

Lecture: Survival

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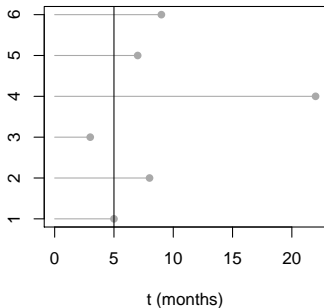
What is survival data?

Is it the same as binomial data?

Censoring

Survivor function, $S(t)$

The survivor function gives the probability of surviving beyond t .

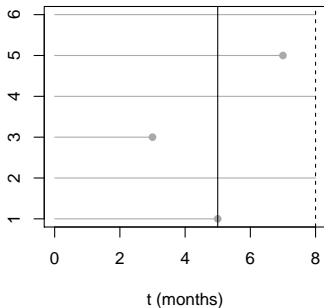


Example: No Censoring

How to estimate the probability of surviving beyond 5 months, $S(t=5)$, when there is no censoring, i.e. we know the time of the event for all subjects?

Survivor function, $S(t)$

The survivor function gives the probability of surviving beyond t .

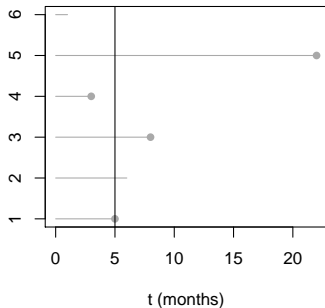


Example: A single right censoring time

How to estimate the probability of surviving beyond 5 months, $S(t=5)$, when there is only a single censoring time at 8 months?

Survivor function, $S(t)$

The survivor function gives the probability of surviving beyond t .



Warning: Censoring during follow-up

The main issue of survival analysis is how to deal with censoring! Has subject 6 died before or after 5 months?

Kaplan-Meier: An estimator of $S(t)$

If a subject is censored before time t , then estimating $S(t)$ simply as the observed proportion with event times greater than t can be biased - the censored subject may have died before time t without our knowledge.

The solution is to look at each event time $t_1 < t_2 < \dots < t_k$. Let d_j and n_j be the number who die and are *at risk* of dying, respectively, at time t_j .

The Kaplan-Meier (KM) estimator

$$\hat{S}(t) = \prod_{j: t_j \leq t} \left(1 - \frac{d_j}{n_j}\right)$$

At risk

At risk means they have not (yet) died nor have been censored. If one already died she is no longer at risk. And if one has been censored she is not considered at risk anymore since even if she will die, we can't observe it.

HIV data

- ▶ Question: A Health Maintenance Organization (HMO) wants to evaluate the survival time of HIV+ members using a follow-up study.
- ▶ Enter: Members diagnosed with HIV from Jan 1, 1989 to Dec 31, 1991 were enrolled into the study.
- ▶ Exit: Follow-up until death due to AIDS or AIDS-related complications, until end of study (Dec 31, 1995), or lost to follow-up.
- ▶ Baseline measures: Age and drug use.

HIV data

OK, let's look at the structure of the data:

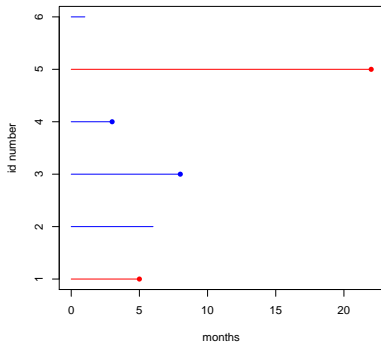
```
hiv <- read.table(  
  "http://www.ats.ucla.edu/stat/R/examples/asa/hmohiv.csv",  
  sep=";", header = TRUE)
```

```
head(hiv)
```

	ID	time	age	drug	censor	entdate	enddate
1	1	5	46	0	1	5/15/1990	10/14/1990
2	2	6	35	1	0	9/19/1989	3/20/1990
3	3	8	30	1	1	4/21/1991	12/20/1991
4	4	3	30	1	1	1/3/1991	4/4/1991
5	5	22	36	0	1	9/18/1989	7/19/1991
6	6	1	32	1	0	3/18/1991	4/17/1991

