Iteration 1: log likelihood = -1553.6348 Iteration 2: log likelihood = -1548.8007 Iteration 3: log likelihood = -1547.6302 Iteration 4: log likelihood = -1547.574 Iteration 5: log likelihood = -1547.5738 Refining estimates: Iteration 0: log likelihood = -1547.5738 Cox regression -- Breslow method for ties 385 298 Number of obs = 385 No. of subjects = No. of subjects = 385 No. of failures = 298 Time at risk = 76522 LR chi2(2) = 38.04 Prob > chi2 Log likelihood = -1547.5738 0.0000 = \_\_\_\_\_ \_t | Haz. Ratio Std. Err. z P>|z| [95% Conf. Interval] \_\_\_\_\_+ arm21.260846.14664141.990.0461.0038391.583654area.9733582.0062712-4.190.000.9611442.9857274 \_\_\_\_\_

We can also include other variables. In a multicentre trial, it is usual to include the centre as a predictor. We can add **centre** to the covariates. Centre is categorical, so we have to create some dummy variables. In Stata, we can do this using the "xi:" (interaction expansion) command:

### xi: stcox arm area i.centre

The "xi:" tells Stata to create the dummy variables and the "i." tells it for which variable these are to be created. We get:

```
. xi: stcox arm area i.centre
i.centre __Icentre_1-9 (naturally coded; _Icentre_1 omitted)
failure _d: status
analysis time _t: time
```

Iteration 0:	5					
Iteration 1:	-					
Iteration 2:	log likeliho					
Iteration 3:	-					
Iteration 4:	-					
Iteration 5: log likelihood = -1530.4617						
Refining estimates:						
Iteration 0:	log likeliho	pod = -1530.	4617			
Cox regression	n Breslow n	method for t	ies			
No. of subject	ts =	385		Numbe	er of obs =	385
No. of failure						
Time at risk	= 76	5522				
					ni2(10) =	
Ten lileslikess	1	4 < 1 1		<b>D</b> 1	1 1 0	0 0000
LOG IIKEIINOOC	d = -1530.4	461/		Prob	> chi2 =	0.0000
Log likelinood	d = -1530.4	461/		Prob	> CN12 =	0.0000
			 Z			
	1 = -1530.4    Haz. Ratio +		Z			
t		Std. Err.		P> z	[95% Conf.	Interval]
t t arm	Haz. Ratio	Std. Err.	-2.42	P> z  0.016	[95% Conf. .5951721	Interval] .9472438
t t arm area	Haz. Ratio +	Std. Err. .0890128 .0059162	 -2.42 -3.86	P> z  0.016 0.000	[95% Conf. .5951721 .9653649	Interval] .9472438 .9885567
t arm area Icentre_2	Haz. Ratio +	Std. Err. .0890128 .0059162 .2033215	-2.42 -3.86 1.58	P> z  0.016 0.000 0.115	[95% Conf. .5951721 .9653649 .9408501	Interval] .9472438 .9885567 1.750724
t arm area _Icentre_2 _Icentre_3 _Icentre_4	Haz. Ratio   .7508482   .976892   1.283421   2.465417   1.323886	Std. Err. .0890128 .0059162 .2033215 .4210099 .3058625	-2.42 -3.86 1.58 5.28 1.21	<pre>P&gt; z  0.016 0.000 0.115 0.000 0.225</pre>	[95% Conf. .5951721 .9653649 .9408501 1.764144 .8417711	Interval] .9472438 .9885567 1.750724 3.445457 2.082126
t arm area _Icentre_2 _Icentre_3 _Icentre_4	Haz. Ratio 	Std. Err. .0890128 .0059162 .2033215 .4210099 .3058625	-2.42 -3.86 1.58 5.28 1.21	<pre>P&gt; z  0.016 0.000 0.115 0.000 0.225</pre>	[95% Conf. .5951721 .9653649 .9408501 1.764144 .8417711	Interval] .9472438 .9885567 1.750724 3.445457 2.082126
t arm area _Icentre_2 _Icentre_3 _Icentre_4 _Icentre_5 _Icentre_6	Haz. Ratio .7508482 .976892 1.283421 2.465417 1.323886 1.112807 .9018402	Std. Err. .0890128 .0059162 .2033215 .4210099 .3058625 .2742678 .2931813	-2.42 -3.86 1.58 5.28 1.21 0.43 -0.32	<pre>P&gt; z  0.016 0.000 0.115 0.000 0.225 0.665 0.751</pre>	[95% Conf. .5951721 .9653649 .9408501 1.764144 .8417711 .6864809 .4768816	Interval] .9472438 .9885567 1.750724 3.445457 2.082126 1.803894 1.705488
t arm area _Icentre_2 _Icentre_3 _Icentre_4 _Icentre_5 _Icentre_6	Haz. Ratio .7508482 .976892 1.283421 2.465417 1.323886 1.112807 .9018402	Std. Err. .0890128 .0059162 .2033215 .4210099 .3058625 .2742678 .2931813	-2.42 -3.86 1.58 5.28 1.21 0.43 -0.32	<pre>P&gt; z  0.016 0.000 0.115 0.000 0.225 0.665 0.751</pre>	[95% Conf. .5951721 .9653649 .9408501 1.764144 .8417711 .6864809 .4768816	Interval] .9472438 .9885567 1.750724 3.445457 2.082126 1.803894 1.705488
t arm area _Icentre_2 _Icentre_3 _Icentre_4 _Icentre_5 _Icentre_6 _Icentre_7	Haz. Ratio .7508482 .976892 1.283421 2.465417 1.323886 1.112807	Std. Err. .0890128 .0059162 .2033215 .4210099 .3058625 .2742678 .2931813 .337384	-2.42 -3.86 1.58 5.28 1.21 0.43 -0.32 -0.54	<pre>P&gt; z  0.016 0.000 0.115 0.000 0.225 0.665 0.751 0.586</pre>	[95% Conf. .5951721 .9653649 .9408501 1.764144 .8417711 .6864809 .4768816 .3447325	Interval] .9472438 .9885567 1.750724 3.445457 2.082126 1.803894 1.705488 1.825792
t arm area _Icentre_2 _Icentre_3 _Icentre_4 _Icentre_5 _Icentre_6 _Icentre_7 _Icentre_8	Haz. Ratio .7508482 .976892 1.283421 2.465417 1.323886 1.112807 .9018402 .7933536	Std. Err. .0890128 .0059162 .2033215 .4210099 .3058625 .2742678 .2931813 .337384 .3410406	-2.42 -3.86 1.58 5.28 1.21 0.43 -0.32 -0.54 -0.53	<pre>P&gt; z  0.016 0.000 0.115 0.000 0.225 0.665 0.751 0.586 0.599</pre>	[95% Conf. .5951721 .9653649 .9408501 1.764144 .8417711 .6864809 .4768816 .3447325 .3458671	Interval] .9472438 .9885567 1.750724 3.445457 2.082126 1.803894 1.705488 1.825792 1.844339

