

# Life\_Table

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## Problem 1

Interval Time Period Events Censor At risk at the beginning of the interval Average number at risk in the  
interval 1 [0,4) 2 1 20 19.5 2 [4,8) 1 1 17 16.5 3 [8,12) 0 3 15 13.5 4 [12,16) 1 2 12 11

## Problem 2

Survival function at the end of the  $i^{\text{th}}$  interval

$$\hat{S}_L(t_i) = \hat{S}_L(t_{i-1}) \left(1 - \frac{d_i}{n_i'}\right)$$

For the  $i^{\text{th}}$  interval:

$$\begin{cases} \hat{f}(t_{mi}) = \frac{\hat{S}_L(t_{i-1}) - \hat{S}_L(t_i)}{t_i - t_{i-1}} \\ \hat{S}_L(t_{mi}) = \frac{\hat{S}_L(t_{i-1}) + \hat{S}_L(t_i)}{2} \end{cases}$$

$$\begin{aligned} \therefore \hat{h}(t_{mi}) &= \frac{2\hat{f}(t_{mi})}{[\hat{S}(t_i) + \hat{S}(t_{i-1})]} = \frac{2\hat{S}_L(t_{i-1}) \left(1 - 1 + \frac{d_i}{n_i'}\right)}{\hat{S}_L(t_{i-1}) \left(1 - \frac{d_i}{n_i'} + 1\right)} \cdot \frac{1}{t_i - t_{i-1}} \\ &= \frac{1}{t_i - t_{i-1}} \cdot \frac{2 \cdot \frac{d_i}{n_i'}}{2 - \frac{d_i}{n_i'}} \\ &= \frac{d_i}{(t_i - t_{i-1})(n_i' - \frac{d_i}{2})} \quad \textcircled{1} \end{aligned}$$

So, based on the definition, it can be proved that equation ① holds.  $\square$

## Problem 3

### Load packages

```
library(survival)
library(tidyverse)
library(ggfortify)
library(dplyr)
library(ggplot2)
library(biostat3)
library(knitr)
```

### Ovarian Cancer:

- futime: survival or censoring time(day)
- fustat: censoring status(censor = 0)
- age: in years
- resid.ds: residual disease present(1=no, 2=yes)
- rx: treatment group
- ecog.ps: ECOG performance status(1 is better)

```
data("ovarian")
attach(ovarian)
```

### Life-table summary stratified by rx

```
res <- summary( survfit( Surv(futime, fustat)~rx, data=ovarian))
cols <- lapply(c(2:6, 8:11) , function(x) res[x])
tbl <- do.call(data.frame, cols)
tbl
```

	time	n.risk	n.event	n.censor	surv	cumhaz	std.chaz	strata	type
1	59	13	1	0	0.9230769	0.07692308	0.07692308	rx=1	right
2	115	12	1	0	0.8461538	0.16025641	0.11340901	rx=1	right
3	156	11	1	0	0.7692308	0.25116550	0.14534809	rx=1	right
4	268	10	1	0	0.6923077	0.35116550	0.17642581	rx=1	right
5	329	9	1	0	0.6153846	0.46227661	0.20849879	rx=1	right
6	431	8	1	0	0.5384615	0.58727661	0.24309822	rx=1	right
7	638	5	1	2	0.4307692	0.78727661	0.31479636	rx=1	right
8	353	13	1	0	0.9230769	0.07692308	0.07692308	rx=2	right
9	365	12	1	0	0.8461538	0.16025641	0.11340901	rx=2	right
10	464	9	1	2	0.7521368	0.27136752	0.15876802	rx=2	right
11	475	8	1	0	0.6581197	0.39636752	0.20207000	rx=2	right
12	563	7	1	0	0.5641026	0.53922466	0.24746807	rx=2	right

### Create life-table stratified by rx

```

ovarian_rx1 <- ovarian |>
  filter(rx == 1) |>
  arrange(futime)

ovarian_rx2<- ovarian |>
  filter(rx == 2)|>
  arrange(futime)

lifet1<-lifetab2(Surv(futime, fustat == 1)~1,ovarian_rx1)
lifet2<-lifetab2(Surv(futime, fustat == 1)~1,ovarian_rx2)
print(lifet1, digits = 2)