Variables

- ▶ time: follow-up time (months)
- ▶ censor: 1 = dead, 0 = censored

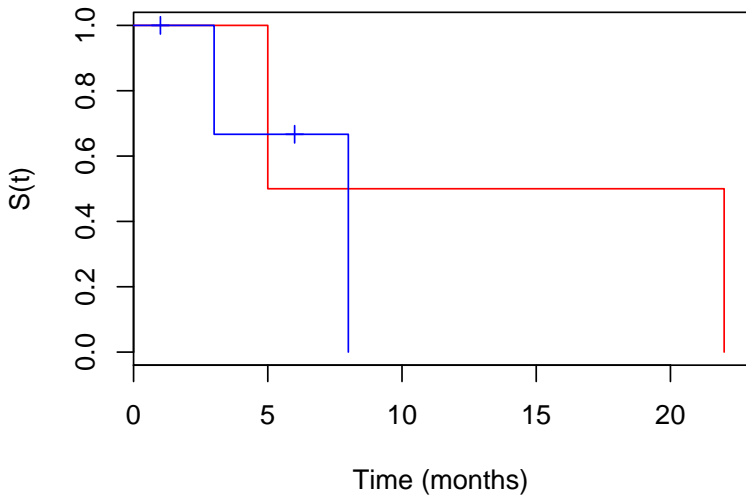


ID	time	drug	censor
6	1	1	0
5	22	0	1
4	3	1	1
3	8	1	1
2	6	1	0
1	5	0	1

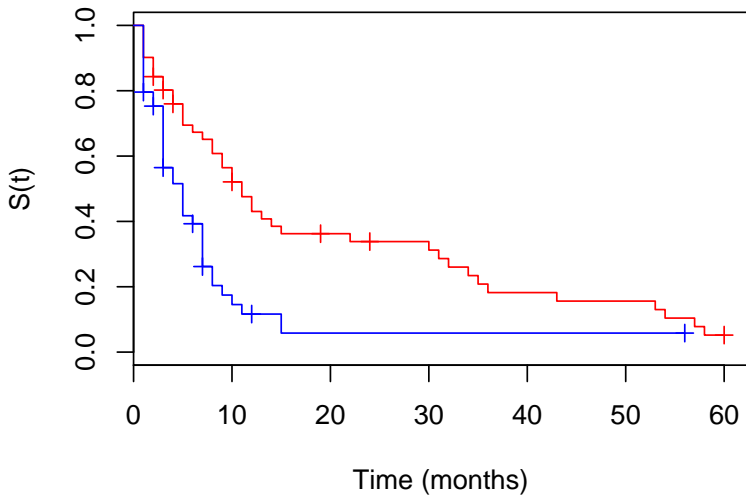
Variables

- ▶ time: follow-up time (months)
- ▶ censor: 1 = dead, 0 = censored

Kaplan-Meier for drug=0 (red) and drug=1 (blue)



Kaplan-Meier for drug=0 (red) and drug=1 (blue)



Test for difference in survivor functions

Proceed as we always do:

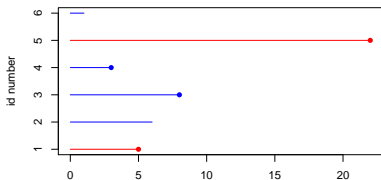
1. **The null.** Assume there is no difference; we call this the null hypothesis (or simply the null).
2. **Find statistic.** Find a statistic (i.e. a function of the data) for which we know the distribution under the null (usually a chisq-distribution).
3. **Test.** See if the value for your statistic is unusually large for what could be expected under the null.

The logrank statistic

The test statistic is the sum of $(O - E)^2/E$ for each group, where O and E are the totals of the observed and expected events.

For each event time we calculate the expected death in each group as the proportion of the subjects at risk times the number of deaths. Then we sum up these expected deaths to get E for each group.

Test for difference in survivor functions - Example 1



Example: 6 subjects

► Drug 0:

$$E = \frac{2}{5}1 + \frac{2}{4}1 + \frac{1}{2}1 + \frac{1}{1}1 = 2.4$$

► Drug 1:

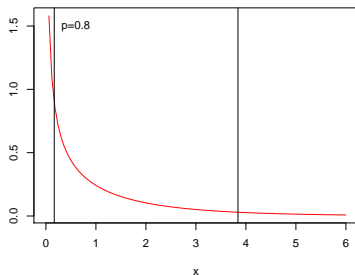
$$E = \frac{3}{5}1 + \frac{2}{4}1 + \frac{1}{2}1 + \frac{0}{1}1 = 1.6$$

The logrank test statistic:

$$\frac{(2 - 2.4)^2}{2.4} + \frac{(2 - 1.6)^2}{1.6} = 0.17$$

Is 0.17 an extrem value under the null?

Chi-Square Density Graph



Test for difference in survivor functions - Example 2

```
hiv$agecat <- cut(hiv$age, c(min(hiv$age), 29, 34, 39,  
                             max(hiv$age)), include.lowest=T)  
survdif(Surv(time=time, event=censor) ~ agecat, data=hiv)
```

Call:

```
survdif(formula = Surv(time = time, event = censor) ~ agecat,  
        data = hiv)
```

	N	Observed	Expected	(O-E) ² /E	(O-E) ² /V
agecat=[20,29]	12	8	19.9	7.10608	12.4419
agecat=(29,34]	34	29	29.4	0.00641	0.0117
agecat=(34,39]	25	20	17.8	0.26894	0.3834
agecat=(39,54]	29	23	12.9	7.98170	11.1799