The only estimates of interest are for **area** and **arm**. The effect is to make the hazard ratio for **arm** a bit smaller, with a lower P value, and reduce the effect of area (hazard ratio closer to 1.00). This is because area is significantly related to centre, some centres had patients with worse ulcers than others.

We can put centre in as strata rather than a categorical variable. This is an option in the stcox command:

### stcox arm area, strata(centre)

We get a very slightly different estimate:

```
. stcox arm area, strata(centre)
   failure _d: status analysis time _t: time
Iteration 0: log likelihood = -1040.5622
Iteration 1: log likelihood = -1028.8549
Iteration 2: log likelihood = -1025.4944
Iteration 3:
               log likelihood = -1024.9019
Iteration 4: log likelihood = -1024.8847
Iteration 5: log likelihood = -1024.8847
Refining estimates:
Iteration 0: log likelihood = -1024.8847
Stratified Cox regr. -- Breslow method for ties
No. of subjects =
                           385
                                                    Number of obs =
                                                                            385
No. of failures =
                           298
Time at risk =
                        76522
                                                   LR chi2(2) = 31.35
Prob > chi2 = 0.0000
Log likelihood = -1024.8847
```

	Haz. Ratio					Interval]
arm	.7657379 .9771864	.0911484	-2.24	0.025	.6063992	
					Stratified	by centre

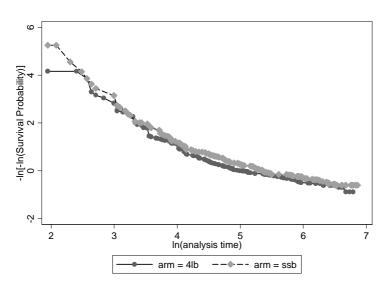
The estimate for treatment is very slightly different. I am not sure why this is, but I think that either analysis is acceptable.