```

	tstart	tstop	nsubs	nlost	nrisk	nevent	surv	pdf	hazard	se.surv
0-59	0	59	13	0	13.0	0	1.00	0.00000	0.00000	0.000
59-115	59	115	13	0	13.0	1	1.00	0.00137	0.00143	0.000
115-156	115	156	12	0	12.0	1	0.92	0.00188	0.00212	0.074
156-268	156	268	11	0	11.0	1	0.85	0.00069	0.00085	0.100
268-329	268	329	10	0	10.0	1	0.77	0.00126	0.00173	0.117
329-431	329	431	9	0	9.0	1	0.69	0.00075	0.00115	0.128
431-448	431	448	8	0	8.0	1	0.62	0.00452	0.00784	0.135
448-477	448	477	7	1	6.5	0	0.54	0.00000	0.00000	0.138
477-638	477	638	6	1	5.5	0	0.54	0.00000	0.00000	0.138
638-803	638	803	5	0	5.0	1	0.54	0.00065	0.00135	0.138
803-855	803	855	4	1	3.5	0	0.43	0.00000	0.00000	0.147
855-1040	855	1040	3	1	2.5	0	0.43	0.00000	0.00000	0.147
1040-1106	1040	1106	2	1	1.5	0	0.43	0.00000	0.00000	0.147
1106-Inf	1106	Inf	1	1	0.5	0	0.43	NA	NA	0.147

	se.pdf	se.hazard
0-59	NaN	NaN
59-115	0.00132	0.00143
115-156	0.00180	0.00212
156-268	0.00066	0.00085
268-329	0.00121	0.00172
329-431	0.00072	0.00115
431-448	0.00435	0.00783
448-477	NaN	NaN
477-638	NaN	NaN
638-803	0.00061	0.00134
803-855	NaN	NaN
855-1040	NaN	NaN
1040-1106	NaN	NaN
1106-Inf	NA	NA

```
print(lifet2, digits = 2)
```

	tstart	tstop	nsubs	nlost	nrisk	nevent	surv	pdf	hazard	se.surv
0-353	0	353	13	0	13.0	0	1.00	0.00000	0.00000	0.000
353-365	353	365	13	0	13.0	1	1.00	0.00641	0.00667	0.000
365-377	365	377	12	0	12.0	1	0.92	0.00641	0.00725	0.074
377-421	377	421	11	1	10.5	0	0.85	0.00000	0.00000	0.100
421-464	421	464	10	1	9.5	0	0.85	0.00000	0.00000	0.100
464-475	464	475	9	0	9.0	1	0.85	0.00855	0.01070	0.100

475-563	475	563	8	0	8.0	1	0.75	0.00107	0.00152	0.126
563-744	563	744	7	0	7.0	1	0.66	0.00052	0.00085	0.141
744-769	744	769	6	1	5.5	0	0.56	0.00000	0.00000	0.149
769-770	769	770	5	1	4.5	0	0.56	0.00000	0.00000	0.149
770-1129	770	1129	4	1	3.5	0	0.56	0.00000	0.00000	0.149
1129-1206	1129	1206	3	1	2.5	0	0.56	0.00000	0.00000	0.149
1206-1227	1206	1227	2	1	1.5	0	0.56	0.00000	0.00000	0.149
1227-Inf	1227	Inf	1	1	0.5	0	0.56	NA	NA	0.149
	se.pdf	se.hazard								
0-353	NaN	NaN								
353-365	0.00616	0.00666								
365-377	0.00616	0.00724								
377-421	NaN	NaN								
421-464	NaN	NaN								
464-475	0.00812	0.01068								
475-563	0.00102	0.00151								
563-744	0.00049	0.00085								
744-769	NaN	NaN								
769-770	NaN	NaN								
770-1129	NaN	NaN								
1129-1206	NaN	NaN								
1206-1227	NaN	NaN								
1227-Inf	NA	NA								