Chisq= 19.9 on 3 degrees of freedom, p= 0.000178

The hazard function

$$h(t) = \lim_{\Delta t \rightarrow 0} \frac{P(t \leq T < t + \Delta t | T \geq t)}{\Delta t}$$

Relationship between survivor function and hazard function

$$S(t) = \exp \left\{ - \int_0^t h(u) du \right\}$$

Model the hazard function - Cox regression

$$\log h(t) = \log h_0(t) + \beta x$$

$$\Leftrightarrow$$

$$h(t) = h_0(t)e^{\beta x}$$

Hazard ratio (or risk ratio) from Cox regression

$$X_1 = \begin{cases} 1 & (\text{Male}) \\ 0 & (\text{Female}) \end{cases}$$

$$X_2 = \begin{cases} 1 & (\text{Blue eyes}) \\ 0 & (\text{Not blue eyes}) \end{cases}$$

$$h(t|X_1 = 0, X_2 = 0) = h_0(t)$$

$$h(t|X_1 = 1, X_2 = 0) = h_0(t)\exp(\beta_1)$$

$$h(t|X_1 = 0, X_2 = 1) = h_0(t)\exp(\beta_2)$$

$$h(t|X_1 = 1, X_2 = 1) = h_0(t)\exp(\beta_1 + \beta_2)$$

Now we can obtain the Hazard ratio (risk ratio) for any combination of groups, e.g.:

$$\text{HR(Male vs Female)} = \frac{h_0(t)\exp(\beta_1)}{h_0(t)} = \exp(\beta_1)$$

Cox regression in R

```
table(hiv$agecat)
```

```
[20,29] (29,34] (34,39] (39,54]  
      12      34      25      29
```

```
coxph(Surv(time=time, event=censor) ~ agecat, data=hiv)
```

Call:

```
coxph(formula = Surv(time = time, event = censor) ~ agecat, data = hiv)
```

	coef	exp(coef)	se(coef)	z	p
agecat(29,34]	1.20	3.33	0.450	2.67	7.5e-03
agecat(34,39]	1.33	3.80	0.458	2.91	3.6e-03
agecat(39,54]	1.91	6.78	0.468	4.09	4.3e-05

```
Likelihood ratio test=20.9 on 3 df, p=0.000109 n= 100, number of events= 80
```

Cox regression in R

```
hiv$drug <- as.factor(hiv$drug)
coxph(Surv(time=time, event=censor) ~ drug + age, data=hiv)
```

Call:

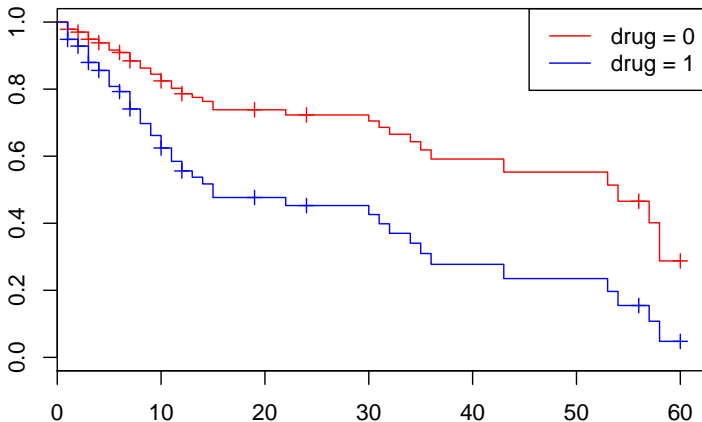
```
coxph(formula = Surv(time = time, event = censor) ~ drug + age,
      data = hiv)
```

	coef	exp(coef)	se(coef)	z	p
drug1	1.0167	2.76	0.2562	3.97	7.2e-05
age	0.0971	1.10	0.0186	5.21	1.9e-07

Likelihood ratio test=39.1 on 2 df, p=3.18e-09 n= 100, number of events= 80

Cox regression in R

```
cox <- coxph(Surv(time=time, event=censor) ~ agecat + drug, data=hiv)
predict <- data.frame(drug=c(0,1), agecat=rep(levels(hiv$agecat)[1], 2))
plot(survfit(cox, newdata=predict), col=c("red","blue"))
legend("topright", legend=c('drug = 0', 'drug = 1'), lty=c(1,1), col=c("red","blue"))
```



Comparison of nested models

Make a likelihood ratio (LR) test to see if there is an significant overall effect of agecat:

```
model1 <- coxph(Surv(time=time, event=censor) ~ drug, data=hiv)
model2 <- coxph(Surv(time=time, event=censor) ~ agecat + drug, data=hiv)
anova(model2, model1)
```

Analysis of Deviance Table

Cox model: response is Surv(time = time, event = censor)

Model 1: ~ agecat + drug

Model 2: ~ drug

loglik Chisq Df P(>|Chi|)

1 -279

2 -290 21.8 3 7.4e-05 ***

Signif. codes:

0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The proportional hazards assumption