# Log minus log survival

And finally, let us check the assumption of proportional hazards. This is easy in Stata. We have a command "stphplot" (survival time proportional hazards plot):

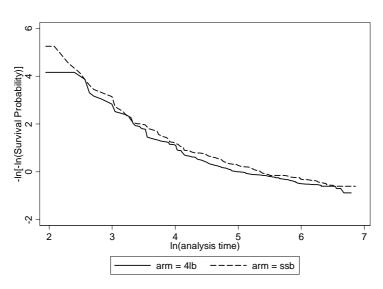
stphplot, by(arm)

We get:



We can tidy this up using all the usual graph options. For example, we can make the marker symbols invisible:

stphplot , by(arm) msymbol(i i)

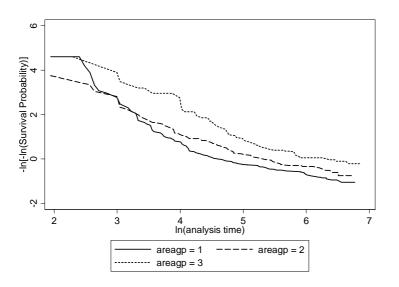


Try checking the assumption of proportional hazards for area, by creating a variable which gives are as three groups: less than  $4 \text{ cm}^2$ ,  $4 \text{ to } 8 \text{ cm}^2$ , more than  $8 \text{ cm}^2$ .

We get:

```
. gen areagp = 1 if area<4
(187 missing values generated)
. replace areagp = 2 if area>=4 & area<=8
(87 real changes made)
. replace areagp = 3 if area>8 & area !=.
(99 real changes made)
.
. stphplot, by(areagp) msymbol(i i i)
        failure _d: status
        analysis time _t: time
```

We get:



Note that second replace command include a instruction to do this only if area is not missing, because the missing data code in Stata is a very large number.

The middle line crosses the other in the same way, showing that the lines are not parallel and the proportional hazards assumption is not well met.

# Checking for change in risk over time

One further point about the analysis is the checking of the assumption that early and late entrants are the same.

We need to create a variable which shows us early and late entrants. One way do this we first order the file by entrance date:

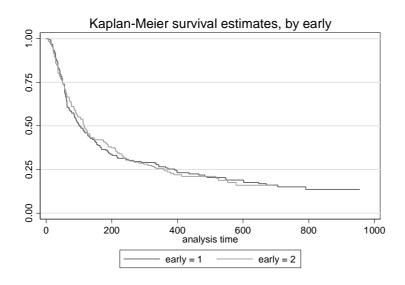
. sort entrance

We now generate a new variable:

```
. gen early = 1
. replace early= 2 if _n > 193
(194 real changes made)
```

We use 193 because there are 387 subjects, 387/2 = 193.5. Now we can draw the two curves:

```
. sts graph, by(early)
failure _d: status
analysis time _t: time
```



There appears to be little difference. We can check with a log rank test:

```
. sts test early
```

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

Log-rank test for equality of survivor functions

early	Events observed	Events expected
1   2	152 146	151.58 146.42
Total	298	298.00
	chi2(1) = Pr>chi2 =	

We could also treat time as continuous (which it is) and do Cox regression:

```
Cox regression -- Breslow method for ties
              386
No. of subjects = 386
No. of failures = 298
Time at risk = 76747
                               Number of obs =
                                            386
                               LR chi2(1) =
Prob > chi2 =
                                            0.70
Log likelihood = -1567.3585
                                           0.4017
_____
     _t | Haz. Ratio Std. Err.
                         z P>|z| [95% Conf. Interval]
entrance | 1.000315 .0003754 0.84 0.402 .9995792 1.001051
_____
                                     _____
```

Either way, there is no evidence for any effect.

If there is an effect, we can adjust for it by putting entrance date into the Cox model:

. stcox arm2 area entrance

```
failure _d: status
  analysis time _t: time
Iteration 0: log likelihood = -1566.596
Iteration 1: log likelihood = -1553.6298
Iteration 2: log likelihood = -1548.8004
             log likelihood = -1548.8004
Iteration 3: log likelihood = -1547.6302
Iteration 4: log likelihood = -1547.5739
Iteration 5: log likelihood = -1547.5738
Refining estimates:
Iteration 0: log likelihood = -1547.5738
Cox regression -- Breslow method for ties
                     385
Log 2
                                            Number of obs =
                                                                  385
                       298
                     76522
                                            LR chi2(3) =
                                                               38.04
                                            Prob > chi2
Log likelihood = -1547.5738
                                                         =
                                                               0.0000
_____
        _t | Haz. Ratio Std. Err. z P>|z| [95% Conf. Interval]
______
   arm21.260748.14743161.980.0481.0025111.585505area.9733601.0062786-4.190.000.9611318.985744entrance1.000002.00038070.010.995.99925651.000749
```

If there is an entrance time effect, this will improve the estimate of the hazard ratio, but the Kaplan Meier curve will still be biased.

There is an SPSS version of this exercise on my website, so you can compare and contrast.

Martin Bland February 2008