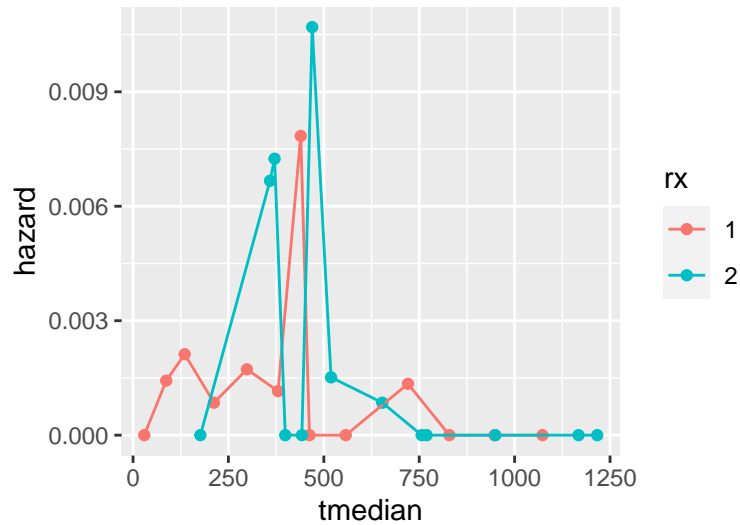
Plot hazard function by rx based on life-table estimate

```
hazard1<-lifet1 |>
  dplyr::select(tstart, tstop, hazard) |>
  mutate(tmedian = (tstart+tstop)/2, rx ="1")

hazard2<-lifet2 |>
  dplyr::select(tstart, tstop, hazard) |>
  mutate(tmedian = (tstart+tstop)/2, rx ="2")

hazard <- rbind(hazard1,hazard2)

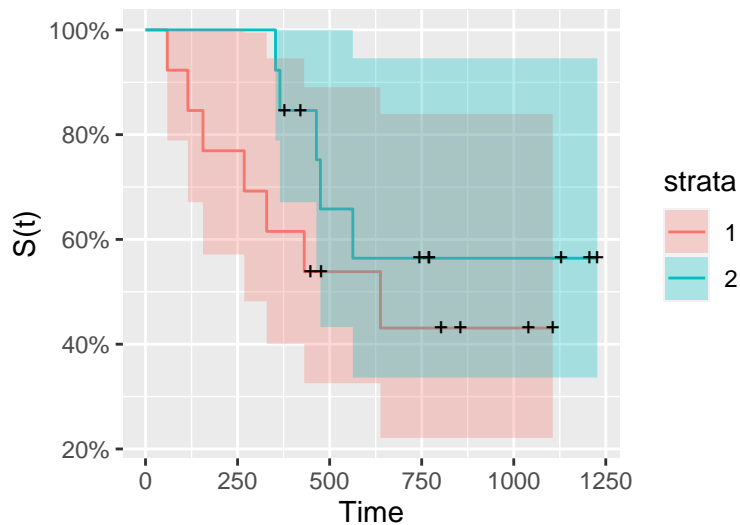
ggplot(hazard, aes(x = tmedian, y = hazard, color = rx)) +
  geom_point()+
  geom_line()
```



### Plot K-M survival function by rx

```
ovarian.survfit <-
  survfit(Surv(futime, fustat)~rx,data= ovarian)

ovarian.survfit |>
  autoplot() +
  ylab("S(t)") +
  xlab("Time")
```



### Median survival time for each treatment group

For the group 1(rx = 1), the median survival time is  $534.5(\frac{431+638}{2})$  days. For the group 2(rx = 2), the median survival time is not sure, because over half of patients are still censored.

## Compare survival function estimations between K-M and F-H methods

### Nelson-Aalen(Fleming-Harrington) and K-M estimators

- Survival function:

$$\hat{S}_F(t) = \begin{cases} 1 & t < t_1 \\ \prod_{t_i \leq t} \exp[-\frac{d_i}{n_i}] & t \geq t_1 \end{cases}$$

$$\hat{S}_K(t) = \begin{cases} 1 & t < t_1 \\ \prod_{t_i \leq t} [1 - \frac{d_i}{n_i}] & t \geq t_1 \end{cases}$$

$$\because \exp[-\frac{d_i}{n_i}] \geq 1 - \frac{d_i}{n_i}$$

So, Fleming-Harrington estimator can always be larger than K-M estimator.

### Describe the analyses and write conclusions

From the survival functions, patients in treatment group 2(rx=2) generally perform better than those in group 1(rx=1). Besides, the median survival time has suggested the same results, but nothing could be referred from the hazard plots. Last but not least, after comparing ECOG performance status in different groups, censored ones in group 2 generally perform better than in group 1.

## References

Edmonson JH, Fleming TR, Decker DG, Malkasian GD, Jorgensen EO, Jefferies JA, Webb MJ, Kvols LK. Different chemotherapeutic sensitivities and host factors affecting prognosis in advanced ovarian carcinoma versus minimal residual disease. Cancer Treat Rep. 1979 Feb;63(2):241-7. PMID: 445